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|------|------------|------|---|-----|-----|--|--|--|----------------------|------------------|---|----------|---|
| 4581 | cg43993462 | 624 | AGTCTCACTTCT TACCAAAAAAAAA A[gap]A[CAATGA ACTGGATTTCAGC CCACTCA | gap | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment). | 5.1E-161 | 5 |
| 4582 | cg43928058 | 463 | CCCACTGTGTGG CCCAGCTCTGG GG[G/gap]CCCTG CCTTGCCCTGCC CCTCCCTG | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q76061 STANNOCALCIN-2 - HOMO SAPIENS (HUMAN), 302 aa. | 1.7E-160 | |
| 4583 | cg43920504 | 134 | ATGTATAATAAG AAATTCACCCCTT C[A/G]GCTCTAT TCACTCTTTATC CTGAG | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13291 SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE - HOMO SAPIENS (HUMAN), 335 aa. | 2.2E-160 | 1 |
| 4584 | cg43920504 | 626 | TGTTCAATTTGG TTTTTCCATTTTC [A/C]GCGCAGAAA GGCCCTTTGTTG GTCTC | A | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13291 SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE - HOMO SAPIENS (HUMAN), 335 aa. | 2.2E-160 | 1 |
| 4585 | cg43920504 | 636 | GGTTTTCCATTT TCACGCAGAAAG [G/T]CCCTTTGTT GGTCTCTGGTGT CAGC | G | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13291 SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE - HOMO SAPIENS (HUMAN), 335 aa. | 2.2E-160 | 1 |
| 4586 | cg43134484 | 1242 | CGAAGTGGCTCT CAGGGGCCAGT GA[G/gap]GGCTG GGCCACACAGAG ATGCATGCG | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92788 RAD GTPASE - HOMO SAPIENS (HUMAN), 308 aa. | 5.8E-160 | |
| 4587 | cg43134484 | 1398 | GGGAGGCTCTTC AGTCCGGTAGCT A[T/C]TTGTTTAC ATGCAGATTTT GTAAT | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92788 RAD GTPASE - HOMO SAPIENS (HUMAN), 308 aa. | 5.8E-160 | |

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|------|------------|-----|---|---|-----|--|--|--------------------------|------------------|---|----------|---|
| 4588 | cg43929687 | 173 | TTGTACTAGGGG GTGGGCTGTTGC C[C/gap]TGGCAC GGCTGGATGAAC ACTTGCA | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB51351 DJ475B7.2 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 717 aa. | 8.5E-160 | |
| 4589 | cg43933630 | 574 | GGTGCGAACGG TTCCGGGCGCTCA GG[C/gap]ACAGT GTGGGGGCGGC CTGCCCTCCT | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC:A-1,3-D -MANNOSIDE B- 1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4 N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa. | 1.4E-159 | 5 |
| 4590 | cg43933630 | 677 | GGCGGACCCCA GGCCGGCCCCAA GCC[C/gap]GACG CCAGGCAGAAC CCTTTGGGCG | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC:A-1,3-D -MANNOSIDE B- 1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4 N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa. | 1.4E-159 | 5 |

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|------|------------|-----|---|---|-----|--|--|----------------------|--------------|--|----------|----|
| 4591 | cg43933630 | 707 | CCAGGCAGAAC CCTTTGGGCGG GGC[C/gap]GTAT CTGGCCCTCCG GGGACGGCAG | C | gap | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC:A-1,3-D -MANNOSIDE B-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa. | 1.4E-159 | 5 |
| 4592 | cg43933630 | 716 | ACCCTTTGGGCG GGGCCGTATCTG G[C/gap]CCTCCG GGGACGGCAGT GACGACAC | C | gap | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC:A-1,3-D -MANNOSIDE B-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa. | 1.4E-159 | 5 |
| 4593 | cg43987224 | 406 | CAACCATTC AAG GGTCAGGGCTCT G[C/gap]CTTCCC ACCAAAGGAGG GCCCCGAAC | C | gap | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene SPTREMBL-ACC:Q15785 HTOM34P - HOMO SAPIENS (HUMAN), 309 aa. | 1.6E-159 | 20 |

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|------|------------|------|---|---|-----|--|--|--|----------------------|------------------|--|----------|----|
| 4594 | cg43987224 | 407 | AACATTCAAGG GTCAGGGGCTCTG C[C/gap]TTCCCA CCAAAGGAGGG CCCGAACA | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15785 HTOM34P - HOMO SAPIENS (HUMAN), 309 aa. | 1.6E-159 | 20 |
| 4595 | cg43987224 | 665 | CTACAAGGGCAG CACTCAGTCTGC A[G/gap]CCCACT TGGGCAGGACA AAGCCAAA | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15785 HTOM34P - HOMO SAPIENS (HUMAN), 309 aa. | 1.6E-159 | 20 |
| 4596 | cg42718246 | 1431 | GCTGCATGTTTT CAACTACAATAA G[T/C]GCACTGTA ATAAAAAGTTTT GTTTA | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13287 HOU - HOMO SAPIENS (HUMAN), 307 aa. | 1.1E-158 | 2 |
| 4597 | cg42831359 | 175 | AGTGGGTTTTGG AACGGGAGGCA GA[G/gap]CATCT GGGACAGACC CTCCTGGAA | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75911 RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE RETSR1 - HOMO SAPIENS (HUMAN), 302 aa. | 2.9E-168 | 1 |
| 4598 | cg42831359 | 333 | CCTGCCTCCCTG TGGGGGTCAGTT A[T/C]ACCCATCA GTCCTGTGCAAA GGTCC | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75911 RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE RETSR1 - HOMO SAPIENS (HUMAN), 302 aa. | 2.9E-168 | 1 |
| 4599 | cg43923892 | 2095 | AAATTACTCCTA AAAAGTTAATA T[C/T]CTGTAAA AAGCAATGCTTT TCAA | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45558 CYCLIN ANIA-6A - RATTUS NORVEGICUS (RAT), 527 aa. | 2.9E-158 | 3 |
| 4600 | cg42910688 | 1140 | TCACCCAGATGT CCCTTTGATGGC C[G/C]TTGTTGAA GGCCATTGGGA CCAATA | G | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa. | 7.7E-158 | 8 |

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| 4601 | cg42910688 | 1389 | GTGTTTCTTCTATG TTTGATAGTAG G/A/GAAGTAAAG CTTACAAAGAAT GCCT | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa. | 7.7E-158 | 8 |
| 4602 | cg42910688 | 1926 | ATGTATAATCAG AAGTCTGAATTT TT/CJATAAAACA TATAGCATAAAA ACTTC | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa. | 7.7E-158 | 8 |
| 4603 | cg42910688 | 1949 | TTTATAAACATA TAGCATAAAAC T/CJTCCAGTACT TTGGTTGACCCCT TGTA | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa. | 7.7E-158 | 8 |
| 4604 | cg43272443 | 1395 | AAGCTTTTTTTTT TTTTTTTTTTTTT gap/GAGACGGAG TCTTGCTCTGTT GCCC | T | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa. | 7.7E-158 | 1 (1p22) |
| 4605 | cg43272443 | 1461 | TGCAGTAGCACG ATCTCGGCTCAC TT/gap/GCACCC TCCGTCCTCAG GTTCAAG | T | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa. | 7.7E-158 | 1 (1p22) |
| 4606 | cg43272443 | 1478 | GGCTCACTTGCA CCCTCCGCTCTCT C/A/GGGTTCAA GCAATTCCTCTG CCTCAG | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa. | 7.7E-158 | 1 (1p22) |

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|------|------------|------|--|---|---|--|--|--|--------------------------|------------------|--|----------|----------|
| 4607 | cg43272443 | 1622 | GCTGGTCTTGAA TTCCTGACCTCA G/GTTGATCCAC CCACCTTGGCCT CCCAA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa. | 7.7E-158 | 1 (1p22) |
| 4608 | cg43921539 | 1602 | CCTGCTCAAGCG GTCCGGGGAAT GG/GTTTGT TTTCCCTTCATTG TTGAG | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14661 SYNTAXIN-16A - HOMO SAPIENS (HUMAN), 303 aa. | 2E-157 | 20 |
| 4609 | cg43921539 | 3347 | TGTTCAAGCTTT TTAAAGTGCTGA G/T/CCTTACAAA CCCCTGAAGGAA GGTGA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14661 SYNTAXIN-16A - HOMO SAPIENS (HUMAN), 303 aa. | 2E-157 | 20 |
| 4610 | cg43921539 | 3476 | CCCAATTTGGTA AAATAACGGATC T/A/GIATTAGAAA CTGTTTAAAGGA GGGC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14661 SYNTAXIN-16A - HOMO SAPIENS (HUMAN), 303 aa. | 2E-157 | 20 |
| 4611 | cg43984495 | 796 | TGTTAACTTCAA TGTAATGTGTAG A/TCTAATACTTT TAGTGGGTACA AGT | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P20774 OSTEOINDUCTIVE FACTOR PRECURSOR (OIF) (OSTEOGLYCIN) - Homo sapiens (Human), 298 aa. | 4.2E-157 | 9 |
| 4612 | cg43048935 | 315 | TACAAAACATGT AGAAGATGCCCTC TT/CJGAGATGGC TTTAAATGCC AGTAT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:P78397 MYD88 - HOMO SAPIENS (HUMAN), 296 aa. | 8.8E-157 | 3 |
| 4613 | cg43048935 | 664 | GCTCTCTTCCTC TCTCTGTGCTTC AT/CJTAGAGGTA TAAATACTGGTA CATTG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:P78397 MYD88 - HOMO SAPIENS (HUMAN), 296 aa. | 8.8E-157 | 3 |

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|------|------------|------|--|-----|-----|--|--|--|----------------------|------------------|---|----------|----|
| 4614 | cg43953563 | 400 | GCAGACTTGTGC TGGTCAGTGAAC A/C/A/C/T/T/T/T/T/T T/T/T/T/CACCACT CTGT | C | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa. | 1.1E-156 | 1 |
| 4615 | cg43953563 | 414 | TCAGTGAACACC T/T/T/T/T/T/T/T/T/T/T gap/T/CACCACTG TGTGACATGGTG AATTA | gap | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa. | 1.1E-156 | 1 |
| 4616 | cg43953563 | 414 | TCAGTGAACACC T/T/T/T/T/T/T/T/T/T/T gap/T/CACCACTG TGTGACATGGTG AATTA | gap | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa. | 1.1E-156 | 1 |
| 4617 | cg43953563 | 597 | ACAGTGTGAAC CCATACCTGTCA T/G/C/GGCAATA GGAATGCATATT GATAAG | G | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa. | 1.1E-156 | 1 |
| 4618 | cg43953563 | 75 | CATGAAGCCACC CATACAATCACA A/T/A/T/T/TATCTA ACACATTTAATTT TGA | T | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa. | 1.1E-156 | 1 |
| 4619 | cg43254730 | 1016 | TGAGATGAGGA ATTTTGAAGAT A/T/A/JATGAAGGC CTAAAAGATCAC TATCT | T | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa. | 1.8E-156 | 22 |
| 4620 | cg43254730 | 279 | TGAGGTATGGG GGTCACTGAGGA GA[C/gap]CCCCA GAGTCACTGACC CCTCCCCG | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa. | 1.8E-156 | 22 |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|---|----------|---------------|
| 4621 | cg43254730 | 283 | GTATGGGGGTCA CTGAGGAGACC CC[C/gap]AGAGT CACTGACCCCTC CCGCCACC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa. | 1.8E-156 | 22 |
| 4622 | cg43329580 | 241 | CTTGTCCTCCAGC CTGTGGGCAGT GC[C/gap]ACACG GCAGGCTAGGG GAGGGGTGA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAA08742 SQV-8-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 327 aa (fragment). | 3.4E-156 | 11 (11q13) |
| 4623 | cg43130238 | 188 | AAAATTACAAAC AGCACTGATATT C[A/G]GCCAGTAT ACAAGTCTGGTC ACAGC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD21222 UBIQUITIN SPECIFIC PROTEASE UBP43 - MUS MUSCULUS (MOUSE), 368 aa. | 7.1E-155 | |
| 4624 | cg43950590 | 885 | TTCTGGAGGGTG GGGAGAAGTGG CT[A/C]AGTGTTA TAAGGTATACTG GACAAAC | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.9E-154 | 7 |
| 4625 | cg43981925 | 2094 | ACAAAGGAACCGC TCGCCGCCGCC GC[C/gap]TCCGG TCACTGGCACGG ACTTCTGA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa. | 6.4E-154 | 8 |
| 4626 | cg43981925 | 710 | CACACACACAGAG ATTTAAAAA [A/gap]TCAAAGG CAATCATTCTAA ATGTAC | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa. | 6.4E-154 | 8 |
| 4627 | cg43981925 | 710 | ACACACACAGAG TTTAAAAA [gap/A]TCAAAGG CAATCATTCTAA ATGTAC | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa. | 6.4E-154 | 8 |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|--|----------|---|
| 4628 | cg43981925 | 737 | CAAAGGCAATCA TTCTAAATGTACT [A/T]TGATAGCAT GTAAAGATGCA AGTA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa. | 6.4E-154 | 8 |
| 4629 | cg43934638 | 966 | GAGAAAGGAGAA GCTTACAAAAA AA[A/gap]AAAAATC CTCTTCTATATTG CAGTGT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa. | 1E-153 | 5 |
| 4630 | cg43934638 | 967 | AGAAGGAGAAG CTTACAAAAA AA[A/gap]AAATC CTCTTCTATATTG CAGTGT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa. | 1E-153 | 5 |
| 4631 | cg43934638 | 968 | GAAGGAGAAGCT TACAAAAA A[A/gap]AAATCCT CTTCTATATTGC AGTGCT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa. | 1E-153 | 5 |
| 4632 | cg43934638 | 970 | GGAGAAGCTTAC AAAAA A[gap]/ATCCTCTT CTATATTGCAGT GTCTCT | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa. | 1E-153 | 5 |
| 4633 | cg43934638 | 1122 | GGCTGAGTTTGT ATTATTACTGATA [T/G]GAAGAATAG AGTACCAATGTC ATTA | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa. | 1E-153 | 5 |
| 4634 | cg43934638 | 1222 | TTCTCAGATTG TAATTCCTCTTT [gap/C]GGGAGCT GAGCTAGTGCTT TTAGGA | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa. | 1E-153 | 5 |

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|------|------------|------|--|----------|-----|--|--|--|--------------------------|------------------|--|----------|----|
| 4635 | cg43934638 | 957 | GTAGAACTGAGA AGGAGAAGCTTA C[gap/A]AAAAAA AAAAAAATCCTC TTCTATA | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa. | 1E-153 | 5 |
| 4636 | cg43934638 | 958 | GTAGAACTGAGA AGGAGAAGCTTA C[A/gap]AAAAAA AAAAAAATCCTCT TCTATAT | A gap | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa. | 1E-153 | 5 |
| 4637 | cg44001553 | 996 | CCCAAGACCTTT AGCCCCCAAAGA G[G/gap]CACGGC CTCACCCCAACT GCCTGAG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92559 MYELOBLAST KIAA0270 - HOMO SAPIENS (HUMAN), 345 aa (fragment). | 3.5E-153 | 19 |
| 4638 | cg44001553 | 167 | ACTCAGGCAGAC TCCAGGGAGGA GG[A/gap]GGGG GTTCCACGGCTG ACGCCCAGG | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92559 MYELOBLAST KIAA0270 - HOMO SAPIENS (HUMAN), 345 aa (fragment). | 3.5E-153 | 19 |
| 4639 | cg44001553 | 264 | GAGGCAGGGAC CCAGGCTCCCAT CC[G/A]AGGTGG CCCCTGTACCTG CCCTGCC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92559 MYELOBLAST KIAA0270 - HOMO SAPIENS (HUMAN), 345 aa (fragment). | 3.5E-153 | 19 |
| 4640 | cg43247677 | 2273 | TGATCCAATAAA GTTGTAAACAG G[C/A]AAAAAAA AAAAAAA CAAGA | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14617 DELTA-ADAPTIN - HOMO SAPIENS (HUMAN), 1153 aa. | 1.7E-152 | 19 |
| 4641 | cg43928724 | 1932 | CCTGGGCCAGG GTCTGTGTGAAT GT[G/gap]GGCAC TGGCCAGGTTTC ATACCTTA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60539 PUTATIVE TUMOR SUPPRESSOR PROTEIN - HOMO SAPIENS (HUMAN), 289 aa (fragment). | 4.1E-152 | 3 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|---|----------|----|
| 4642 | cg43951092 | 104 | TTTTTTTTTTTT TTATCTCCACA[T/ATGACATTTAT TAATAACATTTCT GG | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.5E-152 | 14 |
| 4643 | cg43951092 | 291 | TCTTTAAACTAAAG ACTCCAAGCAGG [G/T]ATCAGATAC AAAACCCCAACTG CAGG | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.5E-152 | 14 |
| 4644 | cg43930854 | 210 | GCTCTATCCACC CCTACAGCTTCC C[C/T]GGCCAAC CAGGTTCAAAGC CCATCA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa. | 2.1E-151 | 12 |
| 4645 | cg43930854 | 325 | CCACAGAGAGA GGATGGGAAACT AG[G/A]GTAGAA GCTACAAGGGCT AAGAACT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa. | 2.1E-151 | 12 |
| 4646 | cg43930854 | 52 | TTTTTTTTTTTT TTTTTTTTTTTT[G /T]TCACTGCAAA TTGTTTATTAAAA CA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa. | 2.1E-151 | 12 |
| 4647 | cg43930854 | 5410 | AGAGGGTTGGAA TGAAGACTCCGA A[G/gap]CCACCA GGATGGGAAACA TGAGGCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa. | 2.1E-151 | 12 |
| 4648 | cg43930854 | 5410 | GAGGGTTGGAAT GAAGACTCCGAA G[gap/G]CCACCA GGATGGGAAACA TGAGGCT | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa. | 2.1E-151 | 12 |

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|------|------------|-----|---|-----|-----|--|--|--------------------------|------------------|---|----------|--|
| 4649 | cg43988751 | 180 | CGGCTCCAAGAA GGCCCCCAAGG GG[G/gap]ACTTA CCTTCAGGGGG CTGAGCCAA | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa. | 7.6E-151 | |
| 4650 | cg43988751 | 180 | GGCTCCAAGAA GGCCCCAAGGG GG[gap/G]ACTTA CCTTCAGGGGG CTGAGCCAA | gap | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa. | 7.6E-151 | |
| 4651 | cg43988751 | 221 | GCTGAGCCAAG GGGAAAGGGG TGG[C/gap]CCCA GAACAGGGGAA GGGCAGGCA | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa. | 7.6E-151 | |
| 4652 | cg43988751 | 230 | AGGGGAAAGG GGTGGCCCCAG AAC/A/GGGGA AGGGCAGGCA TGGGGGGAA | A | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa. | 7.6E-151 | |
| 4653 | cg43988751 | 43 | TTTTTTTTTTTT TTTTTTTTTTTT[G /T]TGAAAAACCA AACCTCAAAAAG CCA | G | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa. | 7.6E-151 | |
| 4654 | cg43988751 | 45 | TTTTTTTTTTTT TTTTTTTTTTGT[G/T]AAAAACCAA ACCTCAAAAAGC CACT | G | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa. | 7.6E-151 | |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|--|----------|----|
| 4655 | cg43135797 | 400 | GGCATGGAGCG TGGGCCACGAG GGC[<i>gap</i>]ACCT CCCCAGGAGCC CACAGCAGCC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O14732 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE 2 (EC 3.1.3.25) (IMP 2) (INOSITOL MONOPHOSPHATASE 2) (MYO- INOSITOL MONOPHOSPHATASE A2) - Homo sapiens (Human), 288 aa. | 1.6E-150 | 18 |
| 4656 | cg43135797 | 44 | TTTTTTTTTTTT TTTTTTTTTTG[C /gap]CCATTATTT TGATTTATTGCAT TCT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O14732 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE 2 (EC 3.1.3.25) (IMP 2) (INOSITOL MONOPHOSPHATASE 2) (MYO- INOSITOL MONOPHOSPHATASE A2) - Homo sapiens (Human), 288 aa. | 1.6E-150 | 18 |
| 4657 | cg43258297 | 60 | TTTTTTTTTTTT TTTTATGGGGC[A/GCGGGGGT CTTATTCGTCA GATT | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB50866 DEOXYRIBONUCLEASE III (DNASE III) - HOMO SAPIENS (HUMAN), 304 aa. | 3.8E-150 | 3 |
| 4658 | cg43919239 | 1089 | ATGCTTTCTGT CCCTGCAGGCG GA[<i>gap</i>]/CIGCTGA ACCTCCGTTGCT GCTGGGAG | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa. | 4.2E-150 | |
| 4659 | cg43919239 | 1167 | CTCTCTAAGTAG GCAATAGATCCA G[G/gap]CCCCCTA GGCTGTCCCCAC AGCCTCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa. | 4.2E-150 | |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|--|----------|----|
| 4660 | cg43919239 | 1167 | TCTCTAAGTAGG CAATAGATCCAG G[gap/G]CCCCCTA GGCTGTCCCCAC AGCCTCT | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa. | 4.2E-150 | |
| 4661 | cg43919239 | 1174 | AGTAGGCAATAG ATCCAGGCCCT A[G/gap]GCTGTC CCACAGCCTCT GTCTTCG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa. | 4.2E-150 | |
| 4662 | cg43919239 | 1175 | GTAGGCAATAGA TCCAGGCCCTA G[G/gap]CTGTCC CCACAGCCTCTG TCTTCGG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa. | 4.2E-150 | |
| 4663 | cg43943351 | 1714 | GGGTGGGCGAG ATTCTGGACTGA GG[AT]GGGCAG GGGAGGGAGAA AGGTGCTC | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa. | 4.5E-150 | 17 |
| 4664 | cg43943351 | 1880 | ACTGGGGCTGA GCCGGGCCCTC CAG[G/gap]CTCA TGCCCGGCTGC AGGTGAACAT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa. | 4.5E-150 | 17 |

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|------|------------|------|---|---|-----|--|--|--------------------------|------------------|---|----------|---|
| 4665 | cg43946935 | 162 | ACCGCAAGGTG TTTGGCGATCCG C[C/gap]GAGAAG TTGTTGGCCCCA GGAGCAT | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O6071 CELL CYCLE CHECKPOINT PROTEIN HRAD1 - HOMO SAPIENS (HUMAN), 282 aa. | 1.8E-149 | |
| 4666 | cg39524115 | 1245 | TTCTCTGCCTC AGCCTCCCAAGT A/A/G]CTGGGATT ACAGGCACGTAC CACCA | A | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA13473 CD89_U11 - HOMO SAPIENS (HUMAN), 275 aa. | 4.8E-149 | |
| 4667 | cg39524115 | 1385 | CCCGCCTTGGC CTCCCAAGTGC TG[G/A]GATTACA GGCATGAGCCA CCACGCC | G | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA13473 CD89_U11 - HOMO SAPIENS (HUMAN), 275 aa. | 4.8E-149 | |
| 4668 | cg39524115 | 1391 | TTGGCCTCCCA AGTGCTGGGATT A/C/T]AGGCATGA GCCACACGCCT GGCCT | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA13473 CD89_U11 - HOMO SAPIENS (HUMAN), 275 aa. | 4.8E-149 | |
| 4669 | cg43930377 | 718 | CAATGTTGTTTAT ATAAGTATACCA[C/gap]ATTATAAG TCTACTGGAGAT CCAAA | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 7.8E-149 | 4 |
| 4670 | cg43917492 | 1706 | CGCCCAAGTGAC TTGCTGAATACC A/T/C]CACAAAAT CTGAACCCAAAG ATGAG | T | C | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa. | 1E-148 | 4 |
| 4671 | cg43917492 | 2086 | ACTTTCATACTG GTTATTTTTTTTT[T/gap]TAATTCTG TCAGTGAGCAGC ATTTC | T | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa. | 1E-148 | 4 |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|---|---------------------|----|
| 4672 | cg43917492 | 2087 | CTTTCATACTGG TTATTTTTTTTTTT T/gap/jAATTCTGT CAGTGAGCAGCA TTTCC | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa. | 1E-148 | 4 |
| 4673 | cg43917492 | 2087 | TTTCATACTGGT TATTTTTTTTTTTT gap/jAATTCTGT CAGTGAGCAGCA TTTCC | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa. | 1E-148 | 4 |
| 4674 | cg43917492 | 3146 | CGAAGCACCGTT GCTCGGAGCAG CC/C/gap/jGGCGG GGAGCAGGAGC TCAGGGACA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa. | 1E-148 | 4 |
| 4675 | cg43917036 | 1328 | AGCATCCCAGAG AAGCTCTGTCTG C/G/A/CTGCAAA GCCATGGCTGCA GACATC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13239 PUTATIVE SRC-LIKE ADAPTER PROTEIN (SLAP) - HOMO SAPIENS (HUMAN), 276 aa. | 1.3E-148 | 8 |
| 4676 | cg43041577 | 2015 | TGAAACCAGAAT CTTTTTTTTTTTTT gap/jAATCTGTA AATAGGTGTACT TTTTCC | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB45767 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment). | 2.7E-148 | 10 |
| 4677 | cg43943919 | 68 | GAGTCAGAACAT TAGACTTATAGT G/G/A/JAGGAGCA GAACGAACCCCT GGCCTG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB46921 DA159A1.1 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 399 aa. | 2.7E-148 | X |
| 4678 | cg44921374 | 1526 | GAAAAAATCTCT CTCAAAACAAAA C/A/gap/jAAAAAA ACCTACACACAA CTGAGTG | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 (12q23) | 12 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|----------|---------------|
| 4679 | cg44921374 | 1652 | ACAAATGTA GTTCTTTTGT [A/gap]AAAAAGG GGTAGGATTAG GTTCA | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |
| 4680 | cg44921374 | 1662 | TAGTTCTTTTG TTAAAAAGGGG [G/gap]TAGGATT AGGTTTCATATA TTAAAG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |
| 4681 | cg44921374 | 2203 | TGCATTTTCAGC AATATTATCGCC A[C/gap]AGACTC TGATTGCTCAGT CCACACA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |
| 4682 | cg44921374 | 400 | AGTTCAACTGTT CTCAATCTATGC T[A/gap]AAAAAAA AAAAATGACAAA TAATAA | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |

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|------|------------|-----|--|-----|-----|--|--|--|----------------------|--------------|---|----------|---------------|
| 4683 | cg44921374 | 412 | CTCAATCTATGC TAAAAA A[A/gap]TGACAA ATAATAAATTCTA CATTTC | A | gap | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |
| 4684 | cg44921374 | 412 | TCAATCTATGCT AAAAA A[gap]/ATGACAA ATAATAAATTCTA CATTTC | gap | A | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |
| 4685 | cg44921374 | 539 | AGCTGTAACCTCA GTGTGGTTTTC A[G/A]CTGCCTAC GTTAGTACCAGG TATTTC | G | A | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |
| 4686 | cg44921374 | 583 | GGTATTCATATA AACTCTGTAGAG G[C/T]CATTTACA TTTCGTAAATTCT GTAA | C | T | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|---|----------|---------------|
| 4687 | cg44921374 | 786 | AATCAACTACTG ATCATAACAGCC C[A/C]ATTAAAA CTCAAAACACTT ATATT | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |
| 4688 | cg44921374 | 855 | ATCCAGCAATGC CAATATAGGTAA TTT[C]TGATAGCC CCTATTGCAAA GTGAT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |
| 4689 | cg43927534 | 317 | TGATGTGTCAIT CTCCCCAGCAG GG[G/gap]AGGG GGTGAATGGCT TGGTTGTA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P23249 PROTEIN MOV-10 - Mus musculus (Mouse), 1004 aa. | 9E-148 | 1 |
| 4690 | cg43965796 | 131 | CAAAAATTCACA GCGCCTGTGAG GA[G/gap]CCCTT GGCTGGAACTG GTGACACCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment). | 9E-148 | 1 |
| 4691 | cg43965796 | 383 | AGCACCTCTCCC AGCTCCAGCCCCA TTC/TGGCTGGA GAGGAAAAGGG CAGAAAA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment). | 9E-148 | 1 |
| 4692 | cg43965796 | 462 | CACACCTACTAC ACAGATGATAAA A[A/gap]TCCCAC AATCGTATCTGT TCATGTT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment). | 9E-148 | 1 |

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|------|------------|------|---|---|-----|--|--|--|----------------------|------------------|--|----------|----|
| 4693 | cg43965796 | 902 | TGCTGTAGGCCT CCTCGAACATGG C[C/gap]TTGCAG GGGAAGCGGGC CTTCAGCT | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment). | 9E-148 | 1 |
| 4694 | cg43942977 | 1171 | TTCTCTCCAGC AGCCTGGGGG CA[G/gap]GGCAG AGCCTCCAGTCG GACCCCTT | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa. | 9.6E-148 | |
| 4695 | cg43942977 | 1173 | CTCTCCAGCAG CCTGGGGGCA GG[G/gap]CAGAG CCTCCAGTCGGA CCCCCTCC | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa. | 9.6E-148 | |
| 4696 | cg43261322 | 1073 | ATGTCACATTTT TGATTCTAGCTA C/TCTGTATTAT TCACCTAGCTTG TCC | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P78380 LECTIN-LIKE OXIDIZED LDL RECEPTOR - HOMO SAPIENS (HUMAN), 273 aa. | 5E-147 | 12 |
| 4697 | cg43261322 | 2207 | CCAGAAAACCCAC CAATCGGCTTTC A/T/ATTTGCATT TTGTAGTTTATG TGAA | T | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P78380 LECTIN-LIKE OXIDIZED LDL RECEPTOR - HOMO SAPIENS (HUMAN), 273 aa. | 5E-147 | 12 |
| 4698 | cg43985545 | 134 | AGAGCAGAAAG GGACACCTCCAT AG/A/TGTGTCTA TGGACCCCATTTT TGCTTT | A | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q15013 HYPOTHETICAL PROTEIN KIAA0110 (HA0666) - Homo sapiens (Human), 274 aa. | 6.3E-147 | 6 |
| 4699 | cg43985545 | 292 | CATCAGCCTATC AGGAAATCTGAG G[G/A]GAGGCAG ACAACCAAGAGG AGAGTT | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q15013 HYPOTHETICAL PROTEIN KIAA0110 (HA0666) - Homo sapiens (Human), 274 aa. | 6.3E-147 | 6 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|---|----------|---|
| 4700 | cg43985545 | 313 | GAGGGGAGGCA GACAACCCAGAAG GA[G]A[AGTTGCT TCCTCTCTCACC AGGAAG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q15013 HYPOTHETICAL PROTEIN KIAA0110 (HA0666) - Homo sapiens (Human), 274 aa. | 6.3E-147 | 6 |
| 4701 | cg42718779 | 1443 | GGGCTGAGAAT GAACCTGACTAG AG[C/G]TTCCTGGA GATACCCAGAGG TCCCCC | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O75712 GAP JUNCTION BETA-3 PROTEIN (CONNEXIN 31) (CX31) - Homo sapiens (Human), 270 aa. | 1.4E-146 | 1 |
| 4702 | cg43937734 | 1520 | GGTTCCTGCGCT CCTTCTGGTGCT C[C/gap]TACTCC AAGTCTATTTCAT TTTTCC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE II) - Homo sapiens (Human), 259 aa. | 3.5E-146 | 8 |
| 4703 | cg43937734 | 2139 | TCCTAGTATTTT CTTACCTGAAG[G/T]AGGGCCATT TATTTTAAATTC ACT | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE II) - Homo sapiens (Human), 259 aa. | 3.5E-146 | 8 |
| 4704 | cg43937734 | 561 | CTCGCTGACCTA ATAAGGCCATGC A[gap/A]GTGTGC GGGGGAGCTAC ATAAAGC | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE II) - Homo sapiens (Human), 259 aa. | 3.5E-146 | 8 |
| 4705 | cg42924529 | 168 | AGTCTGGGACTC CTGGCCCTCCAG G[C/gap]CCCTCC TCTCCAGAGAC CCTGATG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O15120 1-ACYL-SN- GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE BETA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE- BETA) (LPAAT- BETA) - Homo sapiens (Human), 278 aa. | 3.1E-145 | |

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|------|------------|------|--|----------|--|--|--|--------------------------|------------------|---|----------|---|
| 4706 | cg42924529 | 186 | CTCCAGGCCCT C CCTCTCCAGAG A[C]G[CCTGATG CAGCTTGTGGC TGGACC | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O15120 1-ACYL-SN- GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE BETA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE- BETA) (LPAAT- BETA) - Homo sapiens (Human), 278 aa. | 3.1E-145 | |
| 4707 | cg43961927 | 165 | TTATTTAACCCA C GGCCAGGGAG G[C]gap]GAAGCT TCAATCCTGCTG CTTGGTT | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60828 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)) - HOMO SAPIENS (HUMAN), 265 aa. | 4E-145 | |
| 4708 | cg43961927 | 165 | TATTTAACCCA GGCCAGGGAG GC[gap/C]GAAGC TTCATCCTGCT GCTTGGTT | C gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60828 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)) - HOMO SAPIENS (HUMAN), 265 aa. | 4E-145 | |
| 4709 | cg43985220 | 2180 | TAATTAACCTTCAT C TGCCGCTGGATT [C/A]TGTTGAGCC TTTAAAAATATTT CTT | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa. | 5.1E-145 | 8 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|----------|----|
| 4710 | cg43985220 | 2369 | GTGTTGTAAAT TAAAAATGCTTC TGAATAAGTTT TCAAGGTAGGGA GTGAT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa. | 5.1E-145 | 8 |
| 4711 | cg43985220 | 2420 | TTTATTATTGTGT ATATCTAATATA[T/gap]TAAGTATG TGTGATACTAAG GTTTG | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa. | 5.1E-145 | 8 |
| 4712 | cg43985220 | 2421 | TTTATTATTGTGT TATCTAATATAT[T/gap]AAGTATGT GTGATACTAAGG TTTGA | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa. | 5.1E-145 | 8 |
| 4713 | cg43269627 | 319 | TTTGATAATAAGA CAACCTTGTGAT[A/GTCTATTCAA GAAAAGCCAGAG CCCA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q15404 RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1) - Homo sapiens (Human), 277 aa. | 1.1E-144 | 10 |
| 4714 | cg43256169 | 289 | CTGGGTGCCGC ACAGTCTGCTCC CT[G/C]GGGACA GAAACCCACAGG GTCGAGC | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa. | 5.9E-144 | |

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|------|------------|------|---|----------|-----|--|--|--|--------------------------|------------------|---|----------|--|
| 4715 | cg43256169 | 401 | GGGAGGGCACA CAGGCTGGGTG GCA[C]gap]CCAG TGGCCAGGCC CTTAGCTGGG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa. | 5.9E-144 | |
| 4716 | cg43256169 | 414 | GGCTGGGTGGC ACCCAGTGGCCA GG[C]gap]CCCTT AGCTGGGCCGC AGGCAGCAC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa. | 5.9E-144 | |
| 4717 | cg43256169 | 428 | CAGTGGCCAGG CCCCTTAGCTGG GC[C]gap]GCAGG CAGCACTGAGCC GCCTGGAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa. | 5.9E-144 | |
| 4718 | cg43983449 | 945 | CCCTGAAAAGAA ATACACAGCCTA GT[G]CATAGTAT ATCATATAAAGG TTATT | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa. | 7.3E-144 | |
| 4719 | cg43983449 | 952 | AAGAAATACACA GCCTAGTCATAG T[A]G]TATCATAT AAAGGTTATTTT CTTAT | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa. | 7.3E-144 | |
| 4720 | cg43983449 | 1041 | TCCATAGTCCC TTACTAGGCAGT G[C]gap]CACATA AAGTTATTTAGTT AACATT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa. | 7.3E-144 | |
| 4721 | cg43983449 | 343 | CATAAGACAATG GAGCTTTAAAA A[gap]A]GGTTAG GTTTACATCTTT AAAACT | gap A | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa. | 7.3E-144 | |

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|------|------------|-----|--|---|-----|--|--|--|----------------------|------------------|--|----------|----|
| 4722 | cg43983449 | 650 | GTCAGCAAAATG CCTTTGACTGAC G[C/gap]CCTGGA TTATTTTACCACT TAACCT | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa. | 7.3E-144 | |
| 4723 | cg43983449 | 899 | ATGGTAATAGTA ACTAAACTACAT C[C/T]AACCCCTGA AGGTAGAAAAAT CCCTG | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa. | 7.3E-144 | |
| 4724 | cg43983449 | 931 | GAAGGTAGAAAA ATCCCTGAAAAG AATATACACAG CCTAGTCATAGT ATATC | A | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa. | 7.3E-144 | |
| 4725 | cg43925411 | 61 | AAACAAAGGTAC CAGTCGCCGCC GC[G/gap]GGAGG AGGAGGAGCCG GAGCCTCTG | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa. | 9.5E-144 | 10 |
| 4726 | cg43971525 | 103 | ACCTCTGAAGTA AGGCACAAACACA AT/CJTCCATTGT CACTGTGGCAGA AGTCC | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment). | 1.2E-143 | 11 |
| 4727 | cg43971525 | 181 | AAGACTGTGGTC CACGGGCCCTAA GG[C/gap]JACTTG AGCTTTCCCTC AACTGAAG | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment). | 1.2E-143 | 11 |
| 4728 | cg43971525 | 322 | ATGAACATCAAG AATTACTAGACA T[G/T]TAAAAGTG TCTTTAAGTGTC TTTCC | G | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment). | 1.2E-143 | 11 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|--------|----------|
| 4729 | cg44027658 | 1145 | TGAGAGAAATT GAGATGTGTA A[A/gap]TCTAGTT ACTGCCTGTAAA TGGTGT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa. | 2E-143 | 1 (1p21) |
| 4730 | cg44027658 | 191 | GGCCTCGGGCA CCGCGTCCTGTG GG[G/gap]CGGCC GCCTGCCTGCC CGCCCGGCC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa. | 2E-143 | 1 (1p21) |
| 4731 | cg44027658 | 227 | CCTGCCCGCCC GCCCCGAGCCC CTT[G/C]GCTGC CGCCCCCTGGG CGGCCGCTG | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa. | 2E-143 | 1 (1p21) |
| 4732 | cg44027658 | 228 | CTGCCCGGCCG CCCGCAGCCCC TTG[G/C]CTGCC GGCCCCCTGGC GGCCGCTGC | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa. | 2E-143 | 1 (1p21) |

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|------|------------|------|---|---|-----|--|--|--|----------------------|------------------|---|----------|-----------------|
| 4733 | cg44027658 | 249 | CTTGGCTGCCG GCCCCTGGCGG GCC[G/C]CTGCC ATGGGCACCGA CAGCCGCGC | G | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa. | 2E-143 | 1 (1p21) |
| 4734 | cg44027658 | 250 | TTGGCTGCCGG CCCCTGGCGG CCG[C/G]TGCCA TGGGCACCGAC AGCCGCGCG | C | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa. | 2E-143 | 1 (1p21) |
| 4735 | cg43999829 | 1084 | GAAGCAGGGCC CTGACTGCCCCC CC[C/gap]GGCCC CCCTCTCGGGCT CTCTCACC | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa. | 2.1E-143 | 22 (22q11.2) |
| 4736 | cg43999829 | 1198 | TAAATGCAAAGC ACACCTCGGCC GA[G/gap]GCCTG CGCCCTGACATG CTAACCTC | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa. | 2.1E-143 | 22 (22q11.2) |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|---|----------|---------------------|
| 4737 | cg4399829 | 1199 | AAATGCAAGCA CACCTCGCCG AG[G/gap]CCTGC GCCCTGACATGC TAACCTCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa. | 2.1E-143 | 22 (22q11.2) |
| 4738 | cg43917524 | 372 | CTTCCCAGTCTT TTTTTTTTTTTTT T[gap]GAGACAG GGTCTAGCTGTC ACCCAG | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD43025 PTD017 - HOMO SAPIENS (HUMAN), 258 aa. | 3.2E-143 | |
| 4739 | cg44000122 | 153 | CAAAAGGTGGCAA ACATATTATTGC [C/A]TCACTGTAA ATAGAGAAAATC TTGT | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14657 TORSINB - HOMO SAPIENS (HUMAN), 266 aa (fragment). | 6.7E-143 | 9 |
| 4740 | cg44000122 | 399 | GCAGCTGTGCTG TGATTATGAGAC A[G/A]ATACAATG ATTCACTACCTGGC TGGA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14657 TORSINB - HOMO SAPIENS (HUMAN), 266 aa (fragment). | 6.7E-143 | 9 |
| 4741 | cg44000122 | 968 | AGACGGTGAAG GATTCCACAGCC AG[G/C]GCTGTAT TAGCAGCTAGAG CGATGG | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14657 TORSINB - HOMO SAPIENS (HUMAN), 266 aa (fragment). | 6.7E-143 | 9 |
| 4742 | cg44020482 | 132 | GGCAGGGCGGAC CCCAGCCCCCG GGG[G/gap]ACAT GAGGGCCAGGG GAGGGCAGTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q92561 HYPOTHETICAL PROTEIN KIAA0273 - Homo sapiens (Human), 330 aa. | 2.9E-142 | 8 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|---|----------|----------|
| 4743 | cg43334997 | 1155 | CTGCGCTCTGAG ATGAGCTGCCCT C[G]GCTCCCT CCGGGTGGCG CGCCCGG | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75973 C1Q- RELATED FACTOR - HOMO SAPIENS (HUMAN), 258 aa. | 2.9E-142 | |
| 4744 | cg43958563 | 172 | ATGACTGTATTT ATTTGTACAAAA [T/C]GCAGTAACA CTTCTCTTTTCC TCT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa. | 4.7E-142 | 1 (1p35) |
| 4745 | cg43958563 | 341 | AGTGGGAATGA AAACAGGCAGAG G[C/gap]CAGCAG GTTCTCGGCTA GGGCTCT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa. | 4.7E-142 | 1 (1p35) |
| 4746 | cg43958563 | 354 | AACAGGCAGAG GCCAGCAGGTTT CT[C/gap]GGCTA GGGCTCTGCCTA TAACGCCCC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa. | 4.7E-142 | 1 (1p35) |
| 4747 | cg43958563 | 368 | AGCAGGTTTCTC GGCTAGGGCTCT G[C/gap]CTATAA CGCCCTGGTCCT GCTCATC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa. | 4.7E-142 | 1 (1p35) |
| 4748 | cg43958563 | 369 | GCAGGTTTCTCG GCTAGGGCTCTG C[C/gap]TATAAC GCCCTGGTCCTG CTCATCT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa. | 4.7E-142 | 1 (1p35) |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|---|----------|----------|
| 4749 | cg44964063 | 1636 | AAATACAGTTAA ATGTGTTATTTG CT[<i>gap</i>]TTTAAAA TTATAAAAAGCA AAGAGA | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13145 PUTATIVE TRANSMEMBRANE PROTEIN NMA PRECURSOR - Homo sapiens (Human), 260 aa. | 6E-142 | 10 |
| 4750 | cg44964063 | 1639 | TACAGTTAAATG TGTTATTTGCTTT [T/ <i>gap</i>]AAAAATTAT AAAAAGCAAGA GAAGA | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13145 PUTATIVE TRANSMEMBRANE PROTEIN NMA PRECURSOR - Homo sapiens (Human), 260 aa. | 6E-142 | 10 |
| 4751 | cg43951474 | 1863 | ATGGCTCTGCT GTCCTTCCCCAG T[C/ <i>gap</i>]CACCAG GGTGGGGGGA CAGGGGCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76038 SECRETAGOGIN - HOMO SAPIENS (HUMAN), 276 aa. | 6E-142 | |
| 4752 | cg43951474 | 1864 | TGGCTCTGCTG TCCTTCCCCAGT C[C/ <i>gap</i>]ACCAGG GTGGGGGGGAC AGGGGCAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76038 SECRETAGOGIN - HOMO SAPIENS (HUMAN), 276 aa. | 6E-142 | |
| 4753 | cg43951474 | 1918 | AGTGCATTCATT TTGTGCTTTTCTT [G/A]TGGGCTTTC TGCTTAGTCTGA AAGG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76038 SECRETAGOGIN - HOMO SAPIENS (HUMAN), 276 aa. | 6E-142 | |
| 4754 | cg43973724 | 2810 | GCTTTATTCAA CTAAGGTACTTA C[C/T]AAAAACCTT AGTTTTATACA GGTGT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75070 KIAA0483 PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment). | 1.3E-141 | 1 |
| 4755 | cg43119818 | 1895 | AGCCCTGCTTCT GACATAATCCAG T[<i>gap</i>]TAAAAATAA TAATTTTAAAGAA ATAAA | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P00915 CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I) - Homo sapiens (Human), 260 aa. | 6.9E-141 | 8 (8q22) |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|---|----------|----------|
| 4756 | cg43119818 | 2057 | TAGTAATCTGTA AGCATAAGCTTA T[G]gap]CTTAAAT TCAAAGTTTAGTTT GAGGA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P00915 CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I) - Homo sapiens (Human), 260 aa. | 6.9E-141 | 8 (8q22) |
| 4757 | cg43919223 | 206 | ATCTTTTCTTAC AGGATTCTTACC[G/T]CAGGAATAG ATGGACATGGCC TGCC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P41439 FOLATE RECEPTOR GAMMA PRECURSOR (FR- GAMMA) (FOLATE RECEPTOR 3) - Homo sapiens (Human), 243 aa. | 1.4E-140 | 11 |
| 4758 | cg43328633 | 3746 | CCTCAAAGCCAG GTGCTGGCCAAA T[A/G]CCTTGATC ACAGCCTCCATG GCCAG | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O15049 HYPOTHETICAL PROTEIN KIAA0341 - Homo sapiens (Human), 546 aa (fragment). | 1.5E-140 | |
| 4759 | cg43922710 | 125 | CTCTACCCAGCT AAATACACATTAT [G]gap]GCATTTA GCAAACTAACTT ACAAGT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA74897 KIAA0874 PROTEIN - HOMO SAPIENS (HUMAN), 601 aa (fragment). | 4.9E-140 | |
| 4760 | cg43935709 | 449 | ACAACAACATA TTTTGGACAAAA C[A/C]ATTTTTTT TAATCTGCTTG TAAA | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment). | 8E-140 | 20 |
| 4761 | cg43935709 | 505 | TACTTCCTTTTGA GTCTCTGATGGC [C/T]ACAACATTT CAITTGAGATGT TTGG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment). | 8E-140 | 20 |
| 4762 | cg43935709 | 695 | TGCCCATGGTGG AAATGCTGGA A[A/T]TTAAAGGT AAGAAATAAAC ATAGC | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment). | 8E-140 | 20 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|----------|----|
| 4763 | cg43935709 | 92 | GATGGATAGATT TTTTTTTTTTAA[A/G]GAAATTAGC CTCCCTGGGTAC TTAC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment). | 8E-140 | 20 |
| 4764 | cg43935709 | 941 | TCCTGCTTGGCT TTCATTTACAG G[G/gap]CCTGCA GCCTTGCTCTG GAAGGTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment). | 8E-140 | 20 |
| 4765 | cg43950100 | 927 | AGGATGGAAG GTGGAAGGGTAA AT[G/A]GCACAG GGAGAAAAACAA AGTGTTG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa. | 1.7E-139 | 11 |
| 4766 | cg44030891 | 368 | CCCCAGCCCTG GCTGCCCTCTGC GG[C/T]CCCCAC CCGAGCCCTGC CCCTAGGT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99750 MYOGENIC REPRESSOR I-MF - HOMO SAPIENS (HUMAN), 246 aa. | 2.1E-139 | 6 |
| 4767 | cg43936172 | 355 | ACCTCATGTCTC TGGGCCGGGAA GC[C/gap]ACGAT CCCTCATCCATC AGGCCTGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60429 F17127_1 - HOMO SAPIENS (HUMAN), 528 aa. | 2.7E-139 | 19 |
| 4768 | cg43917807 | 1667 | ACTCCTTTAGGC ATGCAGGTAAC G[gap/C]CCCCCA CGCCCCCCCCGC CACCTCCC | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa. | 1.2E-138 | 17 |
| 4769 | cg43917807 | 466 | GAGAAGATTAAAC AAAGTCCTTTCT T[C/T]CAATATCA GGATAGTCATGA GTTC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa. | 1.2E-138 | 17 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|----------|----|
| 4770 | cg43917807 | 467 | AGAAGATTAACA AAGTCCCTTCTT C/C/TAATATCAG GATAGTCATGAG TTGCA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa. | 1.2E-138 | 17 |
| 4771 | cg43917807 | 564 | GAACATATGAGAT TCTTGCTCCCTC C/G/gap/GGGGAG CCAAGGAGCTTG CAACTGG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa. | 1.2E-138 | 17 |
| 4772 | cg43917807 | 723 | AGAGAAATGGACA GTGTGATCCTTG T/T/C/JTGTGCTAG CCATTGGGTGAT GCACC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa. | 1.2E-138 | 17 |
| 4773 | cg43285114 | 427 | GCGGGCACCCCC GTGGGGTCTTTG GC/G/AJGCTCAC AGGACAATGGCA GTGGAGG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD23440 LR8 - HOMO SAPIENS (HUMAN), 270 aa. | 1.9E-138 | 7 |
| 4774 | cg43303845 | 271 | TGGTGTAGCCCC CTGGCCGCCCGA AG/G/gap/JAGGAG CCGGACACTTGT CTCCCGTC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O83263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa. | 1.9E-138 | |
| 4775 | cg43992302 | 1911 | CATTCTCATTG TTTCATGTTTGA C/C/JTTTAAAGT GAAAAAAGAAAA TGGCC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O45934 Y43F4B.5 - CAENORHABDITIS ELEGANS, 595 aa. | 4.5E-137 | 4 |
| 4776 | cg43992302 | 2082 | TTTGCATAAATC ATAAATGTATGT C/C/JTCTCTGTA ATTGTTTTAATGT GTGC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O45934 Y43F4B.5 - CAENORHABDITIS ELEGANS, 595 aa. | 4.5E-137 | 4 |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|--|----------|---|
| 4777 | cg43935076 | 229 | CCAACCCCAAG CATTTGGGTT C[A]G]GCCAAGC CAGACAAGGA CCCACAA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa. | 1.5E-136 | 1 |
| 4778 | cg43935076 | 409 | AAGTAAAGTT TGGTGCGGTG GG[C]gap]CTCAT GCCACACTGATT GGTCAGTA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa. | 1.5E-136 | 1 |
| 4779 | cg43935076 | 410 | AGTAAAGTTT GGTGCGGTGG GC[C]gap]TCATG CCACACTGATTG GTCAGTAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa. | 1.5E-136 | 1 |
| 4780 | cg43935076 | 443 | ACACTGATTGTT CAGTAGACAGG GG[C]gap]CACAT GCCAAACACCAC AGGCATC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa. | 1.5E-136 | 1 |
| 4781 | cg43935076 | 450 | TGGTCAGTAGA CAGGGGCACA TG[C]gap]CAAAAC ACCACAGGGCAT CAGATGCT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa. | 1.5E-136 | 1 |
| 4782 | cg43935076 | 451 | TGGTCAGTAGAC AGGGGGCACAT GC[C]gap]AAACA CCACAGGGCATC AGATGCTG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa. | 1.5E-136 | 1 |
| 4783 | cg43935076 | 629 | ACACTGTTTAA GCAGTATGTTTA A[T]C]TGGATGAT TTCCACAAACTA TCCAC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa. | 1.5E-136 | 1 |

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|------|------------|-----|---|---|-----|--|--|--------------------------|------------------|--|----------|----------|
| 4784 | cg43935076 | 643 | AGTATGTTTAATT GGATGATTTCCAA C/TJAAACTATCC ACGAAGTTTCTA ACCA | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPREMBL-ACC:075937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa. | 1.5E-136 | 1 |
| 4785 | cg43952219 | 675 | CAGTGGTTAGTA GTTTTTTTTTTT T/gap]CCTTTTTT TAAAGCATAAGC AATAG | T | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa. | 2.5E-136 | X |
| 4786 | cg43922796 | 692 | CAGGGCACCAG ACAGCAGCGGC CCCTT/CJTCCCA GGAGGTACAGG AGACAGGA | T | C | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q00004 SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68) - Canis familiaris (Dog), 622 aa. | 3.2E-136 | 1 (1q42) |
| 4787 | cg43947491 | 537 | AACTTTAATTGA ATGAGAATTACA T/CJCTGTCAAAG ACCTGGGCAGTA CACT | T | C | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P30040 ENDOPLASMIC RETICULUM PROTEIN ERP29 PRECURSOR (ERP31) (ERP28) - Homo sapiens (Human), 261 aa. | 1.8E-135 | 12 |
| 4788 | cg43994220 | 136 | TGCCCTTGAAGT CAGTCTGGGTT T/C/gap]CCCAGC TCTGGCTGACCA TTTTGTT | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa. | 5.8E-135 | 19 |
| 4789 | cg43994220 | 186 | TCCCTGAGTGTC TGAGTCCCCGG CA[G/gap]GCGGC CTTCACTCAGGG TCAGCGGG | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa. | 5.8E-135 | 19 |
| 4790 | cg43994220 | 187 | CCCTGAGTGTC GAGTCCCCGGC AG[G/gap]CGGCC TTCACCTCAGGT CAGCGGGC | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa. | 5.8E-135 | 19 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|---|----------|---|
| 4791 | cg43948495 | 1584 | CGCGGAGCGTG CGGTCTGGACCA CQ[C/gap]AAGGG AAACCCCTCAT TTAGCAC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4792 | cg43948495 | 1623 | TCATTTTAGCAC AGCGGCCTGG GC[T/A]GCGTCC AAGCTCTCGTAC TGAATAT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4793 | cg43948495 | 1649 | GCGTCCAAAGCTC TCGTACTGAATA T[A/G]GGCAAAG CTATCTCCTTTG ACGTGA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4794 | cg43948495 | 1707 | TCCGAATGCTCC CAAAGCGGTCAA A[C/T]TCTCGGGC CAGAGCCGCCA GTGACG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4795 | cg43948495 | 1708 | CCGAATGCTCCC AAAGCGGTCAA C[T/C]CTCGGGC CAGAGCCGCCA GTGACGT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4796 | cg43948495 | 2526 | GAGGCTGATCTC GCCGAAGCGCTT G[gap/G]AACTGG TGGAAGAGCCG GTCCTCGA | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4797 | cg43948495 | 2567 | CGGTCCTCGAG GTGCTCGGCGG GCA[G/T]CGCGA GGGCCAAGGCG CCGGGGGACG | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|---|----------|---|
| 4798 | cg43948495 | 2573 | TCGAGGTGCTCGG GCGGGCAGCGC GA[G/C]GGCCAA GGCGCCGGGA CGCGAATC | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4799 | cg43948495 | 2579 | TGCTCGGCGGG CAGCGCAGGG CCA[A/C]GGCGC CGGGGACGCGA ATCACGCG | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4800 | cg43948495 | 28 | TTTTTTCAGGT TAAAAATCCATC C/gap]TCTGTCAA AGGTTTACTGA CAACT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4801 | cg43948495 | 31 | TTTCAGGTTTAA AAATCCATCCTC T[gap/C]GTCAA GGTTTACTGAC AACTTTC | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4802 | cg43948495 | 409 | CTAGCTTGCCCA ATGTCCTTAGTG CT[A/G]ACTGGA GGTACTGCTGG GAAAAGT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4803 | cg43948495 | 463 | GGGTGGGAAGG CGTAGAGCATGC CT[gap/T]GTGCC GTCTCTGCCCTT GGACCCCC | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 4804 | cg43948495 | 510 | CCCCCCTACTGG CAAGCTGATCAC CC[C/gap]TGGCG CCTGCTTCTGTT TCAAGTAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |

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|------|------------|------|---|---|-----|--|--|--|---------------------------------|------------------|---|----------|----|
| 4805 | cg43916993 | 1938 | ATCCGCTTGATT CCACTTGGTTTT GTTAAAGTTTT CCAAATCTTTGG AGAGT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa. | 2.3E-133 | 16 |
| 4806 | cg43916993 | 833 | CCCACAAAGGG GGACGATCACG GCC[C/gap]AGCA AAAGCGATGCTG AGAGGGGAA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa. | 2.3E-133 | 16 |
| 4807 | cg43916993 | 855 | GCCCAGCAAAAG CGATGCTGAGAG G[G/A]GAAACAG TCCAGAGTCCAA CAGCAG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa. | 2.3E-133 | 16 |
| 4808 | cg43916993 | 945 | TATGTATAGGG CCGGGGGCTTC TG[C/gap]CCAGG GCTCCCTGGAC CAGGACGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa. | 2.3E-133 | 16 |
| 4809 | cg43916993 | 947 | TGTATAGGGGCC GGGGGCTTCTG CC[C/gap]AGGGC TCCCCTGGACCA GGACGCCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa. | 2.3E-133 | 16 |
| 4810 | cg34758981 | 1158 | TTTTTATTAATAC AAGTCACITTTT A/CJAAAAATTTG GATTTTTTATAT ATA | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P48307 TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR (TFPI-2) (PLACENTAL PROTEIN 5) (PP5) - Homo sapiens (Human), 235 aa. | 1.6E-132 | 7 |
| 4811 | cg42910848 | 281 | GACAGGTGTGG GAGGTAGCTCGA AA[C/T]ATACAGA GTGTTCCGCAACA CTAGAG | C | T | | | | SILENT- NONCODI NG 886 | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment). | 3.1E-132 | |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|---------------------------|----|
| 4812 | cg42910848 | 295 | GTAGCTCGAAAC ATACAGAGTGTT C[G/A]CAACACTA GAGACGTCCTCT GGCTG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment). | 3.1E-132 | |
| 4813 | cg43317146 | 162 | CAGCTTTGCTGA AACTGTACTTTG G[G/A]CTCCAGA CTTCACTGTCCT TAGGCA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD30567 H5AR - MUS MUSCULUS (MOUSE), 330 aa. | 5.3E-132 | 4 |
| 4814 | cg43317146 | 81 | AGATTCATTTTCT TGAGTGGCACTG [C/gap]CATGCTC ATTCAGTGAAAA CTTGTG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD30567 H5AR - MUS MUSCULUS (MOUSE), 330 aa. | 5.3E-132 | 4 |
| 4815 | cg43317146 | 82 | GATTCATTTTCTT GAGTGGCACTG C[C/gap]ATGCTC ATTCAGTGAAAA CTTGTG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD30567 H5AR - MUS MUSCULUS (MOUSE), 330 aa. | 5.3E-132 | 4 |
| 4816 | cg43957878 | 85 | TCCACTACAAA AATACAGAGGAG A[T/C]AGGGTGTT TCCTGTATCCGC CTCAT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:Q99753 CISPLATIN RESISTANCE ASSOCIATED BETA PROTEIN - HOMO SAPIENS (HUMAN), 252 aa. | 7.1E-132 | 1 |
| 4817 | cg43087636 | 1059 | TTAAAATTATTTC TAGGAAAGTCAAA T/A/AAATATAATA AAGGGTTGAGCC CTC | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P30793 GTP CYCLOHYDROLASE I (EC 3.5.4.16) (GTP-CH-) - Homo sapiens (Human), 250 aa. | 1.5E-131 (14q22.1) | 14 |
| 4818 | cg43087636 | 1145 | AAGTGAACGTGCT AATAGTGTAAAGT A[C/T]GTGCACAA AACCAGTCCAG ATAAC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P30793 GTP CYCLOHYDROLASE I (EC 3.5.4.16) (GTP-CH-) - Homo sapiens (Human), 250 aa. | 1.5E-131 (14q22.1) | 14 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|----------|---------------------|
| 4819 | cg43087636 | 1314 | TTTCTTCTCCA ATAAAAGTGGTG T[A/G]GTGCCGA AAGTGCTAAAT ATTAG | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P30793 GTP CYCLOHYDROLASE I (EC 3.5.4.16) (GTP-CH-I) - Homo sapiens (Human), 250 aa. | 1.5E-131 | 14 (14q22.1) |
| 4820 | cg43918679 | 1275 | TGCCTGTCTACA CCAGTCCTGTCC C[C/gap]AGGACT CCCCCTTCTGTGG TCTGGAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa. | 3E-131 | 21 |
| 4821 | cg43931621 | 1023 | GCATTAGAATGC TGGATGAGACTT A[A/gap]AAGCTT CAGTTCACTGTA AAACTA | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment). | 4.7E-131 | 5 |
| 4822 | cg43931621 | 1025 | ATTAGAATGCTG GATGAGACTTAA A[A/gap]GCTTCA GTTCACTGTAAA AACTAAA | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment). | 4.7E-131 | 5 |
| 4823 | cg43931621 | 760 | AACCGTGTCTAT AATTTTTTAAAG [G/A]AAAAAACCT GCTTTCCAAAC TTAG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment). | 4.7E-131 | 5 |
| 4824 | cg42859936 | 185 | TACTTGGAAATAC ATGCCATTATCT C[T/C]GCATTTTA CAATAAGAAAT CATCA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99644 DELTA SARCOGLYCAN - HOMO SAPIENS (HUMAN), 256 aa. | 8.1E-131 | 5 (5q33) |
| 4825 | cg42382358 | 1842 | CTCCCCACCCAC CACCCTCCCG CG[G/gap]CAAGC CAGCCCCGTGCA CGGAAGCC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P08294 EXTRACELLULAR SUPEROXIDE DISMUTASE [CU-ZN] PRECURSOR (EC 1.15.1.1) (EC-SOD) - Homo sapiens (Human), 240 aa. | 5.7E-130 | 4 (4pter) |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|----------|----|
| 4826 | cg43946922 | 1714 | GGTCCGAGGAC AGAAAGCGCCG GTG[G/gap]CGGG ACGCAGGGGAG GCAGGGTGAC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75190 MSJ-1 - HOMO SAPIENS (HUMAN), 241 aa. | 1.2E-129 | 11 |
| 4827 | cg43946922 | 735 | AGAGATTACAA CAATTTAAAGA C[A/gap]AAAAAA AAAAATGGTCCTA TTATGTG | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75190 MSJ-1 - HOMO SAPIENS (HUMAN), 241 aa. | 1.2E-129 | 11 |
| 4828 | cg43946922 | 745 | AACAATTTTAAA GACAAAAA A[A/gap]TGGTCC TATTATGTGGTC CCAACAA | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75190 MSJ-1 - HOMO SAPIENS (HUMAN), 241 aa. | 1.2E-129 | 11 |
| 4829 | cg43928955 | 225 | GGCGAAGAGCT GGGTCCTGCAG CTC[C/T]GGTGG GAGCCTCCTCAG TTCTTTTC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa. | 1.3E-129 | |
| 4830 | cg43928955 | 254 | GGGAGCCTCCT CAGTTCTTTTCG GAT[C]GCACTCC ACCCCGCGGAAT CCGGTG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa. | 1.3E-129 | |
| 4831 | cg43928955 | 315 | TGCGGAGAGCG GGCTTAGTGCC TC[G/C]CCGGCT TCGTGGCCTCCC AGGCTTC | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa. | 1.3E-129 | |
| 4832 | cg43928955 | 337 | CTCGCCGGCTTC GTGGCCCTCCCA GG[C/T]TCGCTC TGACCCCTGTCTG GGCTGG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa. | 1.3E-129 | |

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|------|------------|-----|--|---|---|--|--|--|--------------------------|------------------|---|----------|----|
| 4833 | cg43928955 | 364 | TCGCTCTGACCC TGCTGGGCTGG ATCJGGAGGCC GGACCGCCCTTC CTGGCG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa. | 1.3E-129 | |
| 4834 | cg43928955 | 460 | AGGATAGACGG GCGGGTGACCC GTG[A/G]CCCG TACCCACGAGTT TGGGTCCC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa. | 1.3E-129 | |
| 4835 | cg43928955 | 486 | CCCCGTACCCAC GAGTTTGGGTCC CTTCTGAGGCAT CTCTCCAGGCCT CTGCC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa. | 1.3E-129 | |
| 4836 | cg43928955 | 667 | TTGAGAACCCCTC TCGAGGAGTCTG G[C/G]CTCATGA GGATGCCAGAAC AAATGG | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa. | 1.3E-129 | |
| 4837 | cg43950545 | 203 | ATCCCCACAAC AGATAGAATGAA TTTCTTTTATAG AGCAAATGACAT GCTTT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa. | 3.5E-129 | 13 |
| 4838 | cg44938448 | 103 | AAGAATCATAGA CAGCTACTACCA C[G/A]GCTGCTTC GTTGGACAAA ATAAC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |
| 4839 | cg44938448 | 963 | CATGTAAAAAGC TGCTTGTTGGC C[C/T]GTTATTC CACTGACCCGTC TGAGT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|----------|---|
| 4840 | cg44938448 | 1149 | CCATGGTAATTT TTCACAAATTAAA [A/G]ACACATTTT GGGTTGTGCAAC AGTG | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |
| 4841 | cg44938448 | 129 | GCTGCTTCGTTT GGACAAAAATAA C[C/G]AGGAGGC ATCCACGGGATT AGTTAC | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |
| 4842 | cg44938448 | 1264 | TTTTCTTTTAA CCTTTTATGCC[T/A]TTCAGTAGG GGAAGTTTCCTT GAAA | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |
| 4843 | cg44938448 | 1311 | GAAAGTTAGAGA GCTGCAATCTC TT/gap/AAGTATC AATGTAAGAAG CAGATG | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |
| 4844 | cg44938448 | 1321 | GAGCTGCAATC TCTTAAGTATCA A[T/C]GTAAAGAA GCAGATGACCCA ATTGG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |
| 4845 | cg44938448 | 1332 | CTCTTAAGTATC AATGTAAAGAAG C[A/C]GATGACC CAATTCGGAAGG TGGTTC | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |
| 4846 | cg44938448 | 166 | ACGGGATTAGTT ACACGGTATCAA C[T/C]TACCACCA CAGCAGAATCAA CAGTG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|---|----------|----|
| 4847 | cg44938448 | 6409 | CGCGGCTGCCC GTTGGTTCCGCC CG[A/G]GCCGTT CTACTCCAGGCA GACGGGA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |
| 4848 | cg44938448 | 6463 | GAAACACGGCG CCTCAGCGTCCC CT[G/C]CCCCGTT GGTCTGCTCGG GCCCTT | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.8E-129 | 1 |
| 4849 | cg43972431 | 1024 | GAAAAGTTTAA CACTGGAGAATT C[G/A]CTATGGTG AGCCTAAGCAAT ATATA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD16888 CDC42 EFFECTOR PROTEIN 3 - HOMO SAPIENS (HUMAN), 254 aa. | 7.1E-129 | 2 |
| 4850 | cg43931286 | 1069 | GGATGTAGTTCC TTTGTAAGGGTG G[G/gap]CAGGCC TCGTAAGAAAGA TGTAGCA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD27775 30S RIBOSOMAL PROTEIN S7 HOMOLOG - HOMO SAPIENS (HUMAN), 242 aa. | 1.4E-128 | 17 |
| 4851 | cg43298916 | 116 | GCTATGGCATCT TTAATTATAAAAA [gap/A]TAAGCAA ATAAAATAACTT GCATCT | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa. | 1.7E-128 | 8 |
| 4852 | cg43298916 | 193 | TTTATATGCACAT GGAGCTTAAAAA gap/A]TGTAATTT AACAAATAATAAT GACA | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa. | 1.7E-128 | 8 |
| 4853 | cg43298916 | 2603 | GTGGTCTCAGG GGAGCAGGGGA AAA[gap/G]ACAT GGCAGAGGAAG TTGGTAAAG | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa. | 1.7E-128 | 8 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|----------|---|
| 4854 | cg43298916 | 425 | ACGAAGCTTTGG AAGTTTAAGGG G[gap/G]AATTGG AGGGAGTAGGG TGGGGAA | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa. | 1.7E-128 | 8 |
| 4855 | cg44128041 | 940 | ATATATTATGG CCGGGCAGGGT GT[G/gap]GGGCC ATGCCTCCTCAG GAGCCGAA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa. | 2.8E-128 | |
| 4856 | cg44128041 | 943 | TATTATGGCCG GGCAGGGTGTG GG[G/gap]CCATG CCTCCTCAGGAG CCGAAGCC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa. | 2.8E-128 | |
| 4857 | cg44128041 | 1082 | TGCAGGACCTCG TGCCACCCCGA GG[G/gap]CTGAG CCTGGTCCCACG AGGGTGCC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa. | 2.8E-128 | |
| 4858 | cg44128041 | 1115 | TGGTCCCACGAG GGTGCCCGTGT CC[C/gap]TGACA GGGCCAGTGCA GTTTGGTGT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa. | 2.8E-128 | |
| 4859 | cg44128041 | 1153 | TGCAGTTTGGTG TGTCCTCCGCCT TT[A]CCAGGAGA AGAACCTGAAGA ACTAT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa. | 2.8E-128 | |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|----------|----------|
| 4860 | cg42891437 | 989 | GGGACAGGGC CTGGAGTCAGAG CTGTGGGGC GTGAGGGCGA AAGGGGAC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75425 ORF3,SPLICEVARIANT_B - HOMO SAPIENS (HUMAN), 235 aa. | 2.4E-127 | 7 (7q21) |
| 4861 | cg42891437 | 991 | GGACAGGGCCT GGAGTCAGAGCT GGGTGGGCGT GAGGGGCGAAA GGGACAA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75425 ORF3,SPLICEVARIANT_B - HOMO SAPIENS (HUMAN), 235 aa. | 2.4E-127 | 7 (7q21) |
| 4862 | cg43995142 | 110 | GTTTCTCATTTTG TTAAGCTGCAA[G/gap]CAAGTTTC TTTCACAATTACA CTTC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60660 ASH2L1 - HOMO SAPIENS (HUMAN), 628 aa. | 8E-127 | |
| 4863 | cg43949897 | 913 | GGAGCCACCAA GCACTTGGAGC TG[G/gap]CCTCG CCCCCTAGGAG GAGAGGGTC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60499 SYNTAXIN 10 - HOMO SAPIENS (HUMAN), 249 aa. | 1.8E-126 | 19 |
| 4864 | cg42549778 | 1633 | TGTGTGTGTGCA CTGCTGTGTGTG T[gap/G]TGCACG CACAGGAAGCCT TTCCACA | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD29690 PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1 - MUS MUSCULUS (MOUSE), 267 aa. | 3.7E-126 | |
| 4865 | cg44002192 | 1646 | GGACTACATCTC CCAGCCCTTCAC G[C/T]GTTAAATA TGAGTGGTTTTA AAAGG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75204 HYPOTHETICAL 25.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 238 aa. | 1.5E-125 | 16 |
| 4866 | cg44002192 | 2337 | AAGACCTTCAGT GTAGATCCAGAT G[G/C]CCCAACCT GTCCTTGTTAAG TTACTT | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75204 HYPOTHETICAL 25.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 238 aa. | 1.5E-125 | 16 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|---|----------|----|
| 4867 | cg44002192 | 2876 | ACTGGTCATCTC CTGAGGACCTGT A/C/A/JATGACCCT GTGGACTGTTCC GCACG | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75204 HYPOTHETICAL 25.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 238 aa. | 1.5E-125 | 16 |
| 4868 | cg43949061 | 863 | GCCCGGGAGTG TTCCGAACGGAG CTG/CJGCTCCG CCACGCCCACTG CTACCCC | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa. | 2.1E-125 | 19 |
| 4869 | cg43307940 | 36 | TTTTTTTGATTTT TTTTTTTTTTTTG /TGTAGCATAGT GAGTGGAGTTTA TTT | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa. | 8.1E-125 | 15 |
| 4870 | cg43307940 | 37 | TTTTTTTGATTTT TTTTTTTTTTTTG G/JTGTAGCATAGT GAGTGGAGTTTA TTTT | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa. | 8.1E-125 | 15 |
| 4871 | cg43307940 | 46 | TTTTTTTTTTTTT TTGGTAGCATAGT T/AJGAGTGGAGT TTATTTTATAAT TTG | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa. | 8.1E-125 | 15 |
| 4872 | cg43307940 | 887 | TGTCAGAAAAAT CAATAGCATCAA A/A/gap/CTGGTC TAACGTAGCACC TAGATT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa. | 8.1E-125 | 15 |
| 4873 | cg44002548 | 1707 | ACCGGAATTTTA TATTAAGGGG C/C/A/JTCCTTTT AAATATATGCCG TGTA | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB45746 HYPOTHETICAL 49.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 454 aa. | 1.1E-124 | 17 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|----------|----|
| 4874 | cg43988302 | 179 | AGCAGGAACCTC CTCACCCACCC TTG/gapJGGGCC TGCCTGAGTCAT TCTCCGT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75352 SL15 PROTEIN - HOMO SAPIENS (HUMAN), 247 aa. | 3.8E-124 | 17 |
| 4875 | cg43988302 | 382 | AAACAATTGCC CAGGATAGTGT A/A/CJACAGCTG GAAATTGCTGCT AGAGGA | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75352 SL15 PROTEIN - HOMO SAPIENS (HUMAN), 247 aa. | 3.8E-124 | 17 |
| 4876 | cg43303925 | 1244 | TTGGTTACAAGA TCCAGACTTGGG C/C/TJGAGCGGT CCCCAGCCCTCT TCATGT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD40851 SIRTUIN TYPE 3 - HOMO SAPIENS (HUMAN), 399 aa. | 4.4E-124 | 11 |
| 4877 | cg43920467 | 661 | AGAGAAAGCCATG AGTTTCCACCAG C/A/GJGACAGT GAGTCCTGAGCA CAACAC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q06136 FOLLICULAR VARIANT TRANSLLOCATION PROTEIN 1 PRECURSOR (FVT-1) - Homo sapiens (Human), 332 aa. | 4.9E-124 | |
| 4878 | cg43920467 | 779 | AAAGAAAGAGAG AGAGAGAGAGA G/A/CJGAGAGAG ACAGAGAGACAG AGAGACA | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q06136 FOLLICULAR VARIANT TRANSLLOCATION PROTEIN 1 PRECURSOR (FVT-1) - Homo sapiens (Human), 332 aa. | 4.9E-124 | |
| 4879 | cg43927337 | 992 | GCAAGATGAATG GGAAAGAAAATA TTT/gapJAGCTTAA GATCTGTTTGCA AATGGA | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa. | 1.1E-123 | 14 |
| 4880 | cg43927337 | 1300 | TGCACTGAGTCA GCTCAAGTGTGC C/A/gapJAAAAAA AAAAAAAAAAAA CAAAACAC | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa. | 1.1E-123 | 14 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|---|---------------------------|----|
| 4881 | cg43927337 | 1318 | GTGTGCCAAAAA AAAAAAAAAAAA A[A/gap]CAAACA CCAACAACAAC AAACAAA | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa. | 1.1E-123 | 14 |
| 4882 | cg43927337 | 830 | TGGGAAGCAAGT GGTCTGAGGGC TC[A/G]GCTGGG ACTGGGAGGGA AAGGGCTA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa. | 1.1E-123 | 14 |
| 4883 | cg43948130 | 519 | TTGTGGTTTTTG TTTTTAAAAAAA [A/gap]GGCCCCC AGGGCAAGTTAT TTACAG | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13243 SPLICING FACTOR, ARGININE/SERINE-RICH 5 (PRE-MRNA SPLICING FACTOR SRP40) (DELAYED-EARLY PROTEIN HRS) - Homo sapiens (Human), 272 aa. | 2.4E-123 | 14 |
| 4884 | cg43948130 | 519 | TGTGGTTTTTGT TTTTTAAAAAAA [gap/A]GGCCCCC AGGGCAAGTTAT TTACAG | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13243 SPLICING FACTOR, ARGININE/SERINE-RICH 5 (PRE-MRNA SPLICING FACTOR SRP40) (DELAYED-EARLY PROTEIN HRS) - Homo sapiens (Human), 272 aa. | 2.4E-123 | 14 |
| 4885 | cg44026811 | 296 | GAGAACAGTTTC ACAATAAATAAT C[G/A]CTTCTCTA AACTGTACAAA TCCTA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03229 ENDOTHELIN 3 PRECURSOR, PLACENTAL SUBTYPE (ET-3) - HOMO SAPIENS (HUMAN), 224 aa. | 2.7E-123 (20q13.2) | 20 |
| 4886 | cg44003626 | 138 | GGCCTCCAGCTA TGGGGTCCAGG GTIC/TTTGAACCT CAGGGCCTGGC AGCTTCA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15025 MRNA (HA1652) FOR ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 296 aa (fragment). | 2.7E-123 | |
| 4887 | cg44003626 | 690 | CATCTCAGCCTC TCATCCAGCTGA G[G/gap]CTCTGG CCACACCGTGCA AGTGGCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15025 MRNA (HA1652) FOR ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 296 aa (fragment). | 2.7E-123 | |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|----------|----------|
| 4888 | cg43271722 | 241 | CAGCTGGGGAG GCCCCGCTTGT TC[C/A]GACCAAG ATTCCCGGAAGC ACCAGC | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SP TREMBL-ACC:O60795 DNA SEQUENCE FROM COSMID 398G5 FROM A REGION OF THE TIP OF THE SHORT ARM OF CHROMOSOME 16, SPANNING 2MB OF 16P13.3. CONTAINS RAR (RAS LIKE GTPASE) LIKE - HOMO SAPIENS (HUMAN), 236 aa (fragment). | 3.1E-123 | |
| 4889 | cg43973009 | 961 | ACAAATGAATCT GTGGATGCATCA A[C/G]CTATCGTC AGTCAAACCCCT TTAAA | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P19075 TUMOR- ASSOCIATED ANTIGEN CO-029 - Homo sapiens (Human), 237 aa. | 3.4E-123 | 12 |
| 4890 | cg44028574 | 2334 | TCGGAACCATCA GCAGAGCCCCA GG[C/G]AGAGTC CTCACCTAAGGG GCTGGTG | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI-15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa. | 4E-122 | 20 |
| 4891 | cg44028574 | 939 | CAAAAGTCATGA GTCCCTGGCTTG G[C/gap]CCCACC ACCTGGTGACTC CCGTCCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI-15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa. | 4E-122 | 20 |
| 4892 | cg43986720 | 1022 | TCTTCGCCGGGA CATCTGCCAGTG G[C/T]CTCCTGG GCAACTCAGAAG CAGGTG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa. | 1.1E-121 | 6 (6p12) |
| 4893 | cg43986720 | 1723 | GTGCTGGGTCTCAC CCGCCCGGGAA TG[C/gap]TTCCG CCGGAGTCTCG CCCTCCCGA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa. | 1.1E-121 | 6 (6p12) |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|----------|----------|
| 4894 | cg43986720 | 1740 | CGGGAATGCTTC CGCCGGAGTCT CG[C/gap]CCTCC GGACCCAAAGTG CTCTGGGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa. | 1.1E-121 | 6 (6p12) |
| 4895 | cg43986720 | 45 | AATTAAATTCCTT AATACAAAATGC[T/gap]TTTTTTTT TTTAAGATATATC TGT | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa. | 1.1E-121 | 6 (6p12) |
| 4896 | cg43986720 | 540 | TCAGGGAGAGA GAGATTGGAAC ATTA/GJAATTTTA TATACAAAACC GGTACA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa. | 1.1E-121 | 6 (6p12) |
| 4897 | cg43986720 | 57 | TAATACAAAATG CTTTTTTTTTTTT[T/gap]AAGATATA TCTGTATTTCTTT GTCG | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa. | 1.1E-121 | 6 (6p12) |
| 4898 | cg43986720 | 657 | ATACTGAAAAA AACCCCTACTCTT TJA/TATTAATAA ACTGTTTTAATTT CTA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa. | 1.1E-121 | 6 (6p12) |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|----------|----------|
| 4899 | cg43986720 | 658 | TACTGAAAAAAA ACCTACTCTTT AATTTTAAATTA ACTGTTTAAATT CTAA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa. | 1.1E-121 | 6 (6p12) |
| 4900 | cg43114691 | 2497 | GATCTGTGTGTC TTTTTTCAGAAAC [G]ATCTGTGACA GGCCCATCAATT TTGA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13109 MELANOMA UBIQUITOUS MUTATED PROTEIN - HOMO SAPIENS (HUMAN), 438 aa (fragment). | 8E-121 | 19 |
| 4901 | cg43932788 | 602 | AACAGCTAGATC AATTTTAGAGAT G[G]gap]CCTAAT AGGCTGGGAA ACAAGTTA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75940 30KDA SPLICING FACTOR - HOMO SAPIENS (HUMAN), 238 aa. | 8.4E-121 | 10 |
| 4902 | cg43958446 | 375 | ATGGAGAGCTCC TCAGCAGGCGG CC[G]A]GGGAGA AGTCAGCCCCAC AGCGGGG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O43089 HYPOTHETICAL 73.5 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 650 aa. | 3.1E-120 | |
| 4903 | cg43923128 | 2111 | TCAAAATTCAG ATATTTTTTTTTT T[gap]GTTCCCT TCTACATAAAAA CCTCA | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa. | 3.2E-120 | 1 |
| 4904 | cg43923128 | 2825 | ACATCTTTTCTTC TGGGCAATAGTA [G]gap]GCCTGGT CTGAAGTCTTAG GTCAAT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa. | 3.2E-120 | 1 |
| 4905 | cg43923128 | 2826 | CATCTTTTCTTCT GGGCAATAGTAG [G]gap]CCTGGTC TGAAGTCTTAGG TCAATT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa. | 3.2E-120 | 1 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|----------|----|
| 4906 | cg43933691 | 1085 | CTGGGCACTCTCT TCTGAGTCTTCT TTC/TCGCATTCA TTTTGGATGTTA ACTTG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14976 PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 248 aa. | 4.1E-120 | 2 |
| 4907 | cg43004093 | 527 | GCTGGGCCAGC TAACCCCTCTGTG TC[G/C]CCTTGG GCAAACAGCCTT CCGGCCG | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa. | 6.6E-120 | |
| 4908 | cg43004093 | 564 | CAGCCTTCGGCC CGCCGGTTTCATT A[G/T]CGTGAAGA TGTTGGAGCGCC GCTTG | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa. | 6.6E-120 | |
| 4909 | cg43963595 | 1291 | TAGAAAGTGCC GTGGAGCCGGC AG[G/gap]JAGGCC CCGCCCGCGCT AGAGAACCA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa. | 8.5E-120 | 17 |
| 4910 | cg43963595 | 1441 | GGCGGCACTCC GCAACGCGTTCC TA[T/C]GTACACC ACCTCCCCCTTCG GCCCTG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa. | 8.5E-120 | 17 |
| 4911 | cg43937103 | 1465 | TTAATGTGACAG TTTTAAAGGATT IACJAGTAGGGA ATCAGAGTCCTT TGCAG | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q14696 HYPOTHETICAL PROTEIN KIAA0081 (HA1009) - Homo sapiens (Human), 233 aa (fragment). | 1.1E-119 | 15 |
| 4912 | cg43937103 | 1527 | CGACTCAATAAC CTCATTTGTTTCT IAGJAAACATTTT CTTTGATAAAGT GCCT | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q14696 HYPOTHETICAL PROTEIN KIAA0081 (HA1009) - Homo sapiens (Human), 233 aa (fragment). | 1.1E-119 | 15 |

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|------|------------|------|--|-----|---|--|--|--|--------------------------|------------------|--|----------|---|
| 4913 | cg43936370 | 957 | CTGTTGTGGAGA AGGTGGCGTTTC C[A/C]CCTTTTCC ATAATAAAATAG AAATG | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:043672 TRANSCRIPTIONAL COACTIVATOR ALY - HOMO SAPIENS (HUMAN), 233 aa (fragment). | 1.1E-119 | |
| 4914 | cg43936370 | 806 | TGTGCGGCCAAT GATGGATTGT TTC/TJTTTTATGTT TTAAATAGGAT TTAA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:043672 TRANSCRIPTIONAL COACTIVATOR ALY - HOMO SAPIENS (HUMAN), 233 aa (fragment). | 1.1E-119 | |
| 4915 | cg43950398 | 898 | AACAAATGAAA CAGATCTCTCCT T[G/T]TACATAAA ACAGCTAAAAAT TTGGC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:075545 HYPOTHETICAL 26.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 230 aa (fragment). | 1.4E-119 | 1 |
| 4916 | cg43950398 | 966 | TCATGTATTGG CTTGAAAAAAA A[gap/A]CAACAA CAAAACAAACAG TTACAAAG | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:075545 HYPOTHETICAL 26.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 230 aa (fragment). | 1.4E-119 | 1 |
| 4917 | cg43972658 | 163 | GGCAGACTCCAT GTGTGTCAAACG C[T/C]GTGCATGA ATCAGGTTTTTA GAAGG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA74894 KIAA0871 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa. | 1.8E-119 | |
| 4918 | cg43972658 | 450 | AAGAAATTTGAT TCITTCCTTTGAT [T/A]CTCTTGGGA AAGAACACATTT CCCA | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA74894 KIAA0871 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa. | 1.8E-119 | |
| 4919 | cg44002087 | 1031 | AAGAGACCACCA GCAGTGACACCT G[G/C]CAATGAC AGATGCAAGCCC AACACC | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:060712 HYPOTHETICAL 26.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 236 aa. | 2.9E-119 | |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|----------------------|----|
| 4920 | cg43256968 | 728 | TACTGAATACAT TGGTCCCTTAGA C[A/G]GCATCAAC AAGCATATTTTA AGAA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPREMBL-ACC:O60648 HYPOTHETICAL 23.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 217 aa (fragment). | 3.7E-119 | 13 |
| 4921 | cg29350504 | 200 | ATAGTTCATGAG TCAAAATTTCAAAT [T/gap]AAATGAAT GACATAATATAT AAAAAT | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05814 BETA CASEIN PRECURSOR - Homo sapiens (Human), 226 aa. | 4.7E-119 (4q21.1) | 4 |
| 4922 | cg29350504 | 251 | AAATAAAGGGAC AAAGTTCATTTT [T/gap]CCATATAA ACTCATTCAAAC ATACT | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05814 BETA CASEIN PRECURSOR - Homo sapiens (Human), 226 aa. | 4.7E-119 (4q21.1) | 4 |
| 4923 | cg43040359 | 557 | CAATAATTTATAT AAATTATTTCTT T[C]CCAAACTAG ATATTTAATAATC CAC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB45737 HYPOTHETICAL 83.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 745 aa (fragment). | 6.6E-119 | |
| 4924 | cg43271520 | 219 | TGCAGACATGCT GTCACTGCTCCA C[A/G]CATCAACG CTGGCAGTCCTT GGGGC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to REMBLNEW-ACC:G339409 T-CELL RECEPTOR GAMMA CHAIN VJCI-3(CII)- CII REGION - HOMO SAPIENS (HUMAN), 318 aa (fragment). | 7.6E-119 7 (7p15) | |
| 4925 | cg43302689 | 490 | GGGAAGCAGGG GATGGGGGAGG TAG[G/gap]CCAG GCCCGCTGGC TCAGGAGGCTC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34087 CGI-92 PROTEIN - HOMO SAPIENS (HUMAN), 265 aa. | 8.5E-119 | 9 |
| 4926 | cg44008583 | 1906 | AGAGTAGTTGAA ATCTTTAGGAAT G[A/T]ACTTCTGA GGCCCAAAAAAT GTGAC | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q15041 HYPOTHETICAL PROTEIN KIAA0069 (HA1508) - Homo sapiens (Human), 226 aa (fragment). | 9.7E-119 | |

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|------|------------|------|---|---|-----|--|--|--------------------------|------------------|---|----------|----------|
| 4927 | cg43067745 | 135 | AATGGATTCTAT TCTGACCAATAC A/C/GJACAGAAA GAGATCACAGAC TCCCTA | C | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |
| 4928 | cg43067745 | 145 | ATTCTGACCAAT ACACACAGAAAG A/G/AJATCACAGA CTCCCTACCTTA GAAGA | G | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |
| 4929 | cg43067745 | 150 | GACCAATACACA CAGAAAGAGATC A/C/TJAGACTCCC TACCTTAGAAGA AGGGA | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |
| 4930 | cg43067745 | 78 | TATTGCATTGAA AGGTCATTGCAG T/G/CJAAAGGTTG GGGATTGCTTGC TGCTA | G | C | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |
| 4931 | cg43108465 | 1231 | TATTTCCACATC ACATCACAGTTC C/C/TJAAAACGAC TTTAAAGTCTCA AAATT | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60666 HYPOTHETICAL 26.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 228 aa. | 4.8E-117 | 1 |
| 4932 | cg43108465 | 756 | TGTGATTGAATT AGTGCATGGTAA T/G/gap]CATGGC ATATACATTGCTT AAGGTG | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60666 HYPOTHETICAL 26.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 228 aa. | 4.8E-117 | 1 |
| 4933 | cg43919033 | 1057 | CATATGTGGACA CCCTCCTGTCCC C/T/gap]GGCCCC TTTCCITTTACCC CAGATT | T | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa. | 6.2E-117 | 1 (1q12) |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|----------|----------|
| 4934 | cg43919033 | 124 | CGCCATCTCTGC AGAAGAACTCCT G[A]gap]GCCACA CACAGAAGGAAA GTTGATC | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa. | 6.2E-117 | 1 (1q12) |
| 4935 | cg43919033 | 894 | TGCTATGAAACA TGTAAGAAAGTGA TTT/AJTCATGGT TTAATTGTGGAT TTTAT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa. | 6.2E-117 | 1 (1q12) |
| 4936 | cg43919033 | 895 | GCTATGAAACAT GTGAAAAGTGAT TTT/AJTCATGGT TAATTGTGGATT TTATT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa. | 6.2E-117 | 1 (1q12) |
| 4937 | cg43919033 | 896 | CTATGAAACATG TGAAAAGTGATT TTT/AJCATGGTTT AATTGTGGATT TATTA | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa. | 6.2E-117 | 1 (1q12) |
| 4938 | cg42893815 | 1119 | TTAATAAAGAA GTGGTGTTGTTTT TTA/CJCCGTGGC CAGATTTTAAAG AACTT | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD45360 APOBEC 2 PROTEIN - HOMO SAPIENS (HUMAN), 224 aa. | 8.6E-117 | 14 |
| 4939 | cg43934644 | 131 | CAGGTGACGCTC GCTCCGCTCGTC C[C]gap]GCTCGT CATGGCCTACCC GGGATAC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P28676 GRANALCIN - Homo sapiens (Human), 217 aa. | 1E-116 | 2 |
| 4940 | cg43935587 | 2560 | CGGTAAGGCTAT CATCAAGACTC TTT/AJGGCTGGTA ATAATATTCAGG TTTAT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q14141 SEPTIN 2 HOMOLOG - Homo sapiens (Human), 424 aa (fragment). | 1.3E-116 | X |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|----------|----|
| 4941 | cg43926002 | 1227 | AGATGCCATCCT CTTTCTCTTTCT [AC]GTTTGCTCA TACTACATTGAG TAGA | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa. | 1.6E-116 | 10 |
| 4942 | cg43926002 | 1321 | TCCTAAAAGCAA AATAAAAACATATT [C/T]GAATGAAAA GACAAGAAAAATC AGGT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa. | 1.6E-116 | 10 |
| 4943 | cg43926002 | 1448 | TCCTTTATTATTA TTTTTTTTTTTTTT gap[GAAAAAAGC TCATTTTCATGCT CTGC | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa. | 1.6E-116 | 10 |
| 4944 | cg43926002 | 2097 | GACACACTATCA TAGTTAACATAG TTT/gapJAAGTTCA GCACCTTGCTCA TTTTAA | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa. | 1.6E-116 | 10 |
| 4945 | cg43926002 | 2302 | TTGCTCTTCAAA CTCCAAGGTTCC C[C/T]TGTTGGCC CTCTCCCTTACC CTGGGA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa. | 1.6E-116 | 10 |
| 4946 | cg43926002 | 2402 | ATAATTTAACTAC CCTTAATTACTTT gap/AJAAAAAAA AAAAAAAAGCCTT ATGAT | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa. | 1.6E-116 | 10 |
| 4947 | cg43926002 | 2417 | CTTAATTACTTAA AAAAAAAATAAA A/gapJGCTTTATG ATTTTCATAACTT ATTG | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa. | 1.6E-116 | 10 |

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|------|------------|------|---|-----|---|--|--|--|--------------------------|------------------|--|----------|----|
| 4948 | cg43926002 | 2417 | TTAATTACTTAAA AAAAAAAAAAAAA gap/AJGCTTTATG ATTTTCATAACTT ATTG | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa. | 1.6E-116 | 10 |
| 4949 | cg42545645 | 214 | TTTCAACAAAAG C AATTTTCTAAGC A/CJTJGCTGCTG TTACCAGACACT TGAGA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76081 REGULATOR OF G PROTEIN SIGNALING - HOMO SAPIENS (HUMAN), 217 aa. | 1.6E-116 | |
| 4950 | cg42545645 | 394 | ATCTTTTATGAAC gap TGCGAATTTGGG gap/GJTCCTGCAA TGGCACTGGTAA GTGAC | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76081 REGULATOR OF G PROTEIN SIGNALING - HOMO SAPIENS (HUMAN), 217 aa. | 1.6E-116 | |
| 4951 | cg4393887 | 770 | AAGCATCTGAA T CTTTTAATGAAC T/GJTGAAAGGACA ACAGCATCTTCC CAAA | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75934 PUTATIVE SPLICEOSOME ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 225 aa. | 3.4E-116 | 1 |
| 4952 | cg43932292 | 3000 | TAAATTTTTTTG A GTCCTTTTGTAA A/GJAGAGTGTGC TGCTGTAAGAAA TCTC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q15631 TRANSLIN - Homo sapiens (Human), 228 aa. | 4.3E-116 | 2 |
| 4953 | cg43921057 | 221 | AGCCAATATAGT T TTCTTCTCCATA T/AJTAACATAAA CAGCTACAAGAA CCCT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB38041 UNR- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa. | 4.3E-116 | 12 |
| 4954 | cg43921057 | 84 | AACTAAAAACAA G TTAGATGTTTCAG A/GAJGCAGTGTA CAATGAACGAGA AATCA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB38041 UNR- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa. | 4.3E-116 | 12 |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|--|----------|---|
| 4955 | cg43258389 | 707 | GAGGGTAACTCT GCTGGACATTCC A[A/C]TTCACTCA TCTGCGTGTCCC CCACA | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:Q22412 T11G6.8 - CAENORHABDITIS ELEGANS, 658 aa. | 1.6E-115 | 5 |
| 4956 | cg42832298 | 51 | ATAACCTTTATT AAAATAGATTTA A[C]TTTAGGAAA GCTCATTTTATAT GAG | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:O75446 MSIN3A ASSOCIATED POLYPEPTIDE P30 - HOMO SAPIENS (HUMAN), 220 aa. | 2.4E-115 | 4 |
| 4957 | cg43307713 | 101 | CTGGCCCCGTCA CGGCCGCTGAA GG[C/gap]AGCAC TGCTGGGCAAG GAGAAACAA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43381 HYPOTHETICAL 42.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 374 aa. | 3.1E-115 | |
| 4958 | cg43307713 | 141 | AGGAGAAACAAG GCCACACCTGCA A[C/A]CTGGGCT GCAGGGTGAGG TGCTCC | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43381 HYPOTHETICAL 42.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 374 aa. | 3.1E-115 | |
| 4959 | cg43307713 | 33 | TTTTTTTTTTTT TTTTTACCAGAA T[A/T]GCTTTTAT TTACATACGAGA AAA | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43381 HYPOTHETICAL 42.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 374 aa. | 3.1E-115 | |
| 4960 | cg43951899 | 221 | CCCTCCAGTTT GGGGTCTAAAC C[G/A]AACAGGA GAGGTGCAGGG GACCAGG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa. | 3.3E-115 | 9 |
| 4961 | cg43951899 | 307 | GCAAGGGGTCC CAGGGCCTGGA GCC[C/gap]GAGG CCCAGCCAAAAG CACACAGCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa. | 3.3E-115 | 9 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|----------|---|
| 4962 | cg43951899 | 369 | TTTATAGTGGGAA GCTCCAGGCCCT G[C/gap]CCCTCC CCGGGGGCCTC GAGGTCGG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa. | 3.3E-115 | 9 |
| 4963 | cg43951899 | 372 | TAGTGGGAAGCT CCAGGCCCTGC CC[C/gap]TCCCC GGGGGCCTCGA GGTCGGGA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa. | 3.3E-115 | 9 |
| 4964 | cg43988647 | 1269 | TCTTTTCTCAG GCCTGAGGGGG AA[C/gap]CATTTT TGGTGTGATAAA TACCCTA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34072 CGI-78 PROTEIN - HOMO SAPIENS (HUMAN), 251 aa. | 3.8E-114 | 1 |
| 4965 | cg43989521 | 1329 | CTTCTGATTGAG CGGTGCCATGG C[C/]GGTCTCC GTGGGCACAGG TTGGGCC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q12381 PRE-MRNA SPLICING FACTOR - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 906 aa. | 5.7E-114 | |
| 4966 | cg43982971 | 1328 | AGCCAGGTGTCT TCCCGGGCCCT GC[C/gap]AGACC CTGCTCACATT CCCTCTGCT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa. | 5.7E-114 | |
| 4967 | cg43982971 | 1529 | GGCTTGGGTGG CGTCGGGGCAG GG[C/gap]GCCG AGGCTGGGAGG AAGCCCTTCT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa. | 5.7E-114 | |
| 4968 | cg43982971 | 1680 | GGTGGCTGCTG GGTGGGGCCGG GAA[C/A]AAGGG CCCCTGACCCCTG TGTGCTGG | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa. | 5.7E-114 | |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|---|----------|---------------|
| 4969 | cg43982971 | 1773 | AGCTTTGTGCCC CTGGATGCGCTA A/C/AJATCACTC TTGTTTGTCCCT GGACT | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPREMBL-ACC:P97765 VWV-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa. | 5.7E-114 | |
| 4970 | cg43948724 | 2006 | TGTGAACCTACC TGCCTTGGAGAG G/G/gap/CCCAGG TCCCAAATCTCT TCAAATT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |
| 4971 | cg43948724 | 2109 | TCAGTTTATGC CCCATTTGGATTA C/gap/TTTTTTTT TTTTTTTTTTTT ACTCT | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |
| 4972 | cg43948724 | 2159 | TTGAAAGCTTTG TTTTGTGGTAGT C/gap/G/CTTTTG GGAAGAATCCAG TATTATC | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |
| 4973 | cg43948724 | 2347 | GAAATGCTGTTA GTAAATTTCTGT G/gap/C/JATTTTTT TTTTTAAATTTGT TTTGC | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |
| 4974 | cg43948724 | 603 | GCATCAGACCTG CATTGAACAGTC C/G/JGTGGAAA GGCCAAGCAGT GACCAGG | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |

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|------|------------|-----|---|-----|---|--|--|--|--------------------------|------------------|---|----------|----|
| 4975 | cg43946376 | 139 | AGCGATATAATT TAAAAGTTTTTTT [gap]/TCATTAGAA ATAAATGTATAAA AATA | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS | 1.9E-113 | 21 |
| 4976 | cg43946376 | 341 | ATTCACCAGGAT ACGACTGTTGGA C/C/AJAGCTGCT GGAGATGGACCT GCTACC | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS | 1.9E-113 | 21 |
| 4977 | cg43946376 | 391 | CCCTCAGCAGCC TCCCCACCACAA G/A/GICAAGTGAT CTCAATGTCCTCC AAACC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS | 1.9E-113 | 21 |
| 4978 | cg43946376 | 832 | AATGTATAAACA TTCTCTGAAACC A/T/C/JAGCAGCCA TAAACAGTGCTG GTCAA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS | 1.9E-113 | 21 |
| 4979 | cg43983566 | 265 | TACAGACAAAT TGGCTTTTATCC C/T/C/JTTTGATAC CAATATATGTGT ATACA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:060487 EPITHELIAL V-LIKE ANTIGEN PRECURSOR - HOMO SAPIENS (HUMAN), 215 aa. | 3.2E-113 | 11 |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|--|----------|---|
| 4980 | cg43971133 | 1167 | TTGTTATATAGT GCTGACTTTTTT [G/T]TTTGAAT AAACAGATTGGT AACC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa. | 6.6E-113 | 4 |
| 4981 | cg43971133 | 125 | CCCCACGCGGA AGGCAACTGCCT GA[G/A]AGCGC GGCGTCGCACC GCCCAGAG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa. | 6.6E-113 | 4 |
| 4982 | cg43971133 | 40 | GCCGGCTGCCC GCCCAGTTGTTA CT[C/T]AGGTGC GCTAGCCTGCG GAGCCCGT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa. | 6.6E-113 | 4 |
| 4983 | cg43971133 | 87 | CCGTCCGTGCTG TTCTGCGGCAAG G[C/gap]CTTTCC CAGTGTCCCCAC GCGGAAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa. | 6.6E-113 | 4 |
| 4984 | cg43257585 | 161 | CGCCCCACCCT GCGCGCTCCTC CGC[gap]/GJCGGG GAAGAACCTGCG CGGCAGGAC | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60682 ACTIVATED B CELL FACTOR-1 - HOMO SAPIENS (HUMAN), 218 aa. | 1.8E-112 | |
| 4985 | cg43934153 | 159 | ATGTCCAGGAAG AAAAAGATTAC A[T/G]GCTGCTC GCAGTAAGTAGG AGCTTT | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBL-ACC:AA42945 RING1 INTERACTOR RYBP - MUS MUSCULUS (MOUSE), 226 aa. | 2.8E-112 | 3 |

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| 4986 | cg43916671 | 898 | TGAAGGCAGAAG CCCACCATGCAG A[G/gap]CTGTGA ATCTAGAGGCTC TGAGCCA | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99470 SDF2 - HOMO SAPIENS (HUMAN), 211 aa. | 5.9E-112 | |
| 4987 | cg42890336 | 1181 | ATAATAAATGCA ATTATAAACTATA [A/T]AAAAAGAGGG TGCAGAGGAGG GAATG | A | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97443 ZINC-FINGER PROTEIN BOP - MUS MUSCULUS (MOUSE), 490 aa. | 1.2E-111 | |
| 4988 | cg43980619 | 386 | TTCAATCCGTCT GTTAAGGGCAG GG[C/gap]CGGGC TAGTGGCAGGA GAAGGTCAG | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q00501 TRANSMEMBRANE PROTEIN DELETED IN VCFS - HOMO SAPIENS (HUMAN), 218 aa. | 2.1E-111 | 22 |
| 4989 | cg43942219 | 944 | GCGAGCGCGAC GCACGGCTGGC CAG[C/T]GACCCCT GCTTCAGCCCCGA CCTCAAA | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |
| 4990 | cg43942219 | 178 | GAATCCACTGGC GAAAGATGCCTT TTC/TTTAGGAAGC AGAGCTCCCTGA CTGGG | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |
| 4991 | cg43942219 | 184 | ACTGGCGAAAGA TGCCTTTCTAGG A[A/G]GCAGAGC TCCCTGACTGGG CTAAGA | A | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |
| 4992 | cg43942219 | 190 | GAAAGATGCCTT TCTAGGAAGCAG A[G/gap]CTCCCT GACTGGGCTAAG ATAGTTC | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |

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|------|------------|------|---|-----|---|--|--|--------------------------|------------------|---|----------|----|
| 4993 | cg43942219 | 208 | AAGCAGAGCTCC CTGACTGGGCTA A/G/AJATAGTTCA GATTGATCTTAG GTCAA | G | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |
| 4994 | cg43942219 | 217 | TCCCTGACTGGG CTAAGATAGTTC A/G/AJATTGATCT TAGGTCAATGGT AAGAC | G | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |
| 4995 | cg43942219 | 48 | TTTTTTTTTTTT TTTTTTTTTAA[A] /G/GAAAAAGTGT TTATTATAGGCA ACA | A | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |
| 4996 | cg43942219 | 49 | TTTTTTTTTTTT TTTTTTTTTAA[A] G/AJAAAAAGTGT TTATTATAGGCA ACAA | G | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |
| 4997 | cg43942219 | 54 | TTTTTTTTTTTT TAAAAAGAAAAA gap/AJGTGTTTAT TATAGGCAACAA CACCA | gap | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |
| 4998 | cg43957889 | 1187 | GATATGGGAAGC TTCTGTGAGTGC A/G/TAAGGATGG GGGCTGGAGTC ATTGTTA | G | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa. | 2.7E-111 | 12 |
| 4999 | cg43957889 | 1551 | ATTACAGGTGTG CACCACCACGCC T/G/AJACTAATTT TGTATTTTAGTA GAGA | G | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa. | 2.7E-111 | 12 |

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|------|------------|-----|--|---|-----|--|--|--|--------------------------|------------------|---|----------|----|
| 5000 | cg43957889 | 203 | AGGCGCAGAGT ATTGGGTTTGGC TG[<i>gap</i>]CCTCG ATTTAAAGAGAC AGAAGCTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:000577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa. | 2.7E-111 | 12 |
| 5001 | cg43957781 | 60 | CTGTTTACTTCA CTAAACCTGGA G[C/T]GAGGCAG GGAAAAGGTACA TCAATG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:075790 SEVEN TRANSMEMBRANE DOMAIN PROTEIN HOMO SAPIENS (HUMAN), 224 aa. | 3.2E-111 | 19 |
| 5002 | cg43960639 | 359 | TGCATCATGAAA CAGAGGCAGGG CC[C/ <i>gap</i>]TAAGC TGCCCAAGAGG CCTGGGCAC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB40416 P24B PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 217 aa. | 9E-111 | |
| 5003 | cg43036790 | 37 | GACCAAGCTGTC TTGTTTTGCGTA C[A/G]TCAACACT ATGCTGCTTCCA ATATT | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:075058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa. | 1.5E-110 | |
| 5004 | cg43036790 | 68 | ACTATGCTGCTT CCAATATTCCTA G[C/T]CATTCCAC AGGTAATGATTT TTCAA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:075058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa. | 1.5E-110 | |
| 5005 | cg43966282 | 846 | ACCTCCCCAGAC AGGCATTCCGAG T[G/C]GGAGGCG GGAGCACGTAC CGCAGGC | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.9E-110 | 12 |
| 5006 | cg43966282 | 880 | GAGCACGTACC GCAGGCGGAGC TAG[G/C]GAGGT CTAGATGGAGG GAGGGTCCA | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.9E-110 | 12 |

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|------|------------|-----|---|---|-----|--|--|--------------------------|------------------|---|----------|----|
| 5007 | cg43950821 | 807 | AGAGCGCGCTC ATAAAGGCAGCT GA[gap]GGGGC ACCTGCCACCCC ACTGATGC | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD41647 MAD2- LIKE PROTEIN - HOMO SAPIENS (HUMAN), 211 aa. | 3.7E-110 | |
| 5008 | cg43950821 | 811 | CGCGCTCATAAA GGCAGCTGAGG GG[G/gap]CACCT GCCACCCCACTG ATGCCCAA | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD41647 MAD2- LIKE PROTEIN - HOMO SAPIENS (HUMAN), 211 aa. | 3.7E-110 | |
| 5009 | cg43325007 | 537 | AATCAGTGTTTT ACTTCAGCAAAC G/GAACCCCTGG GATAACACCCAGT TGGA | G | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa. | 4.8E-110 | 20 |
| 5010 | cg43116651 | 791 | TGGCAAGAAAAT GGACCCACCTTT C/C/TGCACAGG ACCGGAGGCAA AGTCTGT | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD28300 DNA- BINDING PROTEIN PREB - RATTUS NORVEGICUS (RAT), 417 aa. | 1.6E-109 | 2 |
| 5011 | cg43956410 | 189 | TCCTTTCAGTTG CTGGGAGCCGT GA[G/gap]GCCCA GCCCTTTCCCT TCCTCCCA | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEIN RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa. | 7E-109 | 1 |
| 5012 | cg43956410 | 256 | GGGGCCTGGCA GGGGTGGAGTG ATG[T/gap]GATC TAAGGGTCCCTG GAGAAGGGT | T | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEIN RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa. | 7E-109 | 1 |
| 5013 | cg43956410 | 348 | GAGGTCTCAGG GCAAAGGGAAA GGT[G/T]TTTGA TGAAGACTGAGG CAGTGCC | G | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEIN RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa. | 7E-109 | 1 |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|---|----------|----|
| 5014 | cg43956410 | 366 | GAAAGGTGTTTG GATGAAGACTGA G[G/gap]CAGTGC CTACCTCCCTCC ACATCTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEIN RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa. | 7E-109 | 1 |
| 5015 | cg43928772 | 164 | TCCAGAACTAT CTTAGATGAAAT A[T/A]TTGAAGAA TTCAGTTAAATAT TTAT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa. | 8.9E-109 | 2 |
| 5016 | cg43928772 | 329 | TCCAAAGGCAG AACTTGAGCCAA G[C/G]GATAAATA TAAGCAACCAAT GGCT | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa. | 8.9E-109 | 2 |
| 5017 | cg43928772 | 500 | GTCTTAAATAAG TTGCATTTTCAT G[G/gap]CAAGCC CTCCACTGCCAG CAATGGA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa. | 8.9E-109 | 2 |
| 5018 | cg43327495 | 160 | TCAAGAAGAGGA AGAAAAGGCTCT G[C/gap]CTTATA CCATAAAATCA AGTACTC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa. | 5E-108 | 17 |
| 5019 | cg43327495 | 161 | CAAGAAGAGGAA GAAAAGGCTCTG C[C/gap]TTATAC CATAAAATCAA GTACTCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa. | 5E-108 | 17 |
| 5020 | cg43327495 | 229 | GCAGGATATTG TTTCTCCAGTTT T[C]TGGCTCTAA GAAATTACACTT TCAG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa. | 5E-108 | 17 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|--------|---------------|
| 5021 | cg43942004 | 1769 | CCGTGGTCAGA GTGCCACTGCG GGA[G/gap]CTCT GTATGGTCAGGA TGTAGGGGT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa. | 1E-107 | 5 (5q23) |
| 5022 | cg43942004 | 1932 | AGTGTCTCCCG TGTCCTCTCCCT G[C/T]CAAGTCTC AGAAGAGGTTGG GCTTC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa. | 1E-107 | 5 (5q23) |
| 5023 | cg43942004 | 2003 | TCCCTCACCCCG ATGGCCCCAGG CC[C/gap]ACAGC GTGGGAATCAG TTTCCCTT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa. | 1E-107 | 5 (5q23) |
| 5024 | cg43942004 | 2260 | CACCCACCTCAC CAAAACGATGAA G[G/T]TATGCTGT CATGGTCCTTTC TGGAA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa. | 1E-107 | 5 (5q23) |
| 5025 | cg43976960 | 966 | GCTCTCCTTTGC TTGTCTCTTTG C[C/gap]TTCGGT AATATGTATAAA CTTACAT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa. | 1E-107 | 7 (7q21.1) |
| 5026 | cg43976960 | 1076 | GTTTAGTTTGA TAATAAATCTT T[gap]GGAACCTT AAAAAGATCTAG TCTGT | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa. | 1E-107 | 7 (7q21.1) |

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|------|------------|------|--|-----|-----|--|--|--|----------------------|------------------|---|----------|---------------|
| 5027 | cg43976960 | 1087 | GATAATAAATCT TTGGAACCTTTAA ATJAAGATCTAG TCTGTTACACCA TTTA | A | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa. | 1E-107 | 7 (7q21.1) |
| 5028 | cg43976960 | 1221 | ACATTATTATTT TTCATTGTGAGA C/TACTAAAACT GTTAATCAGACT ACA | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa. | 1E-107 | 7 (7q21.1) |
| 5029 | cg43976960 | 2103 | AAATTTAAAACT GGCCTGGTTTGC Ggap/TTTTTTA TCAAGAGAGCTT AACAGA | gap | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa. | 1E-107 | 7 (7q21.1) |
| 5030 | cg43976960 | 2109 | AAAAGTGGCCTG GTTTGCCTTTT Ggap/TJATCAAGA GAGCTTAACAGA TAAAA | gap | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa. | 1E-107 | 7 (7q21.1) |
| 5031 | cg43979124 | 187 | CAAGTTGCTGTT ACAATACTGAGA A/C/AJTTCATGA AAACGGTATTTA ACAAT | C | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD43023 TRANSMEMBRANE 4 SUPERFAMILY PROTEIN - HOMO SAPIENS (HUMAN), 204 aa. | 2.1E-107 | |
| 5032 | cg43979124 | 838 | AATACAGTAAAT TCCAGGTGCCAC C/A/GJAGCTTCAG AGACCACAAGTT TCAAA | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD43023 TRANSMEMBRANE 4 SUPERFAMILY PROTEIN - HOMO SAPIENS (HUMAN), 204 aa. | 2.1E-107 | |
| 5033 | cg43997460 | 2887 | AGCCCGAAAGAA TCTCTTGCTGCT G[C/gap]AAAGAA CAGATTTTATAT TCTTCC | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O18147 T27E9.4 - CAENORHABDITIS ELEGANS, 625 aa. | 3.5E-107 | 3 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|----------|----|
| 5034 | cg43997460 | 4010 | GACATTGTACTC AGTGGGCCTTG GG[<i>gap</i>]CCTAG CCCAGCTCTGAG CAGAGGAC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O18147 T27E9.4 - CAENORHABDITIS ELEGANS, 625 aa. | 3.5E-107 | 3 |
| 5035 | cg43933543 | 205 | TAAGGGTTGGGT CTCCTGATGAAC T[C/A]TAAGTACC CAGTAAGCTCTT CTCTT | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34113 CGI-118 PROTEIN - HOMO SAPIENS (HUMAN), 212 aa. | 3.5E-107 | 6 |
| 5036 | cg43933543 | 45 | TTTTTTTTTTTT TTTTTTTTTACA[C/T]ATCTGCAGC AGATTTTATTAG ATG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34113 CGI-118 PROTEIN - HOMO SAPIENS (HUMAN), 212 aa. | 3.5E-107 | 6 |
| 5037 | cg43948067 | 1147 | TCCTCTGTTTAA GTTAGATCACTT C[A/T]TTCTCAG GTAATGACTTTA TTTT | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa. | 4.5E-107 | 20 |
| 5038 | cg43948067 | 1148 | CTTCTGTTAAG TTAGATCACTTC A[T/A]TTCTCAGG TAATGACTTTATT TTTT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa. | 4.5E-107 | 20 |
| 5039 | cg43948067 | 1149 | TTCTGTTAAGTTT AGATCACTTCATT T/A]TCTCAGGTA ATGACTTTATTTT TTT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa. | 4.5E-107 | 20 |
| 5040 | cg43948067 | 1150 | TCTGTTAAGTTA GATCACTTCATT T/A]TCTCAGGTA TGACTTTATTTT TTC | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa. | 4.5E-107 | 20 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|-------------------|----|
| 5041 | cg43948067 | 1413 | GGTTTATAGCAT AGTAAGGTATTT T[A/G]CACAAAAT ATATTTTAAACT ACAC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa. | 4.5E-107 | 20 |
| 5042 | cg43948067 | 1614 | CCTTAAGGAGAC TGAATATCAATA C[C/gap]AGTTTC CAAGGAGTTCTT GTTGAAT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa. | 4.5E-107 | 20 |
| 5043 | cg43948067 | 1789 | TTATCAAAAAAAA AAAAA A[gap]CTACCCAA AATATAGTTGTAT TTTT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa. | 4.5E-107 | 20 |
| 5044 | cg43948067 | 65 | TTTATTAAACAAA GTTTTCCTTAAT T[C]CACATTTCAA CTTTATTAAATAG TC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa. | 4.5E-107 | 20 |
| 5045 | cg43260407 | 446 | TGCTGCTGTTTA CACAAGTCCAGA C[G/A]CTGCCAG GGCCTGTTGGG ATCAGCT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P28650 ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (EC 6.3.4.4) (IMP- ASPARTATE LIGASE) - Mus musculus (Mouse), 457 aa. | 5.6E-107 | 14 |
| 5046 | cg43260407 | 479 | GGCCTGTTGGG ATCAGCTCAGTC TG[C/T]GACTAAA ACAGCTGGATCA TCGACT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P28650 ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (EC 6.3.4.4) (IMP- ASPARTATE LIGASE) - Mus musculus (Mouse), 457 aa. | 5.6E-107 | 14 |
| 5047 | cg43967668 | 789 | GGTAGGCCCCC CAGAGCTCCATG CT[C/G]GTGCGC GGCGGGGGCT GCTGCTGC | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa. | 5.6E-107 3 (3p22) | |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|----------|-----------------|
| 5048 | cg43967668 | 790 | GTAGGCCCCC AGAGCTCCATGC TC[G/C]TGC GCG GGCGGGGGCTG CTGCTGCC | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05452 TETRANECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa. | 5.6E-107 | 3 (3p22) |
| 5049 | cg43967668 | 845 | GCGGGTCTGGG TCCGAACGCAGT GA[G/gap]CAGCC ACGGCCCCAGGC TGCACGTCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05452 TETRANECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa. | 5.6E-107 | 3 (3p22) |
| 5050 | cg43297716 | 3201 | GGCTGGCTGCATG TCCCCCAGGATG G[G/gap]CTTCGA GAAAGACAAACT TGCTCTGG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P15018 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION- STIMULATING FACTOR) (D FACTOR) (MELANOMA-DERIVED LPL INHIBITOR) (MLPLI) - Homo sapiens (Human), 202 aa. | 1.2E-106 | 22 (22q12.1) |
| 5051 | cg43297716 | 3952 | AGCACATGGCCTT TGGGTGACAAAT TT[C]CTCTTTGA TGAATGTACCCCT GTGGG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P15018 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION- STIMULATING FACTOR) (D FACTOR) (MELANOMA-DERIVED LPL INHIBITOR) (MLPLI) - Homo sapiens (Human), 202 aa. | 1.2E-106 | 22 (22q12.1) |
| 5052 | cg43297716 | 992 | GGGGCCTGTC CAAGGGTGGCT GGG[G/gap]CCCA GGGCATCGCTAA ACCCAAATG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P15018 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION- STIMULATING FACTOR) (D FACTOR) (MELANOMA-DERIVED LPL INHIBITOR) (MLPLI) - Homo sapiens (Human), 202 aa. | 1.2E-106 | 22 (22q12.1) |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|---|----------|---------------|
| 5053 | cg43269003 | 1190 | CAAAAGGATAAA AATGTGAACGAA GTTgapJTAAACAT TCTGACTTGATA AAGCTT | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34784 HYPOTHETICAL 127.9 KD PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 1181 aa. | 1.2E-106 | |
| 5054 | cg43924804 | 89 | GCGCAGGAGGA GGAGGAGGCCG TGG[Ggap]CGAC GGCGATGGCGA CGGGGACGCG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O48696 F3I6.23 PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 525 aa. | 5E-106 | 6 |
| 5055 | cg43982339 | 1043 | ACAGTGGCAAAA ATGAAAAA A[gap/A]TAAAAAT TATAAAAGAGGC AAAAAA | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa. | 1.7E-105 | 12 (12q22) |
| 5056 | cg43982339 | 1043 | ACAGTGGCAAAA ATGAAAAA A[gap/A]TAAAAAT TATAAAAGAGGC AAAAAA | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa. | 1.7E-105 | 12 (12q22) |
| 5057 | cg43982339 | 1087 | AAAAAAGACAC ACTATTCTCTGC C[gap/C]TCTAAA ACACAATTAAAT AAAAGAA | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa. | 1.7E-105 | 12 (12q22) |
| 5058 | cg43982339 | 153 | AACATCTCCCAT CTCTCTGGATTT CTTCTTTTGGCTT CATTATTCCTGC TAACC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa. | 1.7E-105 | 12 (12q22) |

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|------|------------|-----|--|-----|--|--|--------------------------|------------------|---|----------|----|
| 5059 | cg43995374 | 110 | AAGATACGAGAT C CCCGCTGCCCTTG GTC[gap]AATTCT GTTATCAGAAAG ATAGTGA | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa. | 2.8E-105 | 11 |
| 5060 | cg43995374 | 22 | AGGAATAGAAAA A TTTTTTGTA[A/G] TATGGAAGTTGT AAAGCTGTGTTT T | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa. | 2.8E-105 | 11 |
| 5061 | cg43995374 | 384 | CCCAGCCCATGCC gap CTCTCCCCACCA C[gap]/A]AGCACC CCGCCTGACCCT AGTGTC | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa. | 2.8E-105 | 11 |
| 5062 | cg43995374 | 385 | CCCAGCCCATGCC gap TCTCCCCACCCAC A[gap]/A]GCACCC CGCCTGACCCTA GTGTCCA | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa. | 2.8E-105 | 11 |
| 5063 | cg43995374 | 385 | CCCAGCCCATGCC gap TCTCCCCACCCAC A[gap]/A]GCACCC CGCCTGACCCTA GTGTCCA | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa. | 2.8E-105 | 11 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|---|----------|----|
| 5064 | cg43995374 | 385 | CCCAGCCATGCC TCTCCGCACAC A[gap/A]GCACCC CGCCTGACCCTA GTGTCCA | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa. | 2.8E-105 | 11 |
| 5065 | cg43995374 | 741 | AGGAAGAAATGG AAATATCTGTGC A[gap/G]GGCCCA AGCCCGGCCTG GTGCGGGA | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa. | 2.8E-105 | 11 |
| 5066 | cg44005345 | 2155 | CAGCTGAAATTT GTTTCATAGCTG TTT[C]GGTCACCC AGTTCTAGCCAA CCAGG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14493 CPE- RECEPTOR - HOMO SAPIENS (HUMAN), 209 aa. | 5.8E-105 | |
| 5067 | cg44005345 | 2837 | GGTCACACTCAT CTGGTAGTGCAT G[C/gap]CGACGC GCTCCCGGTGCT GAAAGTC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14493 CPE- RECEPTOR - HOMO SAPIENS (HUMAN), 209 aa. | 5.8E-105 | |
| 5068 | cg44005345 | 417 | CAGCCTTCCAGG TCCTCAACTCCC G[C/T]GGACGCT GAACAATGGCCT CCATGG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14493 CPE- RECEPTOR - HOMO SAPIENS (HUMAN), 209 aa. | 5.8E-105 | |
| 5069 | cg43988395 | 981 | TGCAGCAAGTGC CCAGCAGAGCT GC[T/C]GCGCTAT CTGGCATTCTG CGAGGG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60443 ICERE-1 - HOMO SAPIENS (HUMAN), 234 aa. | 1.5E-104 | 7 |

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|------|------------|------|---|---|-----|--|--|--------------------------|------------------|--|----------|----|
| 5070 | cg44912062 | 810 | GGACCGCTGTG GACCTCGGAC CTG[G/gap]ACGC CGTCTGGCTGC GCAGGAGGG | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15834 HEPATITIS DELTA ANTIGEN INTERACTING PROTEIN A - HOMO SAPIENS (HUMAN), 202 aa. | 1.5E-104 | 11 |
| 5071 | cg44912062 | 836 | ACGCCGTCCTG GCTGCGCAGGA GGG[G/gap]CCGC TGGCATGGACTA AGAAATCCT | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15834 HEPATITIS DELTA ANTIGEN INTERACTING PROTEIN A - HOMO SAPIENS (HUMAN), 202 aa. | 1.5E-104 | 11 |
| 5072 | cg43963123 | 1068 | GCCAGGTGCCT GCATCTCACTGG TG[C/T]GGCCGT GGCACCTGAGG GAGCCAC | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.7E-104 | 17 |
| 5073 | cg43963123 | 343 | TCCTTTTTTTTT TTTTTTTTTTTTT GJTTTAAGAACA AAAGCTTTACTC GT | T | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.7E-104 | 17 |
| 5074 | cg43963123 | 346 | TTTTTTTTTTTT TTTTTTTTTTTTT GJTAAGAACA GCTTTACTCGTG CT | T | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.7E-104 | 17 |
| 5075 | cg43963123 | 449 | CCCTCCATGGAA GGCACCCAGGCG GG[G/C]AGGTGG GTCTGCTGGGAT GGGCAGG | G | C | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.7E-104 | 17 |
| 5076 | cg43963123 | 739 | CGGCGTCCCCC ACAAAGCCTGCC AG[G/gap]CTGAG CCCTTGCAATGG CCGTGGCT | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.7E-104 | 17 |

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|------|------------|------|--|---|-----|--|--|--------------------------|------------------|---|----------|--------------------|
| 5077 | cg43963123 | 941 | CTGGGTCGGGG GGAGGGGCACT GCG[G/gap]CCCT GGCCATCAGCCT GGCTGTCTT | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.7E-104 | 17 |
| 5078 | cg43988007 | 1549 | AGGTAGTTTTTA GTGGTTTGGGT TTC[G]TGTGTGTG TGCATGCCCTGTG CTTTT | C | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q92605 MYELOBLAST KIAA0206 - HOMO SAPIENS (HUMAN), 193 aa (fragment). | 3.6E-103 | 5 |
| 5079 | cg43988007 | 315 | AAATTGAGTCCA TCAGCTGTAAAT AIC[gap]AATTTTA TATTGGCTCAA GTGGCT | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q92605 MYELOBLAST KIAA0206 - HOMO SAPIENS (HUMAN), 193 aa (fragment). | 3.6E-103 | 5 |
| 5080 | cg43934831 | 1109 | CTCAGTAGCCTG GGGTTGGTGCA GA[G/gap]CGTCC AGAGAGGCAAG GGCATAAAG | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60610 DIAPHANOUS 1 - HOMO SAPIENS (HUMAN), 1248 aa. | 1.9E-102 | 5 |
| 5081 | cg43934831 | 969 | GCAAAACAATTT CTCAGCCAGGA GG[C/gap]TCCAC CTCCCATTTCCT TGTAAGACA | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60610 DIAPHANOUS 1 - HOMO SAPIENS (HUMAN), 1248 aa. | 1.9E-102 | 5 |
| 5082 | cg43972159 | 894 | TGCTTGCCCTTA CCCCAGCAACG CG[G/gap]CGCGG CCAGAACCCAGAA TGCAATAA | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa. | 2.6E-102 | 7 (12q24.1) |
| 5083 | cg41045063 | 848 | GGGTGGGAGTG TGGTGGGGGGT AGT[G/T]TGTGGC AGGACAAGAGAA GGCAATTG | G | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P32970 CD27 LIGAND (CD27-L) (CD70 ANTIGEN) - Homo sapiens (Human), 193 aa. | 3.3E-102 | 19 (19p13) |

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|------|------------|-----|---|---|-----|--|--|----------------------|------------------|---|----------|----|
| 5084 | cg43943283 | 390 | AATTGAGAGCGT TTTCGCACTCCA G[G]GCTGCT CCTGGCGGCTCT GCGGCC | G | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O76994 INTRONIC PROTEIN 259 - DROSOPHILA MELANOGASTER (FRUIT FLY), 259 aa. | 1.1E-101 | 5 |
| 5085 | cg43966895 | 149 | TTTTTTTTTTTT TTTTTTTTTTTTA /TCCATTTCACT GATTTTTATTAG GG | A | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD42057 NADH:UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT - HOMO SAPIENS (HUMAN), 179 aa. | 2.3E-101 | 7 |
| 5086 | cg43999564 | 34 | AAGCTGAAAATC ACAGGCTGATAG C[C/gap]TCCATTT TAATTAATATTCT ACTAT | C | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL-TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2) (5,10- METHENYL- TETRAHYDROFOLATE SYNTHETASE) (METHENYL-THF SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa. | 2.8E-101 | 15 |
| 5087 | cg43999564 | 65 | TTTAATTAATATT CTACTATTCACT T/C]TTTTTTTGGT TTTTAAAGATGG TTT | T | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL-TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2) (5,10- METHENYL- TETRAHYDROFOLATE SYNTHETASE) (METHENYL-THF SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa. | 2.8E-101 | 15 |
| 5088 | cg43999564 | 70 | TTAATATTCTACT ATTCACITTTTT T/A]TTGGTTTTTA AAGATGGTTTTA TAT | T | A | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL-TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2) (5,10- METHENYL- TETRAHYDROFOLATE SYNTHETASE) (METHENYL-THF SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa. | 2.8E-101 | 15 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|----------|----------|
| 5089 | cg43926487 | 32 | CTCTTTTTTTTTT TTTTTTTTTTTTT/ CJCACGGAACA GCCGTTTTTATT CCA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD27715 CGI-06 PROTEIN - HOMO SAPIENS (HUMAN), 574 aa. | 3.8E-101 | 20 |
| 5090 | cg43958634 | 1217 | TAGATACAGGCA CCGAGCGTCGA GG[G/gap]CACAG CAGCAGGCCGG CCCTGTTCC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa. | 3.8E-101 | 1 (1q32) |
| 5091 | cg43958634 | 1268 | GAAGAAGGGTG GTTGAGCTCCTG GC[C/gap]TCCGG ATCTGCAGCCAC TGATGGCC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa. | 3.8E-101 | 1 (1q32) |
| 5092 | cg43958634 | 227 | ATATAAACATA GAATAAACCGCA G[G/gap]AAGAAA TATTGGTCTGGA ATTCCCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa. | 3.8E-101 | 1 (1q32) |
| 5093 | cg43958634 | 315 | TATCTCCCCCA CACTGGGGCAG GC[G/A]GCGGAA TAAGCTCCAGCG TTCATGC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa. | 3.8E-101 | 1 (1q32) |
| 5094 | cg43958634 | 341 | GCGGAATAAGCT CCAGCGTTCATG C[G/A]CCACTCAC AGGACTGCTTAC CCCCA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa. | 3.8E-101 | 1 (1q32) |
| 5095 | cg43983699 | 1819 | TTTACTGTTACAA TGTCAGCCGC C[gap/C]JAGATGG TATCTCTCTATG GAAAAA | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD20446 AP-3 ADAPTOR COMPLEX MU3A SUBUNIT - HOMO SAPIENS (HUMAN), 418 aa. | 6.2E-101 | 10 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|-------------------|----|
| 5096 | cg43983699 | 189 | TTGCTAGAGGGA AGGAGCTCCTG GCJAGJTACATTC TACTTGGATAGA AGAGAA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC: AAD20446 AP-3 ADAPTOR COMPLEX MU3A SUBUNIT - HOMO SAPIENS (HUMAN), 418 aa. | 6.2E-101 | 10 |
| 5097 | cg43983699 | 36 | TTTTTTTTTTTT TTTTTTTTTTTTTT GJTTCCTTTCATC TTTTTATTGATAG C | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC: AAD20446 AP-3 ADAPTOR COMPLEX MU3A SUBUNIT - HOMO SAPIENS (HUMAN), 418 aa. | 6.2E-101 | 10 |
| 5098 | cg43980312 | 1090 | ACACTTAGAAAT CAAAACCCACGTC AT/AJCCTTGAGA GCAGACGGCCG TTAGCA | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC: P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa. | 7.9E-101 8 (8q22) | |
| 5099 | cg43980312 | 1094 | TTAGAAATCAAA CCCACGTCATCC TT[?/gap]GAGAGC AGACGGCCGTTA GCAAAGG | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC: P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa. | 7.9E-101 8 (8q22) | |
| 5100 | cg43980312 | 2161 | TTTATCATTAAAGT TGCCAGAAATGGC T[C]CTTTAATGA AAACAAAAAACA AAGA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC: P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa. | 7.9E-101 8 (8q22) | |
| 5101 | cg43980312 | 3050 | CGCTCGCTTCCT CCTCCTGCGCCT G[C/gap]TCCCGC CGCCCGCAGCT GCGCCCCG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC: P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa. | 7.9E-101 8 (8q22) | |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|---|----------|----------|
| 5102 | cg43980312 | 521 | GACTTGGACGG CTCACAGTTTAA AA[C/G]AAAAATTA GTGGTAAATAG AAAAAG | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa. | 7.9E-101 | 8 (8q22) |
| 5103 | cg43939240 | 347 | CCTTCCCCCTCCC GGGAGTGGCAG AG[C/gap]CGGGC ACACCACAGGCA GGCCCTCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43399 HD54+INS2 ISOFORM - HOMO SAPIENS (HUMAN), 206 aa. | 1E-100 | |
| 5104 | cg43939240 | 732 | TCTCTTGGCCCC TCCCATTTCCAG A[G/gap]GCTCAA GAGCCCTTTAGG GCAGGGC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43399 HD54+INS2 ISOFORM - HOMO SAPIENS (HUMAN), 206 aa. | 1E-100 | |
| 5105 | cg43939240 | 733 | CTCTTGGCCCCCT CCCATTTCCAGA G[G/gap]CTCAAG AGCCCTTTAGGG CAGGGCA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43399 HD54+INS2 ISOFORM - HOMO SAPIENS (HUMAN), 206 aa. | 1E-100 | |
| 5106 | cg43941552 | 1041 | ACAGGGTCAGTG GAAGCCCCAAC GG[G/gap]AAAGG AAACGCCCGG GCAAAGGGT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 1.6E-100 | |

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|------|------------|------|---|---|---|--|--|--|--------------------------|------------------|---|----------|----|
| 5107 | cg43941552 | 1175 | GAGGATGGGAG TGGGCAGAGGT GGC[G/A]CCCAG GGCCCCGGGAA CTCCTGCCA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 1.6E-100 | |
| 5108 | cg42917153 | 969 | CCCCTTCTATC CTAAACACATCC A[T/A]AAAAAATG TGCTTATCACTG TGCTC | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P45973 HETEROCHROMATIN PROTEIN 1 HOMOLOG ALPHA (HP1 ALPHA) (ANTIGEN P25) - Homo sapiens (Human), 191 aa. | 2.1E-100 | 12 |
| 5109 | cg43252708 | 386 | GGGTGGCTTCT GTCCACTTGCTG A[G/T]CAACTTGT TTTCCTTTTCACA GTGG | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75679 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa. | 2.1E-100 | |
| 5110 | cg43252708 | 393 | CTTCTGTCCACT TGCTGAGCAACT T[G/T]TTTTCCTT TTCACAGTGGAT ATGAC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75679 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa. | 2.1E-100 | |
| 5111 | cg43143591 | 62 | TTATTTTATTTA CAACAGAAATGG T[G]GGCTTTATT CCTCCAATCTTA GGGA | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99966 MELANOCYTE-SPECIFIC PROTEIN 1 - Homo sapiens (Human), 193 aa. | 3.4E-100 | |
| 5112 | cg43925214 | 372 | CCTCTGCACTCG GGCGGATCGTTA A[C/A]TTCCTCAA GTTACAACTGAG TTGCT | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD44480 BUP - HOMO SAPIENS (HUMAN), 195 aa. | 4.3E-100 | 10 |
| 5113 | cg43925214 | 77 | TTTTTTTTTTTT TTTTTTTTTTTT[G /T]TGGAACAA CACCTTATTATT CA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD44480 BUP - HOMO SAPIENS (HUMAN), 195 aa. | 4.3E-100 | 10 |

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|------|------------|-----|--|---|-----|--|--|--|--------------------------|------------------|---|----------|----------|
| 5119 | cg43941550 | 372 | GCTCCCATTTCT CCAGGGTTTGTG C[C/gap]TGCGGT GTGGGCAGAAG CAGCTTCT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 5120 | cg43941550 | 472 | TCCCGTTGGGG CTTCCACTGACC CT[G/T]CTCACCG GAGGCGTCCTA GATGTAG | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 5121 | cg43941550 | 482 | GCTTCCACTGAC CCTGCTCACC GG A[G/gap]GCGTCC TAGATGTAGTAG AGCGGCA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 5122 | cg43941550 | 483 | CTTCCACTGACC CTGCTCACC GG G[G/gap]CGTCCT AGATGTAGTAGA GCGGCAC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 5123 | cg43950149 | 285 | ATATCTTGGCTG TATTATTTCTAC [C/T]GTGAGAAA GAGACTTAGTAT ATGG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa. | 7.1E-100 | 12 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|----------|---|
| 5124 | cg44925165 | 2067 | TGCCAACACCAA GCTCTGAGTTAA C[<i>gap</i>]/TJGTGCTT TCTTCTCCTGGC CCTGACA | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75672 HMGBCG PROTEIN - HOMO SAPIENS (HUMAN), 196 aa (fragment). | 7.1E-100 | |
| 5125 | cg42903839 | 860 | GTAAAGTGAATG TCTAGTATCTTCT [A/G]TTGAGAGTA CTACTATTAATTA AGC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32099 SOUL PROTEIN - HOMO SAPIENS (HUMAN), 205 aa. | 8.6E-100 | 6 |
| 5126 | cg43917034 | 1156 | GAACACTGGCAG TAGAGTGGAGG GG[C/ <i>gap</i>]/CGAAG CCACATCATCAA GGTGAGGG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62302 TESTIS EXPRESSED PROTEIN 261 (TEG-261) - MUS MUSCULUS (MOUSE), 196 aa. | 1.5E-99 | 2 |
| 5127 | cg43917034 | 65 | TTGAGTGCITTC TAGGTGCCAGG CA[C/ <i>gap</i>]/AAAGC CAGGCACTGTTA ATACAAAA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62302 TESTIS EXPRESSED PROTEIN 261 (TEG-261) - MUS MUSCULUS (MOUSE), 196 aa. | 1.5E-99 | 2 |
| 5128 | cg42646578 | 127 | TAATCAGATGTA ATAAAAACAAAT GT[A]/TTAAAATA CAAAAATGTAAT GTATT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD31085 KU70-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 288 aa (fragment). | 2.4E-99 | |
| 5129 | cg43968421 | 663 | TCCCCCGCGGA GCTGACTTCAGC AG[C/ <i>gap</i>]/CCACA GCTGTGGGGCTT CAGCAGCC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43240 HYPOTHETICAL 85.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 754 aa (fragment). | 6.4E-99 | 1 |
| 5130 | cg43327570 | 638 | TACTCCTTCAGA GCACTGCTGAAA AT[C]/GGATCAAA CGTGGAGATCCC CCAGA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75223 WUGSC:H_DJ077023.1 PROTEIN - HOMO SAPIENS (HUMAN), 188 aa. | 3.5E-98 | 7 |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5131 | cg43920704 | 16 | TTTTTTTTTTT TTCTCAAATTA TAGCATTTTATT TTCCA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:G1488414 N8 GENE PRODUCT LONG ISOFORM, N8L PROTEIN=D52 HOMOLOG/LEUCINE ZIPPER PROTEIN {ALTERNATIVELY SPLICED, CLONE HK4A1} - HOMO SAPIENS, 248 aa. | 1.2E-97 | 8 |
| 5132 | cg43925352 | 1925 | GGCCAAAGTAGCT TTTATTCTGGCT G[A/G]CAGACTG TACTTTTGTACT TTAAC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment). | 3.7E-97 | 6 |
| 5133 | cg43925352 | 2077 | TGGTTAACTTCT CCAAAATAGTGT CT[A/G]GAAGGA GTTTCTTTTCTT CTGTT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment). | 3.7E-97 | 6 |
| 5134 | cg43925352 | 2196 | CGCACTCGCCG CTCCTCTTCTCT CG[C/gap]TCCGC CTGGCGCTGG CGAAAGTCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment). | 3.7E-97 | 6 |
| 5135 | cg43925352 | 2225 | CCTGGCGCTG GCGAAAGTCAGC TC[gap/C]TCCGG GGCCTCATCGTC AAACTCAT | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment). | 3.7E-97 | 6 |
| 5136 | cg43981803 | 29 | TTTTTTTTTTT ACAACAAGCCAA [C/A]ACATATGCT TTATGGTTCTGT TTCA | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16635 TFAZZIN - Homo sapiens (Human), 292 aa. | 7.1E-97 | X |
| 5137 | cg43981803 | 31 | TTTTTTTTTTTAC AACAAGCCAA [C/A]ATATGCTTT ATGGTTCTGTTT CAAA | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16635 TFAZZIN - Homo sapiens (Human), 292 aa. | 7.1E-97 | X |

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|------|------------|------|---|---|-----|--|--|--|----------------------|------------------|--|---------|----|
| 5138 | cg43956754 | 1327 | TTCTATTCTGAAAT AACAAATTTTTT T/gap/GAAGGTCA AGTTTTTCAATG GCACA | T | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD40377 PTD014 - HOMO SAPIENS (HUMAN), 187 aa. | 1.4E-96 | 15 |
| 5139 | cg43974514 | 1202 | TTCTACCAAGGT CCAGGACTAAGG C/GA/JTTTTCTC CATAGCCTCAAC ATTTT | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:G545790 DARPP-32=DOPAMINE AND CAMP-REGULATED PHOSPHOPROTEIN - HOMO SAPIENS, 204 aa. | 2.8E-96 | 17 |
| 5140 | cg43988005 | 226 | TGGGGTCACCTG GCTTCCTGGG GA[C/gap]CCGCA AGAGGGGCAG GGAGCAGCA | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q13938 CALCIOPHOSINE - Homo sapiens (Human), 189 aa. | 3.6E-96 | |
| 5141 | cg43935925 | 1130 | GCGTCCATGGC GGCGCGAGCTG CAG[G/gap]CCAG AGCTCACGGTCT CCTCGGGCC | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa. | 4.6E-96 | 16 |
| 5142 | cg43935925 | 148 | AGAGTCTAAAT CAGCCCCAAGAAA TTC/GJAGGATCAA GAAGGGGTAAAA AGCCG | C | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa. | 4.6E-96 | 16 |
| 5143 | cg43935925 | 239 | TCACTGAACACC TGCCCAAGTGTG ATT/CJGGCTTCCA TGCAGGAGACC CAAGTG | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa. | 4.6E-96 | 16 |
| 5144 | cg43925764 | 443 | AATATCAAGACC AATCTAGACTTTT TT/GJTGCTCTTA CATGTGAAATGG ATGT | T | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAC72976 MDC-3.13 ISOFORM 1 - HOMO SAPIENS (HUMAN), 190 aa. | 7.5E-96 | 5 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5145 | cg43925766 | 911 | AAATTCGTGGTT AAAAGCTTCCTA ATCTGGGTAACA GACCATGGGAG AGATAT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC: AAC72976 MDC-3.13 ISOFORM 1 - HOMO SAPIENS (HUMAN), 190 aa. | 7.5E-96 | 5 |
| 5146 | cg42750616 | 143 | GCACCAATGGC TTTGGGCATAAT G[C/gap]CCCTCC TCCATAAGGTCC CTACCTG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC: Q99764 HYPOTHETICAL 48.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 437 aa (fragment). | 1.4E-95 | |
| 5147 | cg43971745 | 1252 | CAGACAGGAAGA GACCACCCCCC CC[gap/C]AAAAA AAGAGCCCTGAA GACCTCTG | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa. | 2E-95 | 1 |
| 5148 | cg43971745 | 1252 | CAGACAGGAAGA GACCACCCCCC CC[gap/C]AAAAA AAGAGCCCTGAA GACCTCTG | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa. | 2E-95 | 1 |
| 5149 | cg43971745 | 306 | CAGCAGGAGG CAGTGGGCTGG CAG[C/gap]CACC CTGGGCACAGAA GAGCAGACG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa. | 2E-95 | 1 |
| 5150 | cg43971745 | 307 | AGGCAGGAGG AGTGGGCTGGC AGC[C/gap]ACCC TGGGCACAGAA GAGCAGACGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa. | 2E-95 | 1 |
| 5151 | cg43971745 | 769 | TGGTCTTGGGG GGTTGTCCCCCT CC[T/C]TCTGGCC TTGGAAGACTCT TCCCTT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa. | 2E-95 | 1 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5152 | cg44924968 | 43 | TTTTTTTTTTTT TTTTTTTTTTTT[G /T]GAAAAACAAAA TAAATTTATTGCT CC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.8E-95 | 7 |
| 5153 | cg44924968 | 44 | TTTTTTTTTTTT TTTTTTTTTTTT[G G/T]AAAAACAAAA TAAATTTATTGCT CCT | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.8E-95 | 7 |
| 5154 | cg43280516 | 666 | CTTCTGGGACCT GCCGGCCTCCC GG[G/gap]CCAGC TGCCCCACCCCT GCCCATGC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43107 PRENYLATED RAB ACCEPTOR 1 (PRA1) - HOMO SAPIENS (HUMAN), 185 aa. | 6.8E-95 | 19 |
| 5155 | cg43280516 | 718 | TGTCCTGCACGG CTCTGCTGCTCG G[G/gap]CCCACA GCGCCGTCCCAT CACAAGC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43107 PRENYLATED RAB ACCEPTOR 1 (PRA1) - HOMO SAPIENS (HUMAN), 185 aa. | 6.8E-95 | 19 |
| 5156 | cg43129980 | 18 | TTTTTTTTTTTT TTTT[A/T]CCTTT CTGAAGAAAAA CTTTTAT | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA76840 KIAA0996 PROTEIN - HOMO SAPIENS (HUMAN), 848 aa. | 6.8E-95 | |
| 5157 | cg43950632 | 1046 | TTTATGTTATATG TTTACAAGCCTG[G/A]ACCCCGCGC CTCTTCCTGCGG ACGC | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa. | 2.3E-94 | 1 |
| 5158 | cg43950632 | 1047 | TTATGTTATATG TTACAAGCCTGC[A/C]CCCCGCGCC TCTTCCTGCGGA CGCG | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa. | 2.3E-94 | 1 |

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|------|------------|------|---|---|-----|--|--|--------------------------|------------------|--|---------|----------|
| 5159 | cg43950632 | 1048 | TATGTTATATGTT TACAAGCCTGCA [C/A]CCCGCGCC TCCTCCTGCGGA CGCGG | C | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa. | 2.3E-94 | 1 |
| 5160 | cg43984244 | 163 | AGTGGGATGA GTGGCATTGCT GG[G/gap]ATATG GGGTAAAGTTG ATAAGGTC | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa. | 2.9E-94 | 2 (2p23) |
| 5161 | cg43984244 | 278 | GCTCTAAAGCAG TCAGTGTACATT TT[gap]AGAGTG AAGAGGGGCATT GCAGGGT | T | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa. | 2.9E-94 | 2 (2p23) |
| 5162 | cg43984244 | 292 | AGTGTACATTT AGAGTGAAGAG GG[G/gap]CATTG CAGGGTGCTAGT CCTCTTAA | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa. | 2.9E-94 | 2 (2p23) |
| 5163 | cg43984244 | 302 | TTAGAGTGAAGA GGGGCATTGCA GG[G/gap]TGCTA GTCCTCTTAAGC TCTGACCG | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa. | 2.9E-94 | 2 (2p23) |
| 5164 | cg43984244 | 69 | ACTGAGGCACCA TATAAAGGTTTC C[G/C]GGAGTCT CTAAAGAGCTGG AGCTAC | G | C | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa. | 2.9E-94 | 2 (2p23) |
| 5165 | cg43993152 | 262 | AACTCCTAACCT CAAGTGATCCGT C[C/T]GCCCTTGG CCTCCCAAAGTG CTGGGA | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27746 CGI-37 PROTEIN - HOMO SAPIENS (HUMAN), 180 aa. | 3.7E-94 | |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|--|---------|-----------------|
| 5166 | cg43993152 | 270 | ACCTCAAGTGAT CCGTCCGCCTTG G[C/gap]CTCCCA AAGTGCTGGAT TACAGGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27746 CGI-37 PROTEIN - HOMO SAPIENS (HUMAN), 180 aa. | 3.7E-94 | |
| 5167 | cg43018426 | 83 | TGTAAAAACCAA TCACCTGCACAC A[C/gap]AAATTAT GTGAAATTAGTT TATATA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P01344 INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A) - Homo sapiens (Human), 180 aa. | 4.3E-94 | 11 (11p15.5) |
| 5168 | cg43951338 | 304 | ATCTCATTTTCTA ATCATGTGCTTTI G[gap]AGACATTT AATACTATTTCAA TTAT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa. | 3.4E-93 | 10 |
| 5169 | cg43951338 | 323 | TGCTTTGAGACA TTTAATACTATTT [C/T]AATTATGCA GAGGAAATAATA TAAT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa. | 3.4E-93 | 10 |
| 5170 | cg43951338 | 455 | GTTCCCTCTCTT CAAACAGCTGGA G[C/gap]TGTACA CAGATGGAAAAA CATTGG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa. | 3.4E-93 | 10 |
| 5171 | cg43951338 | 468 | AAACAGCTGGAG CTGTACACAGAT G[G/gap]AAAAAC ATTTGGTCAGAA AGCAGCA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa. | 3.4E-93 | 10 |
| 5172 | cg43954317 | 182 | TTTCCTTTCTGAT GATTTTAAACTC[T/gap]TAAAGAAC AGGAAAGCATCT GGTAA | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55957 BH3 INTERACTING DOMAIN DEATH AGONIST (BID) - Homo sapiens (Human), 195 aa. | 3.4E-93 | |

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|------|------------|------|---|---|---|--|--|--|--------------------------|------------------|---|---------|---|
| 5173 | cg42669492 | 91 | TGAAAAACATTT CAAAACCCCTCTA A/C/TAAAGTATTT AATGAAAAATAAA TTTAT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34106 CGI-111 PROTEIN - HOMO SAPIENS (HUMAN), 199 aa. | 1.3E-92 | 5 |
| 5174 | cg43968495 | 1534 | CTGGCTCAGCCCC CCGCAGACCTG CC/C/TACCCCTT TCTGCCACCCCC TGACGG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa. | 3.4E-92 | 3 |
| 5175 | cg43968495 | 1597 | CTCCCCCAGGC CTGCTGGGCACA CC/T/C/TATGCCA TCTCCCTCTCCA ACTTCA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa. | 3.4E-92 | 3 |
| 5176 | cg43968495 | 1636 | TCTCCAACITCA TCGGCCCTCAAGC C/T/C/GTGCCCTT CCTGGCTCTACC ACCTG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa. | 3.4E-92 | 3 |
| 5177 | cg43968495 | 1646 | CATCGGCCTCAA GCCTGTGCCCTT C/C/T/TGGCTCTA CCACCTGCTTCC CCAGG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa. | 3.4E-92 | 3 |
| 5178 | cg43968495 | 1652 | CCTCAAGCCTGT GCCCTTCCTGGC T/C/T/TACCCACT GCTTCCCCCAGG GCCACC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa. | 3.4E-92 | 3 |
| 5179 | cg43968495 | 1675 | CTCTACCACCTG CTTCCCCAGGGC C/A/G/CCGCCGG GCTTGGCGGCC TACACTG | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa. | 3.4E-92 | 3 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5180 | cg43968495 | 1732 | TGGCAGCGGCC AATGGGAGCAAG AA[A]G[GCTGAAC GGCAGAAATTCT CCCCCT | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa. | 3.4E-92 | 3 |
| 5181 | cg43968495 | 1767 | CAGAAATTCTCC CCCTACTGAGGC C[G]A[GCTGAGG TACAGGCAGGG GCAGGCA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa. | 3.4E-92 | 3 |
| 5182 | cg43968495 | 2254 | TGTCAGGGGGC ACCCCAAAGAGG GG[G]gap]CACTG CCAGGTAGCTG GGGGAGTGG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa. | 3.4E-92 | 3 |
| 5183 | cg43968495 | 2286 | CAGGTAGCTGG GGGAGTGGCAT GGG[G]gap]CAGG GGCCCAGTTCTC AGCAGCAGA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa. | 3.4E-92 | 3 |
| 5184 | cg43973490 | 1222 | TCCAATAGGAGT ATACTCTTTAATA [G/C]AACTGTATT TGAATAAGAATT CCAT | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P40616 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 1 - Homo sapiens (Human), 181 aa. | 4.9E-92 | |
| 5185 | cg43973490 | 2100 | ATCTTCAGTGAT TCCTTGGCCCTTC G[G]gap]CTGCAG CTCCGAGGCGG TTTCCTCG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P40616 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 1 - Homo sapiens (Human), 181 aa. | 4.9E-92 | |
| 5186 | cg43979776 | 770 | CCCGGTGCTGC CTGCTCTCATCC AG[T/C]TTCCTGG AAGAAATTTTATT CTGTT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O09003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa. | 6.3E-92 | |

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|------|------------|-----|---|---|---|--|--|--|--------------------------|------------------|---|---------|--|
| 5187 | cg43979776 | 791 | CCAGTTTCTTGG AAGAAATTTTATT [C/T]GTTTCTCG TTTTCGGCACCA TGGA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa. | 6.3E-92 | |
| 5188 | cg43979776 | 797 | TC TTGGAAGAA TTTATTCTGTTT [C/A]TCGTTTTCG GCACCATGGAAG AAAT | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa. | 6.3E-92 | |
| 5189 | cg43979776 | 802 | GAAGAAATTTTA TTCTGTTTCTCG TT[C/T]TCGGCAC CATGGAAGAAAT GCAGA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa. | 6.3E-92 | |
| 5190 | cg43979776 | 835 | CCATGGAAGAA TGCAGAACAAAG C[C/T]GTGGTTT CTTTGTGTTTAC TCAT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa. | 6.3E-92 | |
| 5191 | cg43979776 | 856 | AAGCCGTGGTTT TC TTTGTGTTTA [C/T]TCATGGAGC GCAATTGAAATT TTCA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa. | 6.3E-92 | |
| 5192 | cg43979776 | 858 | GCCGTGGTTTTC TTTGTGTTTACT [C/T]ATGGAGCG CAATTGAAATTT CAGG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa. | 6.3E-92 | |
| 5193 | cg43979776 | 865 | TTTCTTTGTGTT TTACTCATGGAG C/T]GCAATTGAA ATTTTCAGGTAC CCTT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa. | 6.3E-92 | |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|---|---------|----|
| 5194 | cg43979776 | 887 | GAGCGCAATTGAC AATTTTCAGGTA C[C/T]CTTTCTAC ATGCTGACGTGC ATTGA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O09003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa. | 6.3E-92 | |
| 5195 | cg43980242 | 1255 | TTTTCCCTTTTTT TTTTTTTTTTTTTT gap]GTTGGCTTT GCGTTAGGATGC TC TG | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P26438 ADP-RIBOSYLATION FACTOR 6 - Homo sapiens (Human), Mus musculus (Mouse), and, 174 aa. | 1.7E-91 | 14 |
| 5196 | cg43980242 | 411 | GCAACTCCCAACG CAGGCCGCAAA GG[C/gap]GCTCT CGCGGCCGAGA GGCTTCGTT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P26438 ADP-RIBOSYLATION FACTOR 6 - Homo sapiens (Human), Mus musculus (Mouse), and, 174 aa. | 1.7E-91 | 14 |
| 5197 | cg43955549 | 222 | TGAAACATACAA ATACAGAAAAAT A[C/A]CCCATTTA ACAAATACTAGT GTAA | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA82983 KIAA1031 PROTEIN - HOMO SAPIENS (HUMAN), 940 aa (fragment). | 1.7E-91 | 16 |
| 5198 | cg43987971 | 40 | TTTTTTTTTTTT TTTTTTGGATGT G[A/T]TATTTTTT AATAGAAACCAC ATC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92535 PHOSPHATIDYLINOSITOL-GLYCAN- CLASS C (PIG-C) - HOMO SAPIENS (HUMAN), 297 aa. | 7.2E-91 | 1 |
| 5199 | cg25236776 | 735 | GCATACGGGGA CCACCTGTGTGC AC[C/gap]AGGAT GCCTGACACCAT GCTGCCCG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa. | 7.2E-91 | |
| 5200 | cg42527756 | 322 | CAAGTACTGGAG CAGCTAGCAAGC T[C/T]ACTCCCCA CTCTCCTCACTT ATCTC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q95221 PIUS - ORYCTOLAGUS CUNICULUS (RABBIT), 425 aa. | 2.4E-90 | 3 |

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|------|------------|-----|---|-----|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5201 | cg43937263 | 240 | CCCCTTGGTTGT CGATGGTGTGGA A/C/gap/ATTGGG GTGAGGGGCAA AATGCCTA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60831 JM4 PROTEIN, COMPLETE CDS (CLONE IMAGE 546750 AND LLNLC110F1857Q7 (RZPD BERLIN)) - HOMO SAPIENS (HUMAN), 178 aa. | 2.4E-90 | |
| 5202 | cg43937263 | 263 | AACATTGGGGTG AGGGGCAAAATG C/C/gap/JTAAGCA GAGCTGGAGGG AGGCAAAAT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60831 JM4 PROTEIN, COMPLETE CDS (CLONE IMAGE 546750 AND LLNLC110F1857Q7 (RZPD BERLIN)) - HOMO SAPIENS (HUMAN), 178 aa. | 2.4E-90 | |
| 5203 | cg44015091 | 194 | TATGAATTTTCTC ATGGAGATAGCA T/C/TTACATCAC AGAGCTGTTGTG AAAA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa. | 4E-90 | 9 |
| 5204 | cg44015091 | 210 | GAGATAGCATTT ACATCACAGAGC TTG/AJTTGTGAAA ATAAAATAAGAA TGAC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa. | 4E-90 | 9 |
| 5205 | cg44015091 | 231 | AGCTGTTGTGAA AATAAAATAAGA AT/CJGTACAGCA CACCTGGAATAT AAAA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa. | 4E-90 | 9 |
| 5206 | cg44015091 | 256 | GTACAGCACACC TGGAATATAAAA A/gap/AJCATCCC AATAACTTACTT GGAGCCC | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa. | 4E-90 | 9 |
| 5207 | cg43963913 | 274 | TTTTTATTATT TTTTTTTTTTTTT GJTGACACAGAC GCGGGCTTTATT AAC | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment). | 5.1E-90 | 11 |

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|------|------------|------|---|---|-----|--|--|--|----------------------|------------------|--|---------|----------------|
| 5208 | cg43963913 | 378 | CGCAACGGTTAA ACCTGGCTCGC GA[C/T]TTAGCGC AGCGCCTGGG GGAAGC | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment). | 5.1E-90 | 11 |
| 5209 | cg43963913 | 511 | CCGTGGCTTCAC ACGCACCGGAA GG[G/gap]AATCT GGGTCAGCCCT CCCTCCAAA | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment). | 5.1E-90 | 11 |
| 5210 | cg43983527 | 1599 | GCGTGCCTTTT GTGGACACAGG AG[C/gap]TCCTC CAGGAGCAGGC TGGGATCCC | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa. | 6.5E-90 | 3 (11q23.3) |
| 5211 | cg43003890 | 733 | AGGAAAGCGATG GGGCCTGCCCT GC[A/C]CACGTG GAGAGGGAGGG AGAGGGGA | A | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14613 HYPOTHETICAL 22.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 210 aa. | 1.3E-89 | 11 |
| 5212 | cg43990642 | 1182 | CCTGCCCATCCT CCCATGAGAGAC TTC/G]TTGTTAGT CAACACATCTGT AAATA | C | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O93501 NO27 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 248 aa. | 2.4E-89 | 1 |
| 5213 | cg43990642 | 2175 | TGTATTCTTGGT TCATTATAACAAA [C/T]TGTCGCTT AAATCCAAAAA AAAA | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O93501 NO27 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 248 aa. | 2.4E-89 | 1 |
| 5214 | cg43916722 | 301 | CCTGTGAGCATA TAAACACACAAA T[G/A]TATGCTG AAGTTGAAGATT AAGAT | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAC78841 MYOTUBULARIN RELATED PROTEIN 6 - HOMO SAPIENS (HUMAN), 465 aa (fragment). | 2.8E-89 | 13 |

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|------|------------|------|---|---|-----|--|--|--------------------------|------------------|---|---------|---|
| 5215 | cg43059113 | 186 | GATGCAGCTCAGG GGTACAAGGCA GTG/TTACAGG GTAGAGTGCAGC CCAAGCC | G | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa. | 7.4E-89 | 3 |
| 5216 | cg43922090 | 577 | AAAAAAGGACCC AACTCTTACTTTA [G/A]GAGTATTAG GCCTGGACTTCC CCTG | G | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa. | 5.2E-88 | 3 |
| 5217 | cg43922090 | 629 | CCGATGCAATAA AGCAAGTTTTAT A[T/gap]ACACTC CCCATATTTTTT CTAACA | T | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa. | 5.2E-88 | 3 |
| 5218 | cg43922090 | 923 | TTGCTGTCTGTC CTCCAGAACCCG T[G/gap]CCAAGG CCTCCGAGTGCC CAGTTAC | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa. | 5.2E-88 | 3 |
| 5219 | cg43922090 | 988 | AGTTACTGAGGC AGCTGGGGAAAA A[C/T]GTTGAGTA AACATGATTCTA CAATT | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa. | 5.2E-88 | 3 |
| 5220 | cg43960450 | 1307 | GGGATTTACTA TTGGTGGGCG TG[C/gap]CAGAC CCTCCCTTGCTT CAGCCAGA | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa. | 8.5E-88 | 8 |
| 5221 | cg43960450 | 1308 | GGGATTTACTAT TGGTGGGCGT GC[C/gap]AGACC CTCCCTTGCTTC AGCCAGAC | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa. | 8.5E-88 | 8 |

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|------|------------|-----|---|-----|-----|--|--|--|--------------------------|------------------|---|---------|---|
| 5222 | cg43960450 | 307 | TTGGTGTGTTGTTA GTAGGCAGGATT G[C/gap]CTTACA CTGGGGAAGAAA GACCAGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa. | 8.5E-88 | 8 |
| 5223 | cg43960450 | 308 | TGGTGTGTTAG TAGGCAGGATTG C[C/gap]TTACAC TGGGGAAGAAA GACCAGCT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa. | 8.5E-88 | 8 |
| 5224 | cg43955651 | 110 | GACAACACTCTT GAGCCTGCAGA GG[gap]CTCAG GCCACACCCACT TCTGCCGC | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa. | 1.1E-87 | 2 |
| 5225 | cg43955651 | 137 | CACGGCCACAC CCACTCTGCCG CA[G/gap]GGACT GTCTGTTGAGGA GCCGAACC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa. | 1.1E-87 | 2 |
| 5226 | cg43955651 | 139 | CGGCCACACCC ACTTCTGCCGCA GG[G/gap]ACTGT CTGTTGAGGAGC CGAACCGT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa. | 1.1E-87 | 2 |
| 5227 | cg43931874 | 307 | CTTGGAGGAGG GCTGCCAAGTGT G[G/gap]CCAGGG GACCCGGCCTC AGGTCTGT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O54745 P65 PROTEIN - RATTUS NORVEGICUS (RAT), 613 aa. | 2.4E-87 | |

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|------|------------|-----|--|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5228 | cg42556108 | 180 | TGGGCTAGAGG GAGGCAGACAT GGG[G/gap]ACCA TGAAGACCCAAA GGGATGGCC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P49913 ANTIBACTERIAL PROTEIN FALL-39 PRECURSOR (FALL- 39 PEPTIDE ANTIBIOTIC) (ANTIMICROBIAL PROTEIN CAP-18) (LL-37) - Homo sapiens (Human), 170 aa. | 2.9E-87 | 3 |
| 5229 | cg43992520 | 165 | TAAGCCTGCAGA GCTGTTTTTTTT [T/gap]CTACACA CGACAAATACTT TGATAT | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa. | 6E-87 | 11 |
| 5230 | cg43992520 | 428 | GGGAAGGGGGC CAAGAAAAAAG AA[T/C]GGCCACT CTCCTTCTGTC CTTCCC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa. | 6E-87 | 11 |
| 5231 | cg43992520 | 530 | AGAAATCAATTG CACATCTCTAGT T[C/gap]GCAAGC GTCAAAGTCACA ACAAAGTC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa. | 6E-87 | 11 |
| 5232 | cg43993006 | 58 | CGGCCGGTCCA CTTTTTTTTTTT TTA/TTAAGGTGT GAGCTTTTATTG CTTAA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43731 ER LUMEN PROTEIN RETAINING RECEPTOR - HOMO SAPIENS (HUMAN), 214 aa. | 7.7E-87 | 22 |
| 5233 | cg43970868 | 855 | TCCTGTCCCAGC CCTGCCTCCAGG G[C/gap]TCCTGG GCTGCCAGGGA CCTTCAGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA19508 Y39A1C.2 PROTEIN - CAENORHABDITIS ELEGANS, 1066 aa. | 9.8E-87 | 12 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|---------|----|
| 5234 | cg43975606 | 1106 | GAGAAATAGAAA GTCTTCAGTGAT G[G/gap]CCTACG CCAAAGCACAGG ATGGGGC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99871 X-LINKED PROTEIN STS1769 - Homo sapiens (Human), 295 aa. | 9.8E-87 | X |
| 5235 | cg43975606 | 1132 | CCTACGCCAAAG CACAGGATGGG GC[G/gap]GGCAG GAAGCCCTCTCC CAAGATCG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99871 X-LINKED PROTEIN STS1769 - Homo sapiens (Human), 295 aa. | 9.8E-87 | X |
| 5236 | cg43068353 | 118 | TGCTAGTGGTCC CTGCAGGCGCC GC[G/gap]GCGAC CGCCTCAGGGG GCCGTTGTT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa. | 1E-86 | 2 |
| 5237 | cg43918822 | 1227 | TAGGGATCACGC ATACCCAGACA G[G/gap]GCAGGC CCATCCTCAGGA GCTGCAG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa. | 1.1E-86 | 15 |
| 5238 | cg43918822 | 1266 | CAGGAGCTGCA GTCACACTCAGC CC[G/gap]GCCTG AGGCAAGGGAT GCAGGGCCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa. | 1.1E-86 | 15 |
| 5239 | cg43918822 | 220 | ACATTCCTTATTC TATTGCTTCAAA G/CJACAGTTTGT GAGAATGGAAGA TAAC | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa. | 1.1E-86 | 15 |
| 5240 | cg43918822 | 500 | AGAGTCTCCAC ATCTGCGAATGG G[G/gap]CCAATG GCACTCACTGTC TCTTCAG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa. | 1.1E-86 | 15 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5241 | cg43918822 | 508 | CCACATCTGCGA ATGGGGCCCAATG G[C/gap]ACTCAC TGTCTCTTCAGG CCCCCAC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa. | 1.1E-86 | 15 |
| 5242 | cg44018226 | 342 | GGCCAGTAGCT GCTGTGACCGA GTC[A/gap]CCAA GATGACCCACAGC AGGACCCCTT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa. | 1.6E-86 | |
| 5243 | cg44018226 | 426 | GTCACGTCGTGA AGGCAGTGTGTG C[C/gap]TCTCGG CCGGCACAGGA GGGGCCCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa. | 1.6E-86 | |
| 5244 | cg44018226 | 638 | CTTCCCTTCAG ATGTTATCTTTG G[G/gap]CCACCC GGCACTATTTT GGAATAG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa. | 1.6E-86 | |
| 5245 | cg43250258 | 617 | TGCATTTCACAG ATAAGCAGGATT CTT/gapJACATCC GGCCCCCAGTG CGTCTCGG | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34116 CGI-121 PROTEIN - HOMO SAPIENS (HUMAN), 175 aa. | 2.6E-86 | 2 |
| 5246 | cg43312336 | 2475 | AGAGTTCAGTGT TCGCAGTCGCAT ATT/ATACAACCA TGTTTCACACAG CCCTG | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43532 RIG-LIKE 7-1 - HOMO SAPIENS (HUMAN), 171 aa. | 7E-86 | 11 |
| 5247 | cg43921099 | 211 | TAAAGCTGGGTG TTGTCAGGCAAA G[C/gap]CCTTCC CTGCTGCCAGG GGTGGGAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa. | 9.7E-86 | |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5248 | cg43921099 | 213 | AAGCTGGGTGTT GTCAGGCAAAGC C[C/gap]TTCCT GCTGCCAGGGG TGGGAGCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa. | 9.7E-86 | |
| 5249 | cg43921099 | 293 | CCCTCACACCCAC GGGAGGCAGCC CA[G/A]AGGCCA CCGGCACAGGG TGGTGGCC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa. | 9.7E-86 | |
| 5250 | cg43921099 | 317 | AGAGGCCACCG GCACAGGGTGG TGG[C/gap]CCCC AGATCATACAGC AGTGGGCAC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa. | 9.7E-86 | |
| 5251 | cg43921099 | 518 | GTCAGTAGCACA TGGGCACCTGCT G[G/gap]CTTCTA GCCACTGCAGG CGGGGCTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa. | 9.7E-86 | |
| 5252 | cg43921099 | 612 | CTAAAGTGCCC TGGAGGAGTGA GC[G/A]GCTGAC TGAAGCCCTCTG GGCACAG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa. | 9.7E-86 | |
| 5253 | cg43966448 | 1167 | TACGCCTTTCAT CCCTCCTTCTAG G[G/gap]CCTATG GCAGTTCTCCCA GGATGTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa. | 1.4E-85 | 22 |
| 5254 | cg43966448 | 1205 | CTCCAGGATGT GTGGCGAGAGC CT[G/gap]GGCCA GCCCACAGCGTT CCTAGTCA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa. | 1.4E-85 | 22 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|---------|----|
| 5255 | cg43966448 | 1207 | CCCAGGATGTGT GGCGAGAGCCT GG[G/gap]CCAGC CCACAGCGTTCC TAGTCAGG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa. | 1.4E-85 | 22 |
| 5256 | cg43966448 | 1335 | CTTCCAGCTGC TGTTTTGTAAAA [G/A]AAAAAGAAA AAAGAAGCCCAA ACTA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa. | 1.4E-85 | 22 |
| 5257 | cg43966448 | 1551 | AGAAAATGATTG ATGGGCTGGG AA[C/gap]CCTGG AGAGCCTCGACT CCGGAAGT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa. | 1.4E-85 | 22 |
| 5258 | cg43966448 | 959 | TCCTGGTTCCT TGCCCGCGTGG GA[C/G]CCCAATA GAACTCAGCCCT TCCATG | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa. | 1.4E-85 | 22 |
| 5259 | cg43923303 | 170 | AAGTGTGGCACC AAAAGGTGGTAG GG[A/G]CGGCTG GGAGGGAGGA CCAGGAC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O43709 PUTATIVE METHYLTRANSFERASE (EC 2.1.1.-) - Homo sapiens (Human), 220 aa. | 2.3E-85 | |
| 5260 | cg43948718 | 276 | GATCAGTTTTGT ACAAGAGTTTTT TT[A/gap]AAAAAAA TCAAATCACAAAC AAAGCT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa. | 3.4E-84 | 17 |
| 5261 | cg43948718 | 378 | CCAGTCTGCCT CTTCACAAACAC TTG[A/ATTCGGCT CTCCTAGGCTTC CGCCT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa. | 3.4E-84 | 17 |

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|------|------------|-----|--|-----|-----|--|--|--|---------------------------------|------------------|--|---------|----|
| 5262 | cg43948718 | 466 | AAGTTAAGAGTG AGGCTGCTTCAG A[G/gap]CCCCCTG GCCCATGTGTCC ATCCAGA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa. | 3.4E-84 | 17 |
| 5263 | cg43948718 | 494 | CCTGGCCCATGT GTCCATCCAGAC T[C/gap]CCAAGT GGAGTGTAGGG CTCCAGG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa. | 3.4E-84 | 17 |
| 5264 | cg43948718 | 496 | TGGCCCATGTGT CCATCCAGACTC C[C/gap]AAGTGG AGTGAGGGCTC CCAGGGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa. | 3.4E-84 | 17 |
| 5265 | cg43934734 | 352 | ACCACCCAAAGT CCTTTCAGGACC C[C/gap]AGGCCT GGCGGCTGTAG GAGAGAGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment). | 7.1E-84 | 20 |
| 5266 | cg43934734 | 470 | CTCCAGACAGGC CGGTGAGGCTA CT[C/T]GACACCC TCACAAAGGGGA AACCCT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment). | 7.1E-84 | 20 |
| 5267 | cg43934734 | 547 | CCCGATGCGGG AGGTTTTGGGCT AG[C/gap]CCTCC CCAGATCCCCG GCCTGAGGG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment). | 7.1E-84 | 20 |
| 5268 | cg44032523 | 19 | TTTTTTTTTCAAT AAAAAA[gap]/A/C CATTATAGTCAT TTCATGTTGGT | gap | A | | | | SILENT- NONCODI NG 955 | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE). 669 aa. | 9.1E-84 | |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5269 | cg44032523 | 22 | TTTTTTTTCATT AAAAAACCCAGJT TTATAGTCATTC ATGTTGGTTGG | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE), 669 aa. | 9.1E-84 | |
| 5270 | cg43945523 | 1372 | AGATTAGCATTT TTCAACTGCTCA GTCCTCTCTT CAATCTTGGAGA CATTC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q63918 SERUM DEPRIVATION RESPONSE (SDR=SERUM DEPRIVATION RESPONSE) - MUS MUSCULUS (MOUSE), 418 aa. | 3.1E-83 | 2 |
| 5271 | cg43919539 | 267 | TCCTTTAAGAAG CCATTGATGGAC Cgap/CJTCATTG ATGGAAAGTTCT GTAAGTG | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa. | 3.5E-83 | 1 |
| 5272 | cg43919539 | 4091 | CCTCTCGGCTTA CAAGCAGGTCCT GAGJGCTCAAAA GGATGCAACCTT GACCA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa. | 3.5E-83 | 1 |
| 5273 | cg43919539 | 609 | AATAAATTTTCT TTTGTTGTGTTT C/TJGAATTTTACA GAAAAAAATACT GAC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa. | 3.5E-83 | 1 |
| 5274 | cg43919539 | 844 | GTCCAGGCCTAG GGATGTCCTTC TTC/GJGAGCCTG TGCTGGTCTAGG AAGCCT | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa. | 3.5E-83 | 1 |
| 5275 | cg43919539 | 879 | CTGGTCTAGGAA GCCTCTTCTTTA GJGgapJAATCAT TTTTTTGTCCCC CGTGAAC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa. | 3.5E-83 | 1 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|---|---------|---------------|
| 5276 | cg43989507 | 110 | ATGCCCCCAGGTG GAAGATGGTTTG C[G/A]GCTGTTCA GCAGCCACGTCT CCTGC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P36639 7,8-DIHYDRO-8- OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE) - Homo sapiens (Human), 156 aa. | 3.9E-83 | 7 (7p22) |
| 5277 | cg43988406 | 1748 | TGTTGCCAAAAT GGTGGCCTGGC TT[G/gap]TCTTCT GAACGTTTGGTT CAAATGT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E47283 DNA FOR ORF1 AND ORF2 FROM CHROMOSOME X - HOMO SAPIENS (HUMAN), 157 aa. | 5E-83 | X (Xp11.4) |
| 5278 | cg43948335 | 1456 | GAAGATTCAACA CTCTGGAAAGCT T[G/T]CAAAGATT ACTGTTCAACCGA GACAA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P38714 ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.19) (ARGININE- TRNA LIGASE) (ARGRS) - Saccharomyces cerevisiae (Baker's yeast), 643 aa. | 6.5E-83 | 6 |
| 5279 | cg43970119 | 234 | AATAATTATCTTG CGTAAAGAGAAA [A/G]GTAGAGCA CAATATATATATA TCAC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88719 CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLTRANSFERASE) (CMP- SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE) - MUS MUSCULUS (MOUSE), 432 aa. | 1E-82 | 12 |
| 5280 | cg43120215 | 256 | AGGCCACCAGG AACTGTTTTTAAA G[C/A]ATAGGC TGCACTAGGAGG AAGTTT | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P78524 P126 (P70) - HOMO SAPIENS (HUMAN), 1137 aa. | 1.3E-82 | 7 |
| 5281 | cg43120215 | 50 | TTAATATCTAAGA TAAAAA gap/[A]CCCAACCA CCAAAACAACCC ATTG | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P78524 P126 (P70) - HOMO SAPIENS (HUMAN), 1137 aa. | 1.3E-82 | 7 |

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|------|------------|-----|--|---|---|--|--|--|--------------------------|------------------|--|---------|---|
| 5282 | cg43921918 | 274 | TGAAAGAACAAA CCAGAAGAATTT TTTATTTTCAGT TAGATTTTGGAA CTTT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa. | 1.5E-81 | 1 |
| 5283 | cg43921918 | 275 | GAAAGAACAAAC CAGAAGAATTT TTTATTTTCAGT AGATTTTGGAA CTTT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa. | 1.5E-81 | 1 |
| 5284 | cg43921918 | 276 | AAAGAACAAACC AGAGAATTTTT TTTATTTTCAGT ATTTTGGAACTT TTT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa. | 1.5E-81 | 1 |
| 5285 | cg43921918 | 282 | CAAACCAAGA ATTTTTTTTCAG TTTATTTTCAGT GAACTTTTATT TAT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa. | 1.5E-81 | 1 |
| 5286 | cg43921918 | 404 | GTATGTATCTGA TCCACACAAATC CTCTCTAATTTA TTTCTGTGTAG TCCTC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa. | 1.5E-81 | 1 |
| 5287 | cg43921918 | 718 | CTGTCTTGTTAA CCTCTCTAATTTA GTAJAAATCTGTT GTTCTGTAAACT GGAC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O60613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa. | 1.5E-81 | 1 |
| 5288 | cg43283313 | 961 | GCGTCCGCTCC CCGGTCAGGAG CGCAGGCGCGA CGAGTACAGTTG CTGCTGCT | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43658 CANDIDATE TUMOR SUPPRESSOR P33ING1 - HOMO SAPIENS (HUMAN), 279 aa. | 1.9E-81 | 4 |

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|------|------------|-----|---|-----|-----|--|--|--|--------------------------|------------------|---|--------------------------|----|
| 5289 | cg43933199 | 470 | TTTGGGGGGGTT GTGCTGGGGG GA[gap/G]GGG GTTCAAATATTTA TTGTATTT | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O75293 NEGATIVE GROWTH- REGULATORY PROTEIN MYD118 (MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118) - Homo sapiens (Human), 160 aa. | 1.9E-81 | 19 |
| 5290 | cg43933199 | 475 | GGGGTGTGC TGGGGGGGAGG GGG[gap/G]TTCA AATATTTATTGTA TTTTTTGT | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O75293 NEGATIVE GROWTH- REGULATORY PROTEIN MYD118 (MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118) - Homo sapiens (Human), 160 aa. | 1.9E-81 | 19 |
| 5291 | cg44030987 | 83 | CGTAAGCAGAAT TAACCAGACAGT TTT/AJCAAACTC GAACTTTGTGTTA ATTAA | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA78495 TYPE II MEMBRANE PROTEIN SIMILAR TO CD69 - HOMO SAPIENS (HUMAN), 149 aa. | 1.9E-81 | |
| 5292 | cg43298483 | 100 | CTAGGCTGGG CTGCCCGGCTCA GC[C/gap]AGCGG GTCTAAACAGTG TGTCAGG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00423 HUEMAP - HOMO SAPIENS (HUMAN), 717 aa. | 2.5E-81 (12q13.3) | 12 |
| 5293 | cg43298483 | 215 | AGTCGGCCCCCTA GTCGTGGGGA TT[G/A]GGCCAG GGAAGGGCAGG GCGGGGCG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00423 HUEMAP - HOMO SAPIENS (HUMAN), 717 aa. | 2.5E-81 (12q13.3) | 12 |
| 5294 | cg43298483 | 340 | GGGTCGAGAG GGCGTGGCGGG CGC[C/gap]GGCC CCGCGCCCCCA GCGCCCCAGCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00423 HUEMAP - HOMO SAPIENS (HUMAN), 717 aa. | 2.5E-81 (12q13.3) | 12 |

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|------|------------|-----|--|-----|---|--|--|--|--------------------------|------------------|--|---------|----|
| 5295 | cg43076394 | 184 | ATTATATAATAA ATTCTTATGACA C/TJTGATTCCAA ATTGTATGTACG AAT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa. | 6.6E-81 | 16 |
| 5296 | cg43076394 | 227 | GTACGAAATTGGC TTGACATAATAA A/C/TJATAAACAT AAGGGCAATTTA AACAT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa. | 6.6E-81 | 16 |
| 5297 | cg43076394 | 261 | AAGGGCAATTTA AACAT AACATTGGCAGT A/G/AJTATGTA AGTCAATTCAAG GTCAG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa. | 6.6E-81 | 16 |
| 5298 | cg43076394 | 354 | TCTTTAGGAAGC AGCCCTGTAACA A/T/CJGTACATTT GTAGATCAGGG GCTAAA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa. | 6.6E-81 | 16 |
| 5299 | cg43076394 | 48 | AAAGTAGATTTT ATTACAGAGCAA A/TJTTCCTATC AATCAATGCTTT AA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa. | 6.6E-81 | 16 |
| 5300 | cg43320682 | 299 | CTGTCAAGCAGA TCTTGAGGGTTA T/G/AJGTTAAGCC TGATAACAGCCT CTTTA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment). | 6.6E-81 | |
| 5301 | cg43321624 | 432 | CAAGGGAGGGG ACAGGCACATGG AG[ap/CJTACCC GAAGTAGGGCA GGGTGTAGT | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60377 P1.11659_5 - HOMO SAPIENS (HUMAN), 188 aa (fragment). | 1.1E-80 | 9 |

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|------|------------|-----|--|---|-----|--|--|--|--------------------------|------------------|--|---------|--|
| 5302 | cg42651270 | 281 | CCGGTGAGGCC AGGGGCAGCAG TGC[G/A]GCTCA GCAGGTGCGAG GCAGGCTTA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75865 R32611_2 - HOMO SAPIENS (HUMAN), 160 aa (fragment). | 1.4E-80 | |
| 5303 | cg42651270 | 88 | TATTGAGCAGCT ACTGGGCAGTGA C[G/T]CTGCCGA GGCGGAATCC CACCACA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75865 R32611_2 - HOMO SAPIENS (HUMAN), 160 aa (fragment). | 1.4E-80 | |
| 5304 | cg42651270 | 92 | GAGCAGCTACTG GGCAGTGACGC TG[C/gap]CGAGG CGGGAATCCCAC CACAGTCC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75865 R32611_2 - HOMO SAPIENS (HUMAN), 160 aa (fragment). | 1.4E-80 | |
| 5305 | cg43969140 | 222 | ATTCCAAATTGCA GGGCCCCAGCA CA[G/C]GGCTGG GCAGGTGAGATA GGGAGGG | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa. | 1.7E-80 | |
| 5306 | cg43969140 | 274 | TGGAGGAAGTAA TCTGGCCCCAGG GC[C/gap]TCAGA GCTGTGAGATGA TATTGGGT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa. | 1.7E-80 | |
| 5307 | cg43969140 | 789 | GGCTGCAGCGG CTCTGCTGAAC TG[C/gap]GGACC CCGCCAGACGC CCACTCTCC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa. | 1.7E-80 | |

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|------|------------|-----|---|-----|-----|--|--|--|--------------------------|------------------|---|---------|----|
| 5308 | cg43270152 | 81 | TCAATTTGGCTC TTCTTGGCTAAA A[A/gap]TTCTCTG GAGGTGGTGG TGATGAT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P39877 CALCIUM-DEPENDENT PHOSPHOLIPASE A2 PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) (PLA2-10) - Homo sapiens (Human), 138 aa. | 4.6E-80 | 1 |
| 5309 | cg43336199 | 139 | TGCCCCCTTCCT AGGGTGGCGGT GG[C/gap]CTCCA GCCAGGGGGGC TTCCAGGTT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60894 MRNA ENCODING RAMP1 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.6E-79 | 2 |
| 5310 | cg43336199 | 140 | GCCCCCTTCCTA GGGTGGCGGTG GC[C/gap]TCCAG CCAGGGGGGCT TCCAGGTTA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60894 MRNA ENCODING RAMP1 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.6E-79 | 2 |
| 5311 | cg43917480 | 788 | TCCTTTAAAAG GAACAAAACTTT A[G/T]TATTTAAT TAGTTGATTTATT TAAT | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15849 THYROID RECEPTOR INTERACTING PROTEIN 3 (TRIP3) - Homo sapiens (Human), 152 aa (fragment). | 1.6E-79 | 17 |
| 5312 | cg42708544 | 123 | CACACACACACA CACACACACACA C[A/gap]CGGATT CCCCATCAAGGG GACATTT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa. | 2.6E-79 | |
| 5313 | cg42708544 | 124 | CACACACACACA CACACACACACA C[gap/A]GGATT CCCATCAAGGG GACATTTG | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa. | 2.6E-79 | |

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|------|------------|-----|---|-----|-----|--|--|----------------------|------------------|--|---------|----------|
| 5314 | cg42708544 | 341 | GAAGACTGCAGC AAAGACATCCAA A[G/gap]CCAACG GCAAGGGAAGC GTCAGCGG | G | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa. | 2.6E-79 | |
| 5315 | cg42708544 | 710 | GCTACTCAGGAG GCTGAGGCGGG AG[A/G]ATCGCTT GAACCCGGGAG GGGAGG | A | G | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa. | 2.6E-79 | |
| 5316 | cg44024149 | 880 | ATCCCTCACCCA TCCTAGAGGCCA G[G/gap]CAGGAG CCCTTCTATACC CACCCAG | G | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa. | 5.3E-79 | 1 (1p35) |
| 5317 | cg44024149 | 986 | GTGCTTAACCAA AGAAGCTGTACT C[C/T]GGGGGT CTCTTCTGAATA AAGCAA | C | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa. | 5.3E-79 | 1 (1p35) |
| 5318 | cg43963131 | 186 | CTGGGATGGATG AGTAAGAGGAG GA[A/C]GGTACA CTAGAGGCTTTG GTAAAC | A | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa. | 6.8E-79 | 6 |
| 5319 | cg43963131 | 228 | GGTAAACATCT TCTCTCCAGAG G[gap/G]TGAAGA TAAATAAACCTTA CAGAGA | gap | G | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa. | 6.8E-79 | 6 |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5320 | cg43963131 | 318 | TGGTTAGGGCA TCCAGGGGTGTC C[C/gap]TTCAC TGTGAAAGACAA ACTGTTG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa. | 6.8E-79 | 6 |
| 5321 | cg43963131 | 331 | CCAGGGGTGTC CCTTCCAATGTG AA[A/gap]GACAA ACTGTTGCATCT TGCATCCT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa. | 6.8E-79 | 6 |
| 5322 | cg43963131 | 369 | CATCTTGCATCC TCATGCAAGGAA G[G/gap]AAGCAC ACTGCCTGGTGA GCCTGTT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa. | 6.8E-79 | 6 |
| 5323 | cg43287619 | 186 | CAATTAGAAAG AAACACACTTTA A[G/A]AAATCAAA ATTCTCAATTCA GGCAG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa. | 6.8E-79 | 12 |
| 5324 | cg43287619 | 517 | TGGAGGCCGA GGTGGGTGGAT CAC[A/G]AGGTC AGGAGATCGAGA CCATCCTG | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa. | 6.8E-79 | 12 |
| 5325 | cg43287619 | 595 | TAAAAAATACAA AAAATTAGCCGG G[C/T]GTGGTGG CGGGCGCCTGT AATCCCA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa. | 6.8E-79 | 12 |
| 5326 | cg43287619 | 611 | TTAGCCGGCGGT GGTGGCGGGCG CC[C/T]GTAATCC CAGCTACTCGGG AGGCTG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa. | 6.8E-79 | 12 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5327 | cg43287619 | 615 | CCGGGCGTGGT GGCGGGCGCCT GTA[A/G]TCCCAG CTACTCGGGAG GCTGAGGC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa. | 6.8E-79 | 12 |
| 5328 | cg43918538 | 1513 | GGCCCCCAGG TGGAGTGCCTGA CA[T/C]AGGGCT CGCTCCAGAGG CGTCTGAC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa. | 8.6E-79 | 16 |
| 5329 | cg43918538 | 592 | TTATTTTACTAT TAAAAA A/gap]TCAAAGGG ACACACTGGGAA TTGAA | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa. | 8.6E-79 | 16 |
| 5330 | cg43918538 | 592 | TATTTTACTATT AAAAA gap/AJTCAAAGGG ACACACTGGGAA TTGAA | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa. | 8.6E-79 | 16 |
| 5331 | cg43918538 | 592 | TATTTTACTATT AAAAA gap/AJTCAAAGGG ACACACTGGGAA TTGAA | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa. | 8.6E-79 | 16 |
| 5332 | cg43250517 | 206 | TTTCAGATGATG GGGTCTGAGATG TTC/GTCTCTCAGG CTGCATCAGCTG TCTTC | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34037 CGI-41 PROTEIN - HOMO SAPIENS (HUMAN), 475 aa. | 1.4E-78 | |
| 5333 | cg43267341 | 968 | TTAGTCTTTTTT TTTTTTTTTTTTT[g ap/TTAATTCATC TGAATCAGAA GCGG | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa. | 1.4E-78 | |

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|------|------------|------|---|---|-----|--|--|--------------------------|------------------|--|---------|--|
| 5334 | cg43267341 | 1035 | GTCTTGTCCTG TCCCCACTCATC C[C/T]TGGTCTGG TCCCCTGTTGCC TATAG | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa. | 1.4E-78 | |
| 5335 | cg43267341 | 1056 | ATCCCTGGTCTG GTCCCCTGTTGC C[T/C]ATAGCCCT TTACCCTGAGCA CCACC | T | C | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa. | 1.4E-78 | |
| 5336 | cg43267341 | 1083 | TAGCCCTTTACC CTGAGCACACAC C[C/gap]AACAGA CTGGGACACAG CCCCCTCG | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa. | 1.4E-78 | |
| 5337 | cg43267341 | 1092 | ACCCTGAGCAC ACCCCAACAGAC T[G/gap]GGGACC AGCCCCCTCGC CTGCCTGT | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa. | 1.4E-78 | |
| 5338 | cg43267341 | 1154 | AACCCCTTTAGA TGGGAGGGAA GA[G/A]GAGGAG AGGGAGGGGA CCTGCCCC | G | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa. | 1.4E-78 | |
| 5339 | cg43267341 | 1167 | GGGAGGGGAAG AGGAGGAGAGG GGA[G/gap]GGGA CCTGCCCCCTCC TCAGGCATC | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa. | 1.4E-78 | |

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|------|------------|------|---|-----|-----|--|--|--------------------------|------------------|---|---------|----|
| 5340 | cg43267341 | 1170 | GAGGGAAGAGG AGGAGAGGGA GGG[G]gap]ACCT GCCCCCTCCTCA GGCATCTGG | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa. | 1.4E-78 | |
| 5341 | cg43267341 | 1198 | CTGCCCCCTCCT CAGGCATCTGG GA[G]gap]GGCCC TGCCCCCATGG GCTTTACCC | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa. | 1.4E-78 | |
| 5342 | cg43267341 | 1200 | GCCCCCTCCTCA GGCATCTGGA GG[G]gap]CCCTG CCCCCATGGCT TTACCCCT | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa. | 1.4E-78 | |
| 5343 | cg42535274 | 74 | CCTGCTGCCACC ACCGAGCCCTC GG[G]gap]CTCCC AGGCGGACAC GGCCACCGC | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43791 SPOP - HOMO SAPIENS (HUMAN), 374 aa. | 1.8E-78 | |
| 5344 | cg43999987 | 1703 | ACACAGCCTGTG GATCCTGGGC AT[C]T]TGGAGG GCGCACACATCA GCAGCC | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q09981 HYPOTHETICAL 107.4 KD. PROTEIN F30H5.1 IN CHROMOSOME III - CAENORHABDITIS ELEGANS, 961 aa. | 4.8E-78 | 15 |
| 5345 | cg43949675 | 116 | ACAAATCACAGC TGATAGACAGCG A[gap/A]CGCTTC CCCATAGAGACC GTGCTCC | gap | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa. | 7.8E-78 | |
| 5346 | cg43949675 | 156 | ACCGTGCTCCAA CTCGGGCCTGG GG[gap/C]ACTGC TCGCTGCTCCCA GGAAGGGG | gap | C | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa. | 7.8E-78 | |

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|------|------------|-----|---|-----|---|--|--|--------------------------|------------------|---|---------|----|
| 5347 | cg43949675 | 238 | AGAGTCCAGGGT C GGAGCGCGCCA CC[C/gap]TCAGC CAGAGCAGCCA CGACAGCCA | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa. | 7.8E-78 | |
| 5348 | cg43949675 | 910 | CCGTCCCTCAG G AAGAACGAACGT G[G/gap]CGCCGC CTCCTCTCGGGA GCTCTCT | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa. | 7.8E-78 | |
| 5349 | cg43259701 | 605 | GGACGAGTCGG G ACCGAGGCTAG GAC[G/A]TGGCC GGCGCTCTCCA GCCCTGCAG | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00496 IPL (IPL) - HOMO SAPIENS (HUMAN), 152 aa. | 1.3E-77 | 11 |
| 5350 | cg44003673 | 110 | GGGAACACCCC ACACCCACACCC TG[gap/C]CCCCC CATACCCCTTCC TCCAGGAG | gap | C | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa. | 1.6E-77 | |
| 5351 | cg44003673 | 216 | TCTCCAGTGTCT C GCTGCCTCCTCC C[C/T]GCAAAGTC TCCACAAAGCAC AGGAC | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa. | 1.6E-77 | |
| 5352 | cg44923000 | 291 | TTTGTTCTTTTA T TATATACACATA T/CJTATCTCAAA ACATAGTTATTTT TA | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA22102 Y75B8A.14 PROTEIN - CAENORHABDITIS ELEGANS, 272 aa. | 4.3E-77 | 12 |
| 5353 | cg44923000 | 294 | GTTTCTTTTATAT A ATACACATATTTT A/JTCTCAAAACA TAGTTATTTTAC TT | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA22102 Y75B8A.14 PROTEIN - CAENORHABDITIS ELEGANS, 272 aa. | 4.3E-77 | 12 |

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|------|------------|------|--|-----|--|--|--|--|--------------------------|------------------|--|---------|----|
| 5354 | cg44923000 | 665 | AGGCATGAGGCT G GATAAAGAACGA A[G/gap]TTTTACT TTTTTTCATTAA ATAAG | gap | | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA22102 Y75B8A.14 PROTEIN - CAENORHABDITIS ELEGANS, 272 aa. | 4.3E-77 | 12 |
| 5355 | cg43112852 | 1152 | CCTGACAAAGCAC T CAGATTCCATTG TTT/AJTCACGTTT TTAGAGATTTAAT TCCA | A | | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA78730 PALBH (EC 3.4.22.17) - HOMO SAPIENS (HUMAN), 813 aa. | 1.1E-76 | |
| 5356 | cg43112852 | 1153 | CTGACAAAGCAC T AGATTCCATTGT TTT/AJACCGTTT TAGAGATTTAAT CCAT | A | | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA78730 PALBH (EC 3.4.22.17) - HOMO SAPIENS (HUMAN), 813 aa. | 1.1E-76 | |
| 5357 | cg42520895 | 97 | AAGAAGGGCTCA G GCGCTCCCG CC[G/gap]GGCCG TGGACAGAGGG GCACAGTTT | gap | | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB51858 ATP-DEPENDENT METALLOPROTEASE YME1L - HOMO SAPIENS (HUMAN), 716 aa. | 2.4E-76 | |
| 5358 | cg43298234 | 1052 | GCTCCTGCCCTAC G ATCCAGGCAGAA A[G/T]ATAGGCAG GGGCTCTTGAA GACGT | T | | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.3E-75 | 7 |
| 5359 | cg43298234 | 1110 | TGTGACCTCCGA G GCCCTCCTGGTG G[G/A]AAGACAG CTGGAAAGGCTG GGAGGA | A | | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.3E-75 | 7 |
| 5360 | cg43298234 | 1147 | AAAGGCTGGGA C GGAGAAGGGAG GGG[C/T]TGGGG GTTCCAGGAGC CATGCGTG | T | | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.3E-75 | 7 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|---|---------|----|
| 5361 | cg43298234 | 1260 | CTGGAGTGGG GTGTGTTAGAGC CC[C/gap]TCACC GGGACTTGCTGT GCGGATGG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.3E-75 | 7 |
| 5362 | cg43298234 | 1287 | CACCGGACTTG CTGTGCGGATG GG[G/gap]CCTGG GCCTCCTTCCTA CAGGGGCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.3E-75 | 7 |
| 5363 | cg43298234 | 584 | CACCGACACGCT GCTGTGAGGT CC[G/C]GGTGAG ATGGAGTGGGTC ACACCTG | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.3E-75 | 7 |
| 5364 | cg43298234 | 644 | AAGAAAGTTCCC TGGGGATGGGA GA[G/T]CGGGTG GGTGCTGCCAAT CTCCAGC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.3E-75 | 7 |
| 5365 | cg43298234 | 825 | CAGTGGAGGAAA ATGTGATAAGC C/A/G/GAGCTTGT GTGCTGGGCAC AGAAAT | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.3E-75 | 7 |
| 5366 | cg43298234 | 897 | CGCAGGCTGGG CCGGAGCCTCT GCC[C/T]GCAGG TTTCTATGCTGTT TCTTAGC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.3E-75 | 7 |
| 5367 | cg43957018 | 539 | GGAGAGCATCA GGGCAGGCCTTT AG[G/gap]CTGTT GCTCTGGGCAG GGGGTGGG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD44697 MUM2 - HOMO SAPIENS (HUMAN), 145 aa. | 2.1E-75 | 17 |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5368 | cg43973471 | 128 | TCCTGAGAACAA ACAAGTAGGCCT G[C/T]TCCTCTCA CCACGTGCTTGT TTATT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14834 DIM1P HOMOLOG - HOMO SAPIENS (HUMAN), 142 aa. | 2.1E-75 | |
| 5369 | cg43918219 | 387 | GAGACAGTGCTG GGCAATGGGG GG[C/gap]CCGCA GGCCTTCTTGT GGGCTGCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q21992 SIMILARITY TO LUPUS LA PROTEINS - CAENORHABDITIS ELEGANS, 1356 aa. | 8.2E-75 | 5 |
| 5370 | cg43918219 | 56 | ATGGTCGATTTT GTCCTTTTCTTC T[[T/gap]TTTTTCC CCATTTTTTCAA GGATG | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q21992 SIMILARITY TO LUPUS LA PROTEINS - CAENORHABDITIS ELEGANS, 1356 aa. | 8.2E-75 | 5 |
| 5371 | cg43918219 | 62 | GATTTTGTCTTTT TTCTTCTTTTTT /gap]CCCCATTTT TTCAAGGATGGA AAGG | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q21992 SIMILARITY TO LUPUS LA PROTEINS - CAENORHABDITIS ELEGANS, 1356 aa. | 8.2E-75 | 5 |
| 5372 | cg43311348 | 334 | TTTTCTGAAAA AGACAGGCCCG GG[C/gap]CCACC CAGGTCCACTT CCACTCAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76055 WUGSC:H_DJ130H16.4 PROTEIN - HOMO SAPIENS (HUMAN), 149 aa. | 1.2E-74 | 22 |
| 5373 | cg43311348 | 336 | TTCTGAAAAAG ACAGGCCCGG CC[C/gap]ACCCA GGTCCACTTCC ACTCAGCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76055 WUGSC:H_DJ130H16.4 PROTEIN - HOMO SAPIENS (HUMAN), 149 aa. | 1.2E-74 | 22 |
| 5374 | cg43311348 | 66 | TTTTTTTTTTTT TTTTTTTTTTTT /TACCTCTTCAG GATTATTGGGT CAG | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76055 WUGSC:H_DJ130H16.4 PROTEIN - HOMO SAPIENS (HUMAN), 149 aa. | 1.2E-74 | 22 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5375 | cg44012742 | 1535 | GGGTGACCACA CTGTACTTGGGG CTG[gap]GGCCC TCTGCCCTGTG TCCCATC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa. | 1.8E-74 | |
| 5376 | cg44012742 | 1537 | GTGACCACACTG TACTTGGGCTG G[G/gap]CCCTCT GCCCTGTGTCC CCATCTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa. | 1.8E-74 | |
| 5377 | cg43272466 | 714 | CCAACCCATGAG CACTCAATTCCA C[A/G]CAGGGC AATACCTCAAGC AGAGAG | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa. | 1.9E-74 | 10 |
| 5378 | cg43272466 | 752 | CTCAAGCAGAGA GAGGCTTCAG GC[C/gap]ACCCC ACTTCTGGCTCT TTCCAGTC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa. | 1.9E-74 | 10 |
| 5379 | cg43272466 | 766 | GGGCTTCAGGC CACCCCACTTCT GG[C/T]CTTTCC AGTCCTAGCAGG TAAAAG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa. | 1.9E-74 | 10 |
| 5380 | cg43984390 | 37 | TTATGTTTACCA GTTTATTACAAA C[G/A]TTATTAGA AAAGGATACAAA TAAGT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD29636 HYPOTHETICAL 15.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 134 aa. | 1.9E-74 | 20 |
| 5381 | cg43984390 | 811 | GGCCAAGGACG GAATGACAGAAG AG[T/G]TGATTAG TAACCAACATATG GCTGTT | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD29636 HYPOTHETICAL 15.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 134 aa. | 1.9E-74 | 20 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5382 | cg42670378 | 154 | TTATTTTAAATGA GAAAAAAAAAAAAA A[gap]CCCTCACA ACGTGAGATTCC TTTAC | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD31392 GLYPICAN-6 - HOMO SAPIENS (HUMAN), 555 aa. | 1.9E-74 | |
| 5383 | cg43969639 | 965 | CCACTCTGCAGT AAGGTGTTTCAA A[AT]CAGAAAAT GCACAAATGAAA AGTTA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa. | 2.3E-74 | 3 |
| 5384 | cg43969639 | 994 | AAAATGCACAAA TGAAAAGTTAAC TTC/TJCCTACAGC ATGGTGTGGCAG GGGAA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa. | 2.3E-74 | 3 |
| 5385 | cg43969639 | 995 | AAATGCACAAAT GAAAAGTTAACT CIC/TJCTACAGCA TGGTGTGGCAG GGGAAA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa. | 2.3E-74 | 3 |
| 5386 | cg43969639 | 996 | AATGCACAAATG AAAAGTTAACTC CIC/TJACAGCAT GGTGTGGCAGG GGAAAT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa. | 2.3E-74 | 3 |
| 5387 | cg43969639 | 1238 | GCCTAATAGGTA TACTCTGGAAGC CIG/AJTAACAGGA AGCTACAATCAA ATCAA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa. | 2.3E-74 | 3 |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|--|---------|--|
| 5388 | cg42332174 | 1196 | GAAAAGCTTATT CATGGCGGTGC AG[G]gap]CTGCA GCCTTCCCTCA GACCAGGA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa. | 1.4E-73 | |
| 5389 | cg42332174 | 235 | AAATTCTTCATG TCTTCTAACGTG gap/AJAAAAAAA AAATCCCATCC AATTA | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa. | 1.4E-73 | |
| 5390 | cg42332174 | 247 | TGCTTCTAAGG TGAAAAA A[A]gap]TCCCAT CCAATTAACAA CTTTCT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa. | 1.4E-73 | |
| 5391 | cg42332174 | 247 | GTCTTCTAAGT GAAAAA A[gap/A]TCCCAT CCAATTAACAA CTTTCT | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa. | 1.4E-73 | |
| 5392 | cg42332174 | 37 | CAGGATTATTA TAATGTTTCCTT T/C]TTTTTTAG CTGAAATGTATT TTTA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa. | 1.4E-73 | |
| 5393 | cg42332174 | 39 | GGATTATTATAA TGTTTCCCTTT T/C]TTTTTAGCTG AAATGTAATTTA TT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa. | 1.4E-73 | |
| 5394 | cg44007500 | 48 | TTTTTTTTTTTT TTTTTTTTTTTTT AJATTGTATAAAA TTTAAATTTTATG A | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45717 HYPOTHETICAL 17.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 153 aa (fragment). | 1.4E-73 | |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|--|---------|--|
| 5395 | cg43981873 | 942 | GGTTTGTGAA CGGCCGTCCA AA[G/A]CTGGCT GGATTCCTAGAA GAGICTG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa. | 1.7E-73 | |
| 5396 | cg43981873 | 1135 | GCCTGCAGGGTT TCCTTGGGCGC GG[C/gap]CCCAA AATTGCCCTTCAA AACAAACC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa. | 1.7E-73 | |
| 5397 | cg43981873 | 1161 | CCCAAAATTGCC TTCAAAACAAAC C[C/gap]GGGACG GTTGAAAGCCTT CGAACCG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa. | 1.7E-73 | |
| 5398 | cg43981873 | 1201 | CTTCGAACCGTG CAGGGGATGCC TT[gap/G]GGCC TGGCCCTTCGCT TCCTCTCT | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa. | 1.7E-73 | |
| 5399 | cg43981873 | 811 | TGCTCAGAAAGG AAGAGGCAGGC GC[C/gap]AGGGG GAACCCCTTCG TGTTTTGT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa. | 1.7E-73 | |
| 5400 | cg43981873 | 824 | AGAGGCAGGCG CCAGGGGGAAC CCC[C/gap]JTCG TGTTTTGTGACC CTCCCTTTT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa. | 1.7E-73 | |
| 5401 | cg44004729 | 287 | TTTTCTTGCTTGA CACTTTATTCTC[G/C]TGAGAGGG GAGGACAGCAG AGGGAG | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P22749 NKG5 PROTEIN PRECURSOR (LYMPHOKINE LAG-2) (T- CELL ACTIVATION PROTEIN 519) - Homo sapiens (Human), 145 aa. | 1.7E-73 | |

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|------|------------|------|---|---|-----|--|--|--------------------------|------------------|---|---------|----|
| 5402 | cg44004729 | 379 | CGGAGGAGCCG GCAGAGGTTGCT GA[G/C]GTTCCC GGGATCTGAGG ACAGGAGC | G | C | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P22749 NKG5 PROTEIN PRECURSOR (LYMPHOKINE LAG-2) (T- CELL ACTIVATION PROTEIN 519) - Homo sapiens (Human), 145 aa. | 1.7E-73 | |
| 5403 | cg43942549 | 2079 | AGAAGAAAGCAA GCAAGGCCGCTT C[C/gap]TGCGGC TAAGTGGACAGG CGACTGC | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q94218 CODED FOR BY C. ELEGANS CDNA CM10H5 - CAENORHABDITIS ELEGANS, 589 aa. | 2.8E-73 | 4 |
| 5404 | cg43933021 | 240 | CTTTTTTTTTT CGAAGTCCCTC [T/gap]TTTTTTT CCTTCAGTGTGG TCCTT | T | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD38506 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa. | 2.8E-73 | 13 |
| 5405 | cg43947751 | 220 | GGATCCTTTTGA GATCATGCTCCC A[C/gap]ATCTATT AAAAGATACATA AGCTTT | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P91086 CODED FOR BY C. ELEGANS CDNA YK134H12.5 - CAENORHABDITIS ELEGANS, 470 aa. | 8.6E-73 | 6 |
| 5406 | cg43048518 | 226 | GTGGATGTCATT GAGCCTTGGA GG[C/gap]CCCAG TCTGGCGGGAG AGAAATCCA | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P50416 CARNITINE O- PALMITOYLTRANSFERASE I, MITOCHONDRIAL LIVER ISOFORM (EC 2.3.1.21) (CPT I) (CPTL-L) - Homo sapiens (Human), 773 aa. | 2.5E-72 | 19 |
| 5407 | cg43048518 | 229 | GATGTCATTGAG GCCTTGAGGC CC[C/gap]AGTCT GGCGGAGAGA AATCCACAC | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P50416 CARNITINE O- PALMITOYLTRANSFERASE I, MITOCHONDRIAL LIVER ISOFORM (EC 2.3.1.21) (CPT I) (CPTL-L) - Homo sapiens (Human), 773 aa. | 2.5E-72 | 19 |
| 5408 | cg43932428 | 386 | ACAGCAGGAATG GGCTGGGGAGG GT[C/gap]CCCCG CAAGCTGGACCC CTTGTTCC | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa. | 2.5E-72 | |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5409 | cg43932428 | 426 | CCCCTTGTTCCG TTCGGCCCGTGA G[G/gap]AGAACG GAACTGGCGGC CAAGGGGA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa. | 2.5E-72 | |
| 5410 | cg42372763 | 150 | ACTGGGAAAGAT CCGAGGTCAGG AA[T/G]AGGCC GTCAATCAGAAG CGCTGAA | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75128 KIAA0633 PROTEIN - HOMO SAPIENS (HUMAN), 1316 aa (fragment). | 3.3E-72 | 7 |
| 5411 | cg43981956 | 854 | GAGTGGCGGA AATGGGGGCA TCA[C/G]CATGCC TGCCGTCGGGTT CCTGCGC | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q63625 CTD-BINDING SR-LIKE PROTEIN RA9 - RATTUS NORVEGICUS (RAT), 1473 aa. | 1.6E-71 | |
| 5412 | cg43292786 | 825 | AAGAAACACAA CTGTACTTTAAA A[T/C]ATGTACAA AGAAAAAATTT CTTTA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA82970 AP-4 CLATHRIN ADAPTOR-RELATED COMPLEX SIGMA4 SUBUNIT - HOMO SAPIENS (HUMAN), 144 aa. | 1.8E-71 | |
| 5413 | cg43951096 | 1405 | TCTGGTTATCTA CCTATAAATTTCA [T/C]GGTATTTCT TTAAACACTGAA GTAC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2E-71 | 17 |
| 5414 | cg43951096 | 1423 | AATTCATGGTA TTTCTTTAAACAC [T/A]GAAGTACTA AAAGCACTGATG ATT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2E-71 | 17 |
| 5415 | cg43951096 | 456 | CCCATGTGAAAA GTTTCCATGCAG TT[gap]ACAAAG GCAGCAGCACAT GCTGTTT | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2E-71 | 17 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|---|---------|---------------------|
| 5416 | cg43934599 | 582 | GGCCAGGCCAG AAGAGTAAGGC AA[C/T]TCAGGAT ACTCCATTATT GAATC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34127 CGI-132 PROTEIN - HOMO SAPIENS (HUMAN), 137 aa. | 3.7E-71 | 10 |
| 5417 | cg43283970 | 1054 | CGGCCCTGCCG TTTAACCCGGCC CT[A/C]JAGAAGAG TGAACACAGAATC CAAATC | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA82971 KIAA1019 PROTEIN - HOMO SAPIENS (HUMAN), 1867 aa (fragment). | 8.1E-71 | 21 (21q22.1) |
| 5418 | cg43271682 | 112 | CGTTGCCCCCCC CCGCCCCCGCC CC[A/G]CATGCTC TGACTCCTTTGG GGTCTG | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa. | 1.3E-70 | 1 |
| 5419 | cg43271682 | 650 | TCAGTCCTGGCC TGGGCAGGAGT CT[G/gap]GCGGA GCCTCTGAGGTG ACGAGACC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa. | 1.3E-70 | 1 |
| 5420 | cg43271682 | 651 | CAGTCCTGGCCT GGCAGGAGTC TG[G/gap]CGGAG CCTCTGAGGTGA CGAGACCA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa. | 1.3E-70 | 1 |
| 5421 | cg43271682 | 90 | AGCGCCCCCTC CCTTAGCCCTAC GT[T/C]GCCCCC CCCCGCCCCCG CCCCACAT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa. | 1.3E-70 | 1 |
| 5422 | cg43271682 | 96 | CCTCCCTTAGCC CTACGTTGCCCC C[gap/A]CCCCGC CCCCGCCCCAC ATGCTCTG | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa. | 1.3E-70 | 1 |

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|------|------------|------|---|---|-----|--|--|--------------------------|------------------|--|---------|----|
| 5423 | cg44032365 | 203 | AACAAAAATTTAA AAAATCACCTAT T[<u>gap</u>]ATCTTACC ACACAACCACTG TTATG | T | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q15170 (PP21) - HOMO SAPIENS (HUMAN), 157 aa. | 3.3E-70 | |
| 5424 | cg43918399 | 1015 | TGCTGTTCTACT ATTTAACTACTG [G/ <u>gap</u>]CAAAAGCC ACTTGCAITTTTC ATTAG | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43415 HYPOTHETICAL 15.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 136 aa (fragment). | 4.2E-70 | 4 |
| 5425 | cg43045396 | 102 | TAGGATACAAG AGGCACCAAGG CC[T/A]GGGGG TGGGGGTGGG GACACTAC | T | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa. | 4.2E-70 | 15 |
| 5426 | cg43045396 | 216 | AGCTCAGAACTA TGACATAATTCCT C[A/ <u>gap</u>]GGGGAG CCTGCATCCCTT CCTGAAA | A | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa. | 4.2E-70 | 15 |
| 5427 | cg43045396 | 222 | GAACATGACAT ATTCCTCAGGG A[G/ <u>gap</u>]CCTGCA TCCCTTCCTGAA AGTAGGA | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa. | 4.2E-70 | 15 |
| 5428 | cg43045396 | 266 | AGTAGGAGCAAG CCAGCTGCCCTC A[C/T]TCTCGGAC ATAAATTCTGGT GCAGA | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa. | 4.2E-70 | 15 |
| 5429 | cg43045396 | 63 | ATGACTTCGAAA CCGTGCAAATGC C[A/G]AACTATGG AGCACTAGGGAT ACAAG | A | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa. | 4.2E-70 | 15 |

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|------|------------|-----|--|---|-----|--|--|--|----------------------|------------------|--|---------|----|
| 5430 | cg43045396 | 64 | TGACTTCGAAAC CGTGCAAAATGCC A[A/G]ACTATGGA GCACTAGGGATA CAAGA | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa. | 4.2E-70 | 15 |
| 5431 | cg43045396 | 65 | GACTTCGAAACC GTGCAAAATGCCA A[A/G]CTATGGAG CACTAGGGATAC AAGAG | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa. | 4.2E-70 | 15 |
| 5432 | cg43045396 | 71 | GAAACCGTGCA ATGCCAAACTAT G[G/C]AGCACTA GGGATACAAGAG GCACCA | G | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa. | 4.2E-70 | 15 |
| 5433 | cg43917991 | 400 | CCTGAGAGGGT GACAGTCACAGC TA[C/T]AAAGAGA GGGCCGAGCTC CTGGTGT | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD23762 ERECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa. | 6.9E-70 | 11 |
| 5434 | cg43967210 | 379 | ACCTCAAGAGAG AGCTAAATCAAT TTC/TJAGGTTTTG GAAAAATTTTATT GCAT | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O44780 CODED FOR BY C. ELEGANS CDNA YK355D7.5 (CODED FOR BY C. ELEGANS CDNA YK373A5.5) - CAENORHABDITIS ELEGANS, 885 aa. | 8.1E-70 | 3 |
| 5435 | cg44922306 | 482 | ATAAGATAAAT GAACACAGTAAT G[A/gap]AAAAAA AAAGAAAGAAAC AGTATGG | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q01469 FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (PSORIASIS-ASSOCIATED FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABP) - Homo sapiens (Human), 135 aa. | 1.8E-69 | 17 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|---------|----------|
| 5436 | cg44922306 | 491 | ATTGAACACAGT AATGAAAAA A[A]gap]GAAAGA AACAGTATGGAG ATTGCT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q01469 FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (PSORIASIS-ASSOCIATED FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABP) - Homo sapiens (Human), 135 aa. | 1.8E-69 | 17 |
| 5437 | cg44922306 | 491 | TTGAACACAGTA ATGAAAAA A[A]gap]GAAAGA AACAGTATGGAG ATTGCT | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q01469 FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (PSORIASIS-ASSOCIATED FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABP) - Homo sapiens (Human), 135 aa. | 1.8E-69 | 17 |
| 5438 | cg42500321 | 110 | CCAGGGCCTGA CTTGGCAGTGGC CC[C]gap]AGGCT GCATGGGCTCA GGTAGGCTC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41588 TESTISIN - HOMO SAPIENS (HUMAN), 314 aa. | 2E-69 | 16 |
| 5439 | cg40985789 | 549 | GGCGTTTCCAA GTCATTTTATCA [A]G]AATTTTG TTTGTTTCCTGA ATCA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P04765 EUKARYOTIC INITIATION FACTOR 4A-I (EIF-4A-I) - Homo sapiens (Human), and Mus musculus (Mouse), 406 aa. | 2.6E-69 | 17 |
| 5440 | cg43292900 | 285 | TTATTCAGAATC ATAAGGGTTTT TTA]T]AAAAAAT CTTACCATTATG AAAGT | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75449 P60 KATANIN - HOMO SAPIENS (HUMAN), 491 aa. | 3E-69 | 6 |
| 5441 | cg43930848 | 1334 | GGTGGGGGTAA TTGTCTCTTGGT GG[G]gap]CCCAG TTAGTGGGCCTT CCTGAGTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75817 RIBONUCLEASE P PROTEIN SUBUNIT P20 - HOMO SAPIENS (HUMAN), 140 aa. | 7.9E-69 | 7 (7q21) |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5442 | cg43323149 | 1471 | TCGGTCTTTTA GTTTAAATTTATT [G/A]GTAAACTG ATGGCAGCAATC CATG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa. | 1E-68 | 1 |
| 5443 | cg41400057 | 183 | AATGGTAGTCAC TGTGAAAACTGC TTTCTCTAAAC ACAGGCTAGCC TGACT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P49901 SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS) - Homo sapiens (Human), 116 aa. | 2.7E-68 | 9 |
| 5444 | cg43955219 | 625 | CATCTCTCCAC TGATGCGCGTG C[C/gap]TAGACC GATGGCAGCCAT CGAATAT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P39194 III ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human); 593 aa. | 6.4E-68 | |
| 5445 | cg43955219 | 691 | GGGTGTTTCCA A CCCCCTGCAG CA[VC]CTAAGAT GGTGGGGGAGA GGGGGT | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P39194 III ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa. | 6.4E-68 | |
| 5446 | cg44004331 | 138 | CAGACAGCAGG C ACTCCAAAGAGG GT[C/G]GGCCTC CTAGGCTGCCCC GGACTAG | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa. | 7.1E-68 | |
| 5447 | cg44004331 | 234 | GAGGGACCCC C TGACCTGCCTCT GG[C/gap]CGCCG AACCCGGGGCC CTCCCCCTGG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa. | 7.1E-68 | |
| 5448 | cg44004331 | 296 | ATCTCAGAAAAC G AAAGGCTGTCCC T[G/T]CTTTGTC AGCCCTAGACCA GGTCT | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa. | 7.1E-68 | |

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|------|------------|-----|--|---|---|--|--|--|--------------------------|------------------|--|---------|----|
| 5449 | cg44004331 | 35 | TTTAGATTGTTGT CTACATTTTATT C/TJTTTCACTCAA CAGAAATAGAAGT TTT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa. | 7.1E-68 | |
| 5450 | cg43980385 | 286 | ACTGCTCAGCCT GGTGGTGGCTG GA[G/C]CTCAGA AATTGGGAGTGA CACAGGA | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa. | 1.5E-67 | 20 |
| 5451 | cg43969533 | 35 | TTTTTTTTTTTT TTTTTTTTTTTTT A/GATTTTAAAA AGCCATTTATTT A | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa. | 1.6E-67 | 7 |
| 5452 | cg43969533 | 37 | TTTTTTTTTTTT TTTTTTTTTTG /TJTTTTAAAAAG CCATTTATTTAA A | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa. | 1.6E-67 | 7 |
| 5453 | cg43951170 | 241 | TCTAATTTCTGGG TTCTGCACCATC A/G/AJGAAGAGA ATATCCTACAGG ACAGTT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27777 RNA POLYMERASE I 16 KDA SUBUNIT - HOMO SAPIENS (HUMAN), 133 aa. | 1.9E-67 | 13 |
| 5454 | cg43951170 | 260 | CCATCAGGAAGA GAATATCCTACA G/G/TJACAGTTCT CCTTGATACTG CATAA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27777 RNA POLYMERASE I 16 KDA SUBUNIT - HOMO SAPIENS (HUMAN), 133 aa. | 1.9E-67 | 13 |
| 5455 | cg44921579 | 625 | GGCTTAGAAGAT GAACCCCTTGAG A/T/CJGGCCACTA AGGAGAATTGAA AAAAA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75477 KE04P - HOMO SAPIENS (HUMAN), 346 aa. | 3.1E-67 | |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5456 | cg44030323 | 422 | AGCCTGGGTCA GAGGCCTGGTG GGC[C/gap]AGCC CAGTGGGACTAG GCAGGAAGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27747 CGI-38 PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 3.9E-67 | |
| 5457 | cg43999983 | 875 | GATTCCACCTG TAATCATAACTT [G/T]TTAACATCA AACTCGACAGCT AACC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43446 HYPOTHETICAL 34.0 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 299 aa. | 1E-66 | |
| 5458 | cg42506346 | 532 | TCAGAGATGAAA AGTCACCTCAGT T[gap/T]JAAAAGC AAAAAGGAAGAT AGAAAAT | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45744 HYPOTHETICAL 66.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 577 aa (fragment). | 3.5E-66 | 2 |
| 5459 | cg44928538 | 1092 | CCGCCCCACTA TGGGCCTACCAT T[A/T]ATAGTGTA TAAC TTGGAGGT TAAA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA34673 CFKBP/SMAP - GALLUS GALLUS (CHICKEN), 577 aa. | 3.5E-66 | 7 |
| 5460 | cg44928538 | 917 | GGTAAAACATT TTAGAAATATTCT [A/T]GAGATGGG CAGGAGAGTCAA AGGGC | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA34673 CFKBP/SMAP - GALLUS GALLUS (CHICKEN), 577 aa. | 3.5E-66 | 7 |
| 5461 | cg44911411 | 1159 | GGGTTTCTGCC ACTCCGGGTCT A[G/gap]GCCCTG CCCCAAATCCAG CCAGTCC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa. | 4.5E-66 | |
| 5462 | cg44911411 | 1160 | GGGTTTCTGCCA CTCCGGGTCTA G[G/gap]CCCTGC CCCCAAATCCAGC CAGTCCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa. | 4.5E-66 | |

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|------|------------|------|---|---|-----|--|--|--------------------------|------------------|---|---------|----|
| 5463 | cg44911411 | 1166 | CTGCCACTTCGG GGTCTAGGCCCT G[C/gap]CCCAAA TCCAGCCAGTCC TGCCCCA | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa. | 4.5E-66 | |
| 5464 | cg44911411 | 714 | TTCTGGATCCCA CAGTGTATGGA G[C/gap]CCCTGA CTCCTCACGTGC CTGATCT | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa. | 4.5E-66 | |
| 5465 | cg43984044 | 948 | CCTTCCCTCCT GGATTCGGGTA G[C/G]AGAGCA GCGCCGCAGGA GGCGGT | C | G | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00455 TTF-J INTERACTING PEPTIDE 20 - HOMO SAPIENS (HUMAN), 385 aa (fragment). | 7.3E-66 | 19 |
| 5466 | cg43984044 | 960 | GGATTCGGGTA GCAGAGGCAGC GC[C/gap]GCAGG AGGCGGGTGCC CGTTTGTC | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00455 TTF-J INTERACTING PEPTIDE 20 - HOMO SAPIENS (HUMAN), 385 aa (fragment). | 7.3E-66 | 19 |
| 5467 | cg43989609 | 192 | AAAAAACCAAC AAAGATTTTTTT [C/T]TTGTATTG CAGGACAAAGTAC AACT | C | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD42992 UBIQUITIN-SPECIFIC PROTEASE 3 - HOMO SAPIENS (HUMAN), 521 aa. | 7.3E-66 | |
| 5468 | cg43989609 | 195 | AAACCAACAAA GATTTTTTTCTT [G/T]TATTGCAG GACAAGTACAAC TGAA | G | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD42992 UBIQUITIN-SPECIFIC PROTEASE 3 - HOMO SAPIENS (HUMAN), 521 aa. | 7.3E-66 | |
| 5469 | cg43989609 | 329 | CTTTGTATATT TACAGGCCAAAAA G/AJAATGATTCC TCAGCAGTCATT GTGA | G | A | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD42992 UBIQUITIN-SPECIFIC PROTEASE 3 - HOMO SAPIENS (HUMAN), 521 aa. | 7.3E-66 | |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5470 | cg42871015 | 100 | CAATGAATTATTT ACCTCAAAATATC[A/gap]AGAGGCC CTGAGGTAGGGT GGCTCC | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O08616 BETA-ALANINE- PYRUVATE AMINOTRANSFERASE PRECURSOR - RATTUS NORVEGICUS (RAT), 512 aa. | 2.5E-65 | 5 |
| 5471 | cg43919145 | 346 | AAAATTGCACTA AAGCTCTGTAAA Gigap/AJAAAAAA TATAATAAATGTC TTATAC | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB52430 DJ703H14.1 PROTEIN - HOMO SAPIENS (HUMAN), 485 aa (fragment). | 3.2E-65 | 1 |
| 5472 | cg43919145 | 352 | GCACTAAAAGCTC TGTAAGAAAAA A[gap/A]TATAATA AATGCTTATAC AAATTT | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB52430 DJ703H14.1 PROTEIN - HOMO SAPIENS (HUMAN), 485 aa (fragment). | 3.2E-65 | 1 |
| 5473 | cg42703392 | 20 | TTTTTTTTTTTT TTTTTT[G/T]TCA GAAGTAGGGTTT TGTTTATTAA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q60778 NUCLEAR FACTOR OF KAPPA LIGHT CHAIN PROTEIN ENHANCER IN B-CELLS INHIBITOR, ALPHA (Kb-BETA) - MUS MUSCULUS (MOUSE), 359 aa. | 4.2E-65 | |
| 5474 | cg43946737 | 229 | GGCGCGCGAGG AGGCTGGCTGG GGC[C/gap]ATCA CGGAGTGCCCAT CCTGCACTG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB42836 DJ22E13.1A.1 (C- TERMINAL PART OF NOVEL PROTEIN DJ22E13.1) (PARTIAL ISOFORM 1) - HOMO SAPIENS (HUMAN), 134 aa (fragment). | 1.1E-64 | 22 |
| 5475 | cg43923225 | 1058 | AAAGTGACCCTA TAGCGCAGGGA GC[G/A]GGGTAG TTCCTTGGCTTT ATGCAIT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa. | 2.2E-64 | 1 |
| 5476 | cg43923225 | 1150 | GATGGTTGTTAT TGAGGATGGGG TG[G/gap]CCATT GGCTAGGGGCC GGCTCTTTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa. | 2.2E-64 | 1 |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5477 | cg43923225 | 258 | ATTTTATTTAA TCCTTTAATTTT[A /TAAAAAAACC CATTAAACAGTAC ATT | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa. | 2.2E-64 | 1 |
| 5478 | cg43923225 | 458 | GGGGAAGAGG CCAGAGAAAGGA GG[A]gap]GGCAG TCAGATCTTAGA CCTGTCGC | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa. | 2.2E-64 | 1 |
| 5479 | cg43929282 | 128 | TGATCATCACAT GAGCCCTCTTCT C/C/TATATACAC ATTGTTAGTGT GAAAA | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20678 HYPOTHETICAL 97.3 KD PROTEIN F52E4.7 IN CHROMOSOME X - CAENORHABDITIS ELEGANS, 848 aa. | 2.9E-64 | |
| 5480 | cg43929282 | 301 | TAAAGGAAAATT TCCCATCCAGTC A/T/CJTGAGAAAT GCTAAAGGCATT TTATG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20678 HYPOTHETICAL 97.3 KD PROTEIN F52E4.7 IN CHROMOSOME X - CAENORHABDITIS ELEGANS, 848 aa. | 2.9E-64 | |
| 5481 | cg44924736 | 1579 | TTTTTTTTTTTC ACATTACCGAAAT G/gap]GCCAAGT AATGTGGTGTGA TTACTA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q27244 T09F3.2 - CAENORHABDITIS ELEGANS, 384 aa. | 5.6E-64 | 3 |
| 5482 | cg44924736 | 1580 | TTTTTTTTTTTC CATTACCGAAAGT G/gap]CCAAGTAA TGTGGTGTGATT ACTAT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q27244 T09F3.2 - CAENORHABDITIS ELEGANS, 384 aa. | 5.6E-64 | 3 |
| 5483 | cg42381630 | 643 | GTTTCATTAAAATT CTCCCAATAAAGT C/gap]TTTACAGC CTTCTGCAAAAA AAAAA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa. | 5.9E-64 | |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5484 | cg42381630 | 662 | ATAAAGCTTTAC AGCCTTCTGCA A/A/GJAAAAAAAA AAAAAAAAAAAA AAAAA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa. | 5.9E-64 | |
| 5485 | cg44001502 | 1002 | GATTATTTATTG TAATACCTCACAJ G/AJACGTTGTAC CATATCCATGCA CATT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14849 MLN64 MRNA - HOMO SAPIENS (HUMAN), 445 aa. | 7.6E-64 | |
| 5486 | cg44001502 | 1009 | TTATTGTAATACCT TCACAGACGTTG [T/C]ACCATATCC ATGCACATTTAG TTGC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14849 MLN64 MRNA - HOMO SAPIENS (HUMAN), 445 aa. | 7.6E-64 | |
| 5487 | cg42367764 | 486 | ATTCACACACCTC TCCTCCCCAGCC G[ap/G]CAACGG GGGTGCCAGGA GCCCCAGG | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q14210 E48 ANTIGEN PRECURSOR - Homo sapiens (Human), 128 aa. | 9.7E-64 | 8 |
| 5488 | cg42367764 | 622 | AGGATGAAGCCA CCCCACAGAGG AT[G/gap]CAGCC CCCAGCTGCATG GAAGGTGG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q14210 E48 ANTIGEN PRECURSOR - Homo sapiens (Human), 128 aa. | 9.7E-64 | 8 |
| 5489 | cg43132517 | 399 | GGTTAATAAATT ACTAGGTCTATT TT[C]GAATAACA AATTGAGTACTT TTATT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa. | 2.6E-63 | |
| 5490 | cg43132517 | 419 | TATTTGAATAAC AAATTGAGTACTI T/C]TTATTAGACC TAAGTGAACCTT TAT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa. | 2.6E-63 | |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5491 | cg43132517 | 424 | TGAATAACAAAT TGAGTACTTTTAT [T/G]AGACCTAAG TGGAACCTTTATC TGAA | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa. | 2.6E-63 | |
| 5492 | cg43132517 | 442 | CTTTTATTAGAC CTAAGTGGAAC TTTCATCTGAAT CTGAATTTTCCA AGGGG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa. | 2.6E-63 | |
| 5493 | cg43968715 | 284 | CAGTTTCTTTCA CAAAACAGCATT CIG/AJAGGAGA AGGGAAGTTCC CACATT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q60888 HYPOTHETICAL 13.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 119 aa. | 3.3E-63 | 22 |
| 5494 | cg43933863 | 284 | ACGTATTAGGAA CAAAATTAAGAGT TTT/AJTITTTGGG TTTTAACTGCA CTTTA | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD25962 ZINC RING FINGER PROTEIN SAG - HOMO SAPIENS (HUMAN), 113 aa. | 1.1E-62 | |
| 5495 | cg43933863 | 286 | GTATTAGGAACA AATTAAGAGTTTT [T/A]JTITGGGTTT TAACTGCACCTT TATT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD25962 ZINC RING FINGER PROTEIN SAG - HOMO SAPIENS (HUMAN), 113 aa. | 1.1E-62 | |
| 5496 | cg43950549 | 1039 | GGACGGGCTGA ACCAGCGCTACT TC[C/gap]GCAAG CGTGCCCTCTAC CTGGCCCCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa. | 1.4E-62 | |
| 5497 | cg43988710 | 64 | ATCTTGTGGGGA CTCTTTTGCCTA A[G/C]CTGGTTCC CAAATCATGGAG GGAAA | G | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34051 CGI-56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa. | 1.4E-62 | |

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|------|------------|------|---|-----|--|--|----------------------|------------------|--|-------------------|---------------|
| 5498 | cg43308257 | 1097 | CGACGTTTTCGGG CAGTGTTCCTTG T[Gap]CCCGTG GGCCGGGAGC GAGTAAAG | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa. | 2.9E-62 | |
| 5499 | cg43308257 | 1135 | GGAGCGAGTAA GTCTGGGCCAG GC[AT]AAAAA AAAAA AAAAA | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa. | 2.9E-62 | |
| 5500 | cg43308257 | 439 | TGAGCGAGATT CTACAGTGAGAT C[C/T]TGGACAAG AAGTTCACAGTG ACTGT | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa. | 2.9E-62 | |
| 5501 | cg44015973 | 1734 | AAGAAGAGGCCT CCATTTTTTTTT T[Gap]CTTTTTTT ATTGGTGTAGTT ACGA | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa. | 3E-62 (3p24.2) | 3 (3p24.2) |
| 5502 | cg44015973 | 2224 | GTAAAGTAA ACTTTACCATGC C[Gap]/TTTTTTT TTTTGTGGCC TAACAT | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa. | 3E-62 (3p24.2) | 3 (3p24.2) |
| 5503 | cg44015973 | 2225 | GTAAAGTAA ACTTTACCATGC C[T/Gap]TTTTTT TTTTGTGGCCT AACATT | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa. | 3E-62 (3p24.2) | 3 (3p24.2) |
| 5504 | cg44015973 | 2236 | AACTTTACCATG CCTTTTTTTTTT T[Gap]GTTGGCCT AACATTGAGGCC TTAA | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa. | 3E-62 (3p24.2) | 3 (3p24.2) |

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|------|------------|-----|--|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5505 | cg43981475 | 211 | CTGGAAGAAG CTGTTGTCGT TTT[<i>gap</i>]GATTGT CCTCTGCCAGCA GATCTGC | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34088 CGI-93 PROTEIN - HOMO SAPIENS (HUMAN), 291 aa. | 4.8E-62 | |
| 5506 | cg43981475 | 415 | TCCGCTCTTTTC TGGCCCTGGAG GC[C/ <i>gap</i>]ATGAG GCTGAAGAAGAG CCCAGGAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34088 CGI-93 PROTEIN - HOMO SAPIENS (HUMAN), 291 aa. | 4.8E-62 | |
| 5507 | cg43950850 | 41 | CAATGAGACTTT ATTGGCAGTGGG C[C/ <i>gap</i>]JAGATT GGTAGTCTGCT AACTCTA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I- B14.5B) (C1-B14.5B) - Homo sapiens (Human), 119 aa. | 7.8E-62 | 11 |
| 5508 | cg43961684 | 192 | CAAAATAAAAAG ATCCACGTTCT TTATTTCTCTAC ACAAAACGCGTT TTTTAA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa. | 1.2E-61 | 19 |
| 5509 | cg43961684 | 44 | TTTTTTTTTTT TTTTTTTTTTT[G /TTGTTCCAGA AGAGAAATTTAA TCT | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa. | 1.2E-61 | 19 |
| 5510 | cg43961684 | 46 | TTTTTTTTTTT TTTTTTTTTTTGT G/TTTCCAGAA GAGAAATTTAAT CTAA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa. | 1.2E-61 | 19 |
| 5511 | cg43961684 | 466 | CATTGTGGGCTC AGTGGGGGGCT CC[C/ <i>gap</i>]AGGCC CCAGCAGGCC CACAGAGGG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa. | 1.2E-61 | 19 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5512 | cg43983897 | 339 | CAAGATACCGAC TTTCTGGCCCTG G[C/gap]CCTAAT CCTAAACTCTCC TCCITIG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTRMBL- ACC:Q19300 CODED FOR BY C. ELEGANS CDNA YK20F8.5 - CAENORHABDITIS ELEGANS, 929 aa. | 1.8E-61 | 6 |
| 5513 | cg43983897 | 341 | AGATACCGACTT TCTGGCCCTGGC C[C/gap]TAATCC TAAACTCTCCTC CTTGCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTRMBL- ACC:Q19300 CODED FOR BY C. ELEGANS CDNA YK20F8.5 - CAENORHABDITIS ELEGANS, 929 aa. | 1.8E-61 | 6 |
| 5514 | cg43983897 | 377 | CTCTCCTCCTTT GCAAGCTGACAA A[G/T]CAAGGATT TGATGTCTCGA GAGGC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTRMBL- ACC:Q19300 CODED FOR BY C. ELEGANS CDNA YK20F8.5 - CAENORHABDITIS ELEGANS, 929 aa. | 1.8E-61 | 6 |
| 5515 | cg44926530 | 1746 | ACACTGACAAAT TCCTAAGTTAAT G[G/gap]CTTTAG CCCAACATTTT AGTCAGT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa. | 2.1E-61 | X |
| 5516 | cg44926530 | 213 | AGGGCACAAAAG CCAGCAGCATAA A[gap/A]GAAACA TGAATAATGACT GAGAATT | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa. | 2.1E-61 | X |
| 5517 | cg44926530 | 368 | CAACATGCACA TAGTATTCCTAC A[A/T]GAATATTG CCTTAATATTGT CAATA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa. | 2.1E-61 | X |
| 5518 | cg42701870 | 133 | TTGCTTTGAGAG TGATGCGATGTA TG[A/T]ATATATA TGATAAATGATT ATAAC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q07325 GAMMA INTERFERON INDUCED MONOKINE PRECURSOR (MIG) - Homo sapiens (Human), 125 aa. | 3.4E-61 | 4 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5519 | cg43918476 | 1426 | TGAAATAACTGG GTTTAAAAAAA A[A/gap]GTTTAAA ATGAAGCCCAAG TTTTAA | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34122 CGI-127 PROTEIN - HOMO SAPIENS (HUMAN), 121 aa. | 6.3E-61 | 2 |
| 5520 | cg43918476 | 174 | TATTGTGACAGC AAATGCACATAG TTG[gap]CTGTAG GTAAGGCATGCT ACTAGGA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34122 CGI-127 PROTEIN - HOMO SAPIENS (HUMAN), 121 aa. | 6.3E-61 | 2 |
| 5521 | cg43298020 | 572 | CTTGAATAAAAC ACAAGCCTCCGT TTATJAAAAAAA AAAAAAA AAAGA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa. | 7E-61 | |
| 5522 | cg43982373 | 27 | GTCGACTTTTTT TTTTTTTTTTT[G /TTGAGCAACAG AGATAGTCTTTA TTC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD38195 MINDIN PRECURSOR - RATTUS NORVEGICUS (RAT), 330 aa. | 8.8E-61 | 4 |
| 5523 | cg43285334 | 364 | AAGAAGGTTCTT CTAGGAGGCC CG[C/gap]CCCTC CAAATGGTCATT TCCTCTTT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa. | 1.9E-60 | 1 |
| 5524 | cg43285334 | 367 | AAGGTTCTTCTA GGAGGCCCCGC CC[C/gap]TCCAA ATGGTCATTTCT CTTTCTG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa. | 1.9E-60 | 1 |
| 5525 | cg43285334 | 795 | GTCAAAGCCCTG GGCGCAGCAT GC[C/gap]TACGG TTCCTAACCCCTG GGCTTTTG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa. | 1.9E-60 | 1 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|----------------------|----|
| 5526 | cg43919806 | 592 | AACTCAGGAGGC AGAGGCTGCAGT G[A/G]GCTGAGA TTGCACCACTGC ACTCTA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O18216 Y53C12B.2 - CAENORHABDITIS ELEGANS, 277 aa. | 2.3E-60 | 2 |
| 5527 | cg43916931 | 1543 | TTGCATTTTATT CAAATGTTATCT C/gap]TTTTTTC TTTGAGAAATAA ACTGT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P91125 CODED FOR BY C. ELEGANS CDNA YK110H1.3 - CAENORHABDITIS ELEGANS, 299 aa. | 9.5E-60 | 1 |
| 5528 | cg43916931 | 1827 | TATATGTAATTG TGTTTAAAGAG C/G]TGATACTGA TTTTCATATGACA ATG | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P91125 CODED FOR BY C. ELEGANS CDNA YK110H1.3 - CAENORHABDITIS ELEGANS, 299 aa. | 9.5E-60 | 1 |
| 5529 | cg42886005 | 106 | CAAAGAGAACAG GAATGGCTGACT C/T]C]GCATAAAT TGCCCGAAGATT ATCCA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P22486 GALANIN PRECURSOR - Homo sapiens (Human), 123 aa. | 1.3E-59 (11q13.3) | 11 |
| 5530 | cg42886005 | 174 | TTCAGGTTACAG CACACAGACAAA C/G]ATGCCCGAG GAGGCTCTCAG GACCGCT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P22486 GALANIN PRECURSOR - Homo sapiens (Human), 123 aa. | 1.3E-59 (11q13.3) | 11 |
| 5531 | cg43985327 | 68 | TTCTCTTTGTCC AGTTCCTTTATT G/T]GGGGCAGG GCACCAAGAAGA GGCCC | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa. | 2.1E-59 | 1 |
| 5532 | cg43985327 | 80 | CAGTTCCTTTATT GGGGGCAGGGC A/C]gap]CAAGAA GAGGCCCTCCG CTCCCCAA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa. | 2.1E-59 | 1 |

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|------|------------|-----|---|---|-----|--|--|--------------------------|------------------|--|---------|----|
| 5533 | cg43958640 | 105 | GGAGCCCCACG AATGTGAGGCCT GG[C/gap]CCCTT CCTCCAGGCCTC CAGGCCCC | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43653 PROSTATE STEM CELL ANTIGEN - HOMO SAPIENS (HUMAN), 123 aa. | 2.7E-59 | |
| 5534 | cg43958640 | 99 | ATTCAGGGAGCC CCACGAATGTGA G[G/gap]CCTGGC CCCTTCCTCCAG GCCTCCA | G | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43653 PROSTATE STEM CELL ANTIGEN - HOMO SAPIENS (HUMAN), 123 aa. | 2.7E-59 | |
| 5535 | cg43978473 | 190 | GACGGGCCCC CCATGCTGTCGG GG[C/gap]CCAGG GCTGCTGTCCGC AAAGAGCG | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa. | 3.5E-59 | 11 |
| 5536 | cg43939569 | 895 | TCITTTGTACAG AACTTCATCCTC C[C/gap]GGGAAC CGGGCTGGACA GGGCTGGG | C | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa. | 3.5E-59 | 17 |
| 5537 | cg43939569 | 357 | AGAAAGGAGAAA GGAGAGTTACAA G[A/T]TGCCAACT CCACCATTACCC CTCCT | A | T | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa. | 3.5E-59 | 17 |
| 5538 | cg43253949 | 531 | GTCGACTGTTGC TTGCTGGTCGCA G[A/gap]CTCCCT GACCCCTCCCTC ACCCCTC | A | gap | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa. | 4.3E-59 | 12 |

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|------|------------|-----|---|-----|-----|--|--|--|--------------------------|------------------|---|---------|----------|
| 5539 | cg43253949 | 628 | CCCAGCCCTAGT GTCAGGGCGGG GG[C/gap]CTGGA GCAGCCCGAGG CACTGCAGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa. | 4.3E-59 | 12 |
| 5540 | cg43253949 | 710 | CTCGCCAGTCCG GTCGCTGGCTTC G[C/gap]GCCGCC ATGGCAATGAGA CAGACGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa. | 4.3E-59 | 12 |
| 5541 | cg43253949 | 710 | TCGCCAGTCCG GTCGCTGGCTTC GC[gap]C/GCCGC CATGGCAATGAG ACAGACGC | gap | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa. | 4.3E-59 | 12 |
| 5542 | cg44011422 | 883 | AGGCCACCCTG CCTCTACCCCAAC CA[G/gap]GGCCC CGGGCCTGTTA TGTCAAAC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa. | 4.4E-59 | 1 (1q12) |
| 5543 | cg44011422 | 885 | GCCACCCTGCCT CTACCCCAACCAG G[G/gap]CCCCGG GGCCTGTTATGT CAAAC TG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa. | 4.4E-59 | 1 (1q12) |

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|------|------------|-----|--|---|-----|--|--|----------------------|------------------|---|---------|----------|
| 5544 | cg44011422 | 895 | CTCTACCCAACC AGGCCCGGG GC[<i>gap</i>]TGTTA TGTCAAACTGTC TTGGCTGT | C | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa. | 4.4E-59 | 1 (1q12) |
| 5545 | cg44011422 | 806 | CAGTGGCCAAGA TCACAGTGGCCA C[<i>gap</i>]GCCACG GCCACAGTCATG GTGGCCA | G | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa. | 4.4E-59 | 1 (1q12) |
| 5546 | cg44011422 | 807 | AGTGGCCAAGAT CACAGTGGCCAC G[<i>gap</i>]CCACGG CCACAGTCATGG TGGCCAC | G | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa. | 4.4E-59 | 1 (1q12) |
| 5547 | cg44011422 | 834 | CACGGCCACAGT CATGGTGGCCAC G[<i>gap</i>]CCACAG CCACTAATCAGG AGGCCAG | G | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa. | 4.4E-59 | 1 (1q12) |
| 5548 | cg44005977 | 604 | AAAATCTGTGGT ATAACAATGTAC T[<i>gap</i>]ATGTTCTG TAGCTCTTTACT GAAGG | G | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76071 WD40 PROTEIN CIAO 1 - HOMO SAPIENS (HUMAN), 339 aa. | 4.4E-59 | |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5549 | cg43063845 | 740 | GTATTCCGGATT AGCAACCCAGGA A[A/C]CCATCACT TCTGAAGACTCT AAACT | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O57683 146KDA NUCLEAR PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1307 aa. | 5.4E-59 | |
| 5550 | cg44914411 | 778 | GTCCCCCAGGCT GGAGTGCAGTG GC[G/A]CGATCAT GCTCACTGCAGC CTCAAT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment). | 7.2E-59 | 22 |
| 5551 | cg44914411 | 803 | GGATCATGCTC ACTGCAGCCTCA A[T/C]CTCCTGGG CTCAAGTGATCC TCCTG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment). | 7.2E-59 | 22 |
| 5552 | cg44914411 | 891 | CCACCGTGTCTG GCCTCTATTCTT GT[C/A]ATTGAAT GAGATGCTATGA GGCCC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment). | 7.2E-59 | 22 |
| 5553 | cg44914411 | 915 | GTAATTGAATGA GATGCTATGAGG C[C/G]CTGAGCG ACCCACAGGAAA GTACTT | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment). | 7.2E-59 | 22 |
| 5554 | cg43959535 | 322 | TGACTTTTGAAG ACGTGGCTGTGA A[C/A]TTTTCCCA GGAGGAATGGA GTCTCC | C | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92967 ZINC FINGER PROTEIN ZFP6 - HOMO SAPIENS (HUMAN), 431 aa (fragment). | 9.2E-59 | 19 |
| 5555 | cg43924537 | 126 | AGTGCTCGACTT TCTGGTGGCAG GG[C/gap]CCAGA GCTCACGGACAC CACTGACA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa. | 1.2E-58 | |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5556 | cg43924537 | 128 | TGCTCGACTTTC TGGTGGCAGGG CC[C/gap]AGAGC TCACGGACACCA CTGACAGT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa. | 1.2E-58 | |
| 5557 | cg43924537 | 55 | TTTTTTTTTTTT TTTTTTAGAAA T/A/AACTCTTGT ATTGTAGCACAT TTC | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa. | 1.2E-58 | |
| 5558 | cg43986278 | 2035 | TCTAAATGAATTA CAGGTACAGATG [G/T]TATGCTAGG TGGAGTATGCTT GATA | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q60395 PAC CLONE DJ0911H05 FROM 7Q21-Q22, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 133 aa (fragment). | 1.9E-58 | 7 |
| 5559 | cg44915744 | 710 | ATACAGAGTTTT ATTTTGAGTTTT [C/T]TTTTTGTC ATTGTCCTCATG CCTG | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q08765 GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2) - Homo sapiens (Human), and Rattus norvegicus (Rat), 117 aa. | 1.9E-58 | 16 |
| 5560 | cg42717343 | 615 | AAATGCTGTGCC AGGCATCTCTAA G[C/gap]TCTGCC CTTACTCTGTGT GGGTTTA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P15267 KIDNEY ANDROGEN- REGULATED PROTEIN PRECURSOR (KAP) - Homo sapiens (Human), and Mus musculus (Mouse), 121 aa. | 1.9E-58 | |
| 5561 | cg42346579 | 137 | CTGCGATCACTC CAGCCGGTGTG GT[C/T]ACAGCCC CACTGGGCTCCT CCACCC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P42128 MYOCYTE NUCLEAR FACTOR (MNF) - Mus musculus (Mouse), 617 aa. | 2.2E-58 | |
| 5562 | cg42346579 | 151 | GCCGGTGTGGT CACAGCCCCACT GG[G/gap]CTCCT CCACCCGGGAC CTTTTGACC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P42128 MYOCYTE NUCLEAR FACTOR (MNF) - Mus musculus (Mouse), 617 aa. | 2.2E-58 | |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|---|---------|---|
| 5563 | cg42346579 | 204 | GGGCTCTCCAGT GGAAGAGCGG AG[<i>gap</i>]CAGAG GCGGTGGTGGC AGTGGCTGG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P42128 MYOCYTE NUCLEAR FACTOR (MNF) - Mus musculus (Mouse), 617 aa. | 2.2E-58 | |
| 5564 | cg43916632 | 144 | ATTTTACTCAA CAGTCTGCCTTT GATGTTTTCTT TCCATAAACAAA TAC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15155 BET1P HOMOLOG - HOMO SAPIENS (HUMAN), 118 aa. | 2.5E-58 | 7 |
| 5565 | cg43961591 | 1282 | CAGAGTGGTCT GTCACCAGCTTG G[<i>gap</i>]/G/ACGCTG TCACCAACGTGC AGTCCAG | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:O35414 STATHMIN-LIKE PROTEIN B3 (RB3) - Rattus norvegicus (Rat), 189 aa. | 3.1E-58 | |
| 5566 | cg43997941 | 581 | AGCTGGGTTAGA GAGAACTCAAAT TT/CJCTGATGGA AAACAAAACCGA ACAAA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O08612 SRC5H3 BINDING PROTEIN - MUS MUSCULUS (MOUSE), 494 aa (fragment). | 3.6E-58 | 8 |
| 5567 | cg43930685 | 1505 | TCTTGAGACAGA CATTAGCTTTCT G/C/GJCTTCCCTA TTCTCATAAGCA GCTAC | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa. | 4E-58 | |
| 5568 | cg43930685 | 1506 | CTTGAGACAGAC ATTAGCTTTCTG C/C/GJTTCCCTAT TCTCATAAGCAG CTACG | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa. | 4E-58 | |
| 5569 | cg42466209 | 111 | AGAGCCACCGG CAAGACAGCGTG ACIG[<i>gap</i>]CTGCT CACCTTCATCCT GCTGCTCA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75827 DJ71L16.5 (KIAA0267 LIKE PUTATIVE NA(+)/H(+) EXCHANGER) - HOMO SAPIENS (HUMAN), 616 aa (fragment). | 2.2E-57 | |

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|------|------------|------|--|---|-----|--|--|--|--------------------------|------------------|---|---------|----|
| 5570 | cg43931116 | 257 | ACAACAAAGATG GCCGTGATGAGT G[G/A]GTATAATA TATTATATATAT ATAT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa. | 2.8E-57 | 12 |
| 5571 | cg43931116 | 532 | TAACACACACTT CTAAGCCACCTG T[G/A]ACCAACTT GGGAATTTCTGG CCCC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa. | 2.8E-57 | 12 |
| 5572 | cg43931116 | 543 | TCTAAGCCACCT GTGACCAACTTG G[G/gap]AATTC TGGCCCTTGG GGACCACA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa. | 2.8E-57 | 12 |
| 5573 | cg43931116 | 553 | CTGTGACCAACT TGGGAATTTCTG G[C/gap]CCCTTG GGGACCAACATCT CAGCCCT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa. | 2.8E-57 | 12 |
| 5574 | cg43924285 | 1009 | TGGGGTGATTTC TGCCCTTTTTTT [G/T]TTTTGTAAG AAAGAGGTTCCCT TCAT | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa. | 4.2E-57 | 15 |
| 5575 | cg43924285 | 1172 | AACTCTGTTTTT TAAATAAAAAA G[A/C]CTTACATG GTCAGGGATTGA TGGA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa. | 4.2E-57 | 15 |
| 5576 | cg43924285 | 219 | ACAGCTCCTTAG AAGGCCAATAAT A[A/C]AGTTGGAA AAAAGGGAGTTT CCACG | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa. | 4.2E-57 | 15 |

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|------|------------|-----|--|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5577 | cg43924285 | 351 | CACTGGGTAACCC TCCAGGCAGGA GC[C/gap]ACAGG CTGGAACAGGC GAACACTTT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa. | 4.2E-57 | 15 |
| 5578 | cg43924285 | 674 | TAAGCATTTCAGA CTTTAGAAATAA G[T/A]TTTTCATT TCAACTTTTATT ATAA | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa. | 4.2E-57 | 15 |
| 5579 | cg43924285 | 675 | AAGCATTTCAGAC TTTTAGAATAAGT [T/A]TTTCATTC AACTTTTATTAT AAC | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa. | 4.2E-57 | 15 |
| 5580 | cg43924285 | 711 | ACTTTTATTATA ACATGAGCTAAA[C/gap]TTTAAAGAA ACAACCCTAGTC TTCTA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa. | 4.2E-57 | 15 |
| 5581 | cg43964035 | 270 | AGGTACACAAGA GTTTGTGACACA A[A/gap]TAAAATA AGAATAC TTCAC ACACGT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa. | 7.5E-57 | 5 |
| 5582 | cg43964035 | 275 | CACAAGAGTTTG TCAGACAAATAA A[A/gap]TAAGAAT ACTTCACACACG TATCAA | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa. | 7.5E-57 | 5 |
| 5583 | cg43964035 | 278 | AAGAGTTTGTCA GACAAATAAAT A[A/gap]GAATAC TTCACACACGTA TCAACAC | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa. | 7.5E-57 | 5 |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5584 | cg43964035 | 281 | AGTTTGTGACAGAC AAATAAAATAAG A[A]gap]TACTTCA CACACGTATCAA CACCAT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa. | 7.5E-57 | 5 |
| 5585 | cg43964035 | 310 | TTACACACACGTA TCAACACCATAC A[A]gap]GGCATT ATTCTTCACACA GTAACAT | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa. | 7.5E-57 | 5 |
| 5586 | cg44032150 | 279 | CCTGAGGTCCTA AAACGATTGCAG A[G]gap]CCTTGG GGTGCCCGGTG CGGCTGCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q18886 CODED FOR BY C. ELEGANS CDNA CEESM21F - CAENORHABDITIS ELEGANS, 221 aa. | 7.5E-57 | 14 |
| 5587 | cg44032150 | 713 | TCTGTGTGTGAC AGAAGAGATTTT A[A]CJACACAGTG TGGGAAGTTTCT ATTTT | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q18886 CODED FOR BY C. ELEGANS CDNA CEESM21F - CAENORHABDITIS ELEGANS, 221 aa. | 7.5E-57 | 14 |
| 5588 | cg44032150 | 714 | CTGTGTGTGACA GAAGAGATTTTA A[A]CJACACAGTG GGGAAGTTTCTA TTTTT | A | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q18886 CODED FOR BY C. ELEGANS CDNA CEESM21F - CAENORHABDITIS ELEGANS, 221 aa. | 7.5E-57 | 14 |
| 5589 | cg43982355 | 490 | CATAGAAAACCT TGGAAAAAACCT TTC/TJTATAAAAC ACTGTTTCAATAT AATT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43290 HYPOTHETICAL 12.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 103 aa (fragment). | 7.5E-57 | |
| 5590 | cg43982355 | 500 | TTTGGAATAAAC TTTCTATAAAACA [C]gap]TGTTTCAA TATAATTTTATTA GCAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43290 HYPOTHETICAL 12.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 103 aa (fragment). | 7.5E-57 | |

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|------|------------|-----|--|-----|-----|--|--|--|--------------------------|------------------|---|---------|----|
| 5591 | cg43982355 | 703 | TCAAGAACTAGA AATGAACCTGCAC G[C/T]GTAGTGTC ACTTAAAGCAAA GCTTC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43290 HYPOTHETICAL 12.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 103 aa (fragment). | 7.5E-57 | |
| 5592 | cg43979919 | 118 | CTCTATTTATATA TATATATATATA[g ap/T]AAAAGGTTTC TTTAGCAGTTAA ATAG | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q18580 CODED FOR BY C. ELEGANS CDNA YK30B3.5 - CAENORHABDITIS ELEGANS, 755 aa. | 1.2E-56 | 1 |
| 5593 | cg43979919 | 122 | TATTTATATATAT ATATATATAAAA A[gap]GGTTCTTT AGCAGTTAAATA GATTC | A | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q18580 CODED FOR BY C. ELEGANS CDNA YK30B3.5 - CAENORHABDITIS ELEGANS, 755 aa. | 1.2E-56 | 1 |
| 5594 | cg43919432 | 204 | GTTTGAAAAGTT CACTCTAAAGAA T[G/A]AAGTCACC TGTTGTCACGT CCTCC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa. | 1.2E-56 | 15 |
| 5595 | cg43919432 | 281 | TACCATCCTGTG GCTCCTTAAGGA G[G/T]CTTCTCTC TTTAATTCTCCAT GAGG | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa. | 1.2E-56 | 15 |
| 5596 | cg44926486 | 124 | AACGTACATGGT TTAATACAACAA C[gap/A]AAAAAA ATTAATCAAGT GAAACGT | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa. | 1.5E-56 | 3 |
| 5597 | cg44926486 | 131 | ATGGTTTAATAC AACAAACAAAAA A[gap/A]TTTTAATC AAGTGAAACGTA ATAAAC | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa. | 1.5E-56 | 3 |

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|------|------------|------|--|-----|-----|--|--|--|--------------------------|------------------|---|---------|---|
| 5598 | cg44926486 | 77 | ATAATTGCTCAC AAAGATTTCATAG A[gap/T]TTTTTTT TTATTGTTAAGCT GCAAC | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa. | 1.5E-56 | 3 |
| 5599 | cg44926486 | 86 | CACAAAGATTCA TAGATTTTTTTTTT gap/TJATTGTTAA GCTGCAACGTAC ATGGT | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa. | 1.5E-56 | 3 |
| 5600 | cg43991184 | 1164 | AAACCATGTGGG TGACACAAAGCCA G[G/gap]CACTGC CAAGTGGAACAT GAGGTTA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment). | 2E-56 | 1 |
| 5601 | cg43968980 | 232 | CGTTGCCCCCTC AGCCTCTAGGAG G[C/gap]CTCAGG ATTATGGCGTCC ATCTTAT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.5E-56 | 5 |
| 5602 | cg43968980 | 262 | GGATTATGGCGT CCATCTTATGAT A[T/C]TGGCCAAA AGGAGACAGTCT TGGAG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.5E-56 | 5 |
| 5603 | cg43968980 | 268 | TGGCGTCCATCT TATGATATTGGC C[A/G]AAAGGAG ACAGTCTTGGAG GTGCTG | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.5E-56 | 5 |
| 5604 | cg43968980 | 360 | GGGAAAGGAATC TTTAGGCAGACT G[C/gap]CATCCA GGGACTGCTATT CTGTTCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.5E-56 | 5 |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5605 | cg43968980 | 361 | GGAAGGAATCT TTAGGCAGACTG C[C/gap]ATCCAG GGACTGCTATTG TGTCAC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.5E-56 | 5 |
| 5606 | cg43968980 | 45 | TTTTTTTTTTT TTTTTTTTTTT /TGTATTTAGGG ATGCATTTTGAA TAT | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.5E-56 | 5 |
| 5607 | cg43968980 | 48 | TTTTTTTTTTT TTTTTTTTTAGT /TJTAGGGATG CATTTGAATATT TA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.5E-56 | 5 |
| 5608 | cg43968980 | 49 | TTTTTTTTTTT TTTTTTTTTAGT /AJTTAGGGATG ATTTGAATATT AT | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.5E-56 | 5 |
| 5609 | cg43968980 | 559 | GGAGCAGGAG CTGAGGTGGAG ACG[G/gap]CCAC TGCCCTCTCTCAG CCTCTGTTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.5E-56 | 5 |
| 5610 | cg43306180 | 951 | AGCCACCCACCT CCAACACCTCCT GATGCGTCTGA TGCTCCACCCAG GCCAG | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD10847 CHEMOKINE - HOMO SAPIENS (HUMAN), 113 aa. | 5.3E-56 | |
| 5611 | cg43306180 | 959 | ACCTCCAACACC TCCTGAGCGTCT GATTTGCTCCCA CCAGGCCAGCT CTCCTC | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD10847 CHEMOKINE - HOMO SAPIENS (HUMAN), 113 aa. | 5.3E-56 | |

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|------|------------|-----|---|-----|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5612 | cg43306180 | 960 | CCTCCAACACCT CCTGAGCGTCTG ATTATGCTCCAC CAGGCCAGCTCT CCTCC | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD10847 CHEMOKINE - HOMO SAPIENS (HUMAN), 113 aa. | 5.3E-56 | |
| 5613 | cg44001479 | 864 | TTTCCGCACCAA CGCGCCCGCCA TG[G/gap]CTGTG CCGACACCAGAC CCCGAGTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD39918 HSPC040 PROTEIN - HOMO SAPIENS (HUMAN), 109 aa. | 1.4E-55 | 6 |
| 5614 | cg44001479 | 295 | CTGCAGATAAAA CCATCATCAGAA ATGTTTATTAAAT TAATTGCATATTT TGAG | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD39918 HSPC040 PROTEIN - HOMO SAPIENS (HUMAN), 109 aa. | 1.4E-55 | 6 |
| 5615 | cg43935092 | 599 | CAGCCTGCTGTA CTGGCCATGCTG G[gap/G]CCAGCC CCACCTGGAGCT CAGTAAA | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD26992 VAMP5-LIKE PROTEIN HOMO SAPIENS (HUMAN), 116 aa. | 1.8E-55 | 2 |
| 5616 | cg44019498 | 366 | AAAAGAAAGAAA GAAGAAATGGAAA A[G/A]AAAAAGAG AAAAAAACCACC ACAAA | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45970 HYPOTHETICAL 43.5 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 392 aa. | 1.8E-55 | 15 |
| 5617 | cg44019498 | 457 | TGGTGAAGACTT TTGGTAGCAAAA TTC/TTTGCACGGT TCTTAAATGGG AGTCT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45970 HYPOTHETICAL 43.5 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 392 aa. | 1.8E-55 | 15 |
| 5618 | cg43917388 | 313 | AAGAAAACTTT GTAATCAATATC CTT/CJGCTCATAA GTAAAAGTGGAA AAGAA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q22453 SIMILARTO LDL RECEPTOR-RELATED PROTEIN. NCBI GI: 1055166 - CAENORHABDITIS ELEGANS, 1357 aa. | 2.3E-55 | 1 |

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|------|------------|-----|--|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5619 | cg43917989 | 829 | CGCCTTGCTGGT TCTGAGCCCTGG GG[A]CTCGGAC CACTGACCCCTGG CGCTTG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD23762 ERECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa. | 2.3E-55 | 11 |
| 5620 | cg43928349 | 129 | AAAAAGTGCTGC TGCGGGCCGACG AC[G/gap]CCAGT GCTGGCCCTCA GGGGGCCCC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5621 | cg43928349 | 181 | CAGCCGGCGAG GGCGGGGACTT CCG[C/gap]CGCC AATCCCTGAGGG GGTAACATC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5622 | cg43928349 | 182 | AGCCGGCGAGG GGCGGGGACTT CGC[C/gap]GCCA ATCCCTGAGGG GGTAACATCG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5623 | cg43928349 | 238 | CAATCCCTGAGC TGGGCAGGGTG GG[C/gap]CCCCG TCACCCCCCTGG GCTGCCCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5624 | cg43928349 | 241 | TCCCTGAGCTGG GCAGGGTGGGC CC[C/gap]GCTCA CCCCCTGGGC TGCCCCACCC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |

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|------|------------|-----|--|---|-----|--|--|----------------------|------------------|---|---------|--|
| 5625 | cg43928349 | 247 | AGCTGGGCAGG GTGGGCCCCGC TCA[C/gap]CCCC CTGGGCTGCC ACCCGGGGT | C | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5626 | cg43928349 | 252 | GGCAGGGTGGG CCCCGCTCACCC CC[C/gap]TGGC TGCCACCCCG GGGTGTTCC | C | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5627 | cg43928349 | 293 | GGGGTGTCCC GCCGACTTCTGG GC[G/gap]GGGCC TCCCGGGCCAG GCCTGCCCG | G | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5628 | cg43928349 | 307 | GACTTCTGGGCG GGGCTCCCCG GC[C/gap]AGGCC TGCCGGGGGCG GGGCCCCGAG | C | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5629 | cg43928349 | 329 | GGCCAGGCCCTG CCGGGGGCGGG GCC[C/gap]GAGC AGCCGGACTGG CCAGGTTCAG | C | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5630 | cg43928349 | 345 | GGCGGGGCCCCG AGCAGCCGGAC TGG[C/gap]CAGG TTCAGCGCGCCT CAGTAGGGT | C | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|--|---------|---|
| 5631 | cg43928349 | 415 | GGACACCTGGG AGATGCGCCGC GAG[G/gap]ACCG CCACAGCTTCCG CGCGAACTG | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5632 | cg43928349 | 450 | GCTTCCGCGCG AACTGGCTGCTG CG[C/gap]ACCTC AGAGGGCTGCC CCGCGACCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment). | 4.1E-55 | |
| 5633 | cg42904952 | 109 | CCTTGAAGTGAT CTCTAGGCCCCA G[C/gap]CCCCAA TCCGCCACCAT CCGTGCT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41781 CYTOPLASMIC PHOSPHOPROTEIN PACSIN2 - HOMO SAPIENS (HUMAN), 486 aa. | 6E-55 | |
| 5634 | cg43926664 | 28 | TTTTTTTTTTTT TTTTTTTTTTAT /CJTTCACAAAGAT AATCTTTATTCAT A | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43805 NUCLEAR AUTOANTIGEN FO 14 KDA - HOMO SAPIENS (HUMAN), 119 aa. | 9.8E-55 | 9 |
| 5635 | cg43978709 | 487 | GTAAGAAGATTTT ATTGTTCTATAG A/GCACTTCTGA AAAGAGATCTAA TTGA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O42204 INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16) - Gallus gallus (Chicken), 262 aa. | 1.3E-54 | |
| 5636 | cg43978709 | 582 | TGAAGGCGTTAC AGCCCTCCTCTC C/A/GJAGGCTCA GGGCTGAGAAC GGTTAGC | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O42204 INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16) - Gallus gallus (Chicken), 262 aa. | 1.3E-54 | |
| 5637 | cg43927929 | 216 | GCCACAGCCTCC CGAGTAGCTGG GA/TCTACAGGT GCCCGCCACCA CACCCAG | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P35250 ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (A1 40 KD SUBUNIT) (RF- C 40 KD SUBUNIT) (RFC40) - Homo sapiens (Human), 354 aa. | 1.6E-54 | 7 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5638 | cg43927929 | 417 | TAAAGGACAGTC ATGTTGGCTCCA G[C/gap]CTAAGG CGGCATTTTCC CCATCAG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P35250 ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (A1 40 KD SUBUNIT) (RF- C 40 KD SUBUNIT) (RFC40) - Homo sapiens (Human), 354 aa. | 1.6E-54 | 7 |
| 5639 | cg41664708 | 437 | TCACITTTACACG CTCATGGACTGA G[T/A]TTTACTC ACCTTTTATGAA AGCAC | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1- ALPHA) - Homo sapiens (Human), 114 aa. | 2E-54 | 1 |
| 5640 | cg41664708 | 446 | ACGCTCATGGAC TGAGTTTATACT C[A/G]CCTTTTAT GAAAGCACTGCA TGAAT | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1- ALPHA) - Homo sapiens (Human), 114 aa. | 2E-54 | 1 |
| 5641 | cg43135067 | 688 | GCCCCGGAGCC CCATCCTGGGCC TG[C/gap]CCTGG CTGGCCAGGAC CCCAGCGGT | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAAB3094 X11L2 - HOMO SAPIENS (HUMAN), 369 aa (fragment). | 6.1E-54 | 19 |
| 5642 | cg43983352 | 1027 | GATTTGCAGCTG GTTCTCCAGGG A[A/G]TTGGCCC CGAAGCTGGCTC AGTTCA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD45832 WUGSC:H_DJ0747G18.5 PROTEIN - HOMO SAPIENS (HUMAN), 261 aa (fragment). | 6.9E-54 | 11 |
| 5643 | cg43983352 | 1039 | GTTCTCCAGGG AATTGGCCCGA A[G/gap]CTGGCT CAGTTCACCTCC AGGACCT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD45832 WUGSC:H_DJ0747G18.5 PROTEIN - HOMO SAPIENS (HUMAN), 261 aa (fragment). | 6.9E-54 | 11 |
| 5644 | cg43123055 | 318 | TAAGCCACGCTG TTGTGTCTGCC C[gap/T]ATTATTG GTGTCATTTCTG CAGTAT | gap | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P08949 NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN B] - Homo sapiens (Human), 121 aa. | 8.8E-54 | 2 |

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|------|------------|-----|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5645 | cg43243118 | 170 | GATATTATTGTC TTGACGCTGGTG [C/T]CAAAATAAA TATTTAGAAAGTG TTTT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SP TREMBL- ACC:Q92599 MYELOBLAST KIAA0202 - HOMO SAPIENS (HUMAN), 508 aa (fragment). | 9.9E-54 | 5 |
| 5646 | cg43957121 | 174 | TTAATGCTTTGG CAGATGAAGTAA C[G/A]TTTGAAA CTGTTTGTGAAA ATAGT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SP TREMBL- ACC:O60067 HYPOTHETICAL 74.7 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 649 aa. | 1.7E-53 | 4 |
| 5647 | cg43957121 | 425 | GCTTCCCAGACA GTCAAGGCCGG AG[G/gap]TCGCT CCTGTCCTGTGG TCTGACCC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SP TREMBL- ACC:O60067 HYPOTHETICAL 74.7 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 649 aa. | 1.7E-53 | 4 |
| 5648 | cg43946151 | 80 | CATAAAGTGCAT CTTATTAAAAAT [G/A]TATAAAAC CACATAAATTCA GGGC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SP TREMBL- ACC:Q62179 SEMAPHORIN C (SEM C) - MUS MUSCULUS (MOUSE), 782 aa (fragment). | 2.3E-53 | 15 |
| 5649 | cg43958224 | 284 | TTGCTGTTTGT ACCGGGGCTCT GC[C/gap]CTGGT CCTGTCACCCCT GAGACGTC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment). | 2.3E-53 | 19 |
| 5650 | cg43958224 | 285 | TGCTGTTTGT CCGGGGCTCTG CC[C/gap]TGGTC CTGTCACCCCTG AGACGTCC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment). | 2.3E-53 | 19 |
| 5651 | cg43958224 | 489 | CAACACCCATTA GAAGCACCTGGA A[G/gap]GGGGGT TTTGGGAAACGG GCTCAGA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment). | 2.3E-53 | 19 |

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|------|------------|-----|---|-----|-----|--|--|--|----------------------|--------------|---|---------|----|
| 5652 | cg43928097 | 224 | TCTAACATTATT TATTCAGGTTT G/gapTTTTTTTT TGGCAACTATAA ATTA | G | gap | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Similar to SPTREMBL- ACC:Q62739 RABIN3 - RATTUS NORVEGICUS (RAT), 460 aa. | 4.3E-53 | |
| 5653 | cg43969772 | 231 | TAAATCATATAA AAATGTTTAAAGT A/gapJAAAAAAA AAAAGAAAGAGA AAGAA | A | gap | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa. | 4.9E-53 | 14 |
| 5654 | cg43969772 | 243 | AAATGTTTAAAG TAAAAA A/gapGAAAGA GAAAGAAAGA GGAGGTA | A | gap | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa. | 4.9E-53 | 14 |
| 5655 | cg43969772 | 243 | AAATGTTTAAAGT AAAAA A/gapA/GAAAGA GAAAGAAAGA GGAGGTA | gap | A | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa. | 4.9E-53 | 14 |
| 5656 | cg43969772 | 31 | TTTTTTTTTTT TTTTTTTTTTT TTTAACTAAAGG ACATTTATTATT TT | A | T | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa. | 4.9E-53 | 14 |
| 5657 | cg43934126 | 297 | GCATGGCCGCC ACGTGAGCTCAA AC/GTTCCGTTT ATTCAAAGCAG TAATAA | G | T | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Similar to SPTREMBL- ACC:O60372 R33683_3 - HOMO SAPIENS (HUMAN), 103 aa (fragment). | 4.9E-53 | |
| 5658 | cg43983169 | 953 | GTTTATTGTGCA GAACAGACAGTG ATTAATAACACT AGAGAAATATTT TCAAC | T | A | | | | SILENT- NONCODING | UNCLASSIFIED | Human Gene Similar to SWISSPROT- ACC:P52926 HIGH MOBILITY GROUP PROTEIN HMGI-C - Homo sapiens (Human), 109 aa. | 7.7E-53 | 12 |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|---------|----|
| 5659 | cg43986294 | 1277 | TGTGGTTTTTGT GTTTTTTTTTTT T/gap]CTTTTCC ATAGGAAAGAAT ATATA | T | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O22730 UNKNOWN PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 240 aa. | 5.9E-52 | |
| 5660 | cg43986294 | 1333 | GTAATCCTAAT TCAAAGATGGCT C[A/G]TGTGTA GGGCATTGAGTT TGATTT | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O22730 UNKNOWN PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 240 aa. | 5.9E-52 | |
| 5661 | cg43980016 | 384 | TTTTTTTTTTTT TTTTTTTTTTTT[G]CCTGCATAAAA TACTGTTTATTT G | T | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62509 ZINC FINGER PROTEIN - MUS MUSCULUS (MOUSE), 354 aa (fragment). | 7.1E-52 | 1 |
| 5662 | cg42732394 | 160 | GTAGAGTTAAGG GCTTGGCAAGTT G[C/gap]CCACTC CTATCCCTGGTC TAGCTGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60516 EUKARYOTIC INITIATION FACTOR 4E-BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 100 aa. | 9.1E-52 | 5 |
| 5663 | cg42732394 | 243 | TCACCTCCCTCC AGATTAGATGAG G[C/gap]CCAGCT GGCCTTTGGATG CCCCAGG | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60516 EUKARYOTIC INITIATION FACTOR 4E-BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 100 aa. | 9.1E-52 | 5 |
| 5664 | cg42732394 | 245 | ACTCCCTTCCAG ATTAGATGAGGC C[C/gap]AGCTGG CCTTTGGATGCC CCAGGAA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60516 EUKARYOTIC INITIATION FACTOR 4E-BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 100 aa. | 9.1E-52 | 5 |
| 5665 | cg44923668 | 377 | AAACAAGCTTGG TCTCTTCTCTGC C[A/T]GGGTACCA CAGGGACACAC GCCAAG | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD45963 ASPARTYL PROTEASE - HOMO SAPIENS (HUMAN), 518 aa. | 1.2E-51 | 11 |

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|------|------------|------|---|-----|-----|--|--|--|--------------------------|------------------|---|---------|----------|
| 5666 | cg43241808 | 1106 | TTTCTCAAAACA TCTGCCACCTGA G[G/gap]CTAAGC CTACACACGGCG TGGCTGA | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41781 CYTOPLASMIC PHOSPHOPROTEIN PACSIN2 - HOMO SAPIENS (HUMAN), 486 aa. | 1.2E-51 | |
| 5667 | cg43241808 | 137 | ATTTTTCCTCA AATACTAGACAT G/T]TAAAGGAAC TGTTAAACTGAA AAAG | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD41781 CYTOPLASMIC PHOSPHOPROTEIN PACSIN2 - HOMO SAPIENS (HUMAN), 486 aa. | 1.2E-51 | |
| 5668 | cg43916927 | 392 | AGCCATAAGTTA AAAAGAAGACAA G[C/gap]TGAAGC TACACACATGGC TGAIGTC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60829 JM27 PROTEIN, COMPLETE CDS (CLONE IMAGE 145745 AND IMAGE 257878) - HOMO SAPIENS (HUMAN), 102 aa. | 1.9E-51 | |
| 5669 | cg43980942 | 553 | ATTTCATTAACTT AAAAGGTGGACA IT/A]AATGTTTAT TTTAAATCTAATT GAA | T | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P09132 SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) - Homo sapiens (Human), 144 aa. | 3.9E-51 | 5 (5p21) |
| 5670 | cg44014613 | 277 | AATAGCAGCAAA CTGGGAAAAAAA A[gap/A]CCTCCT GTCCATAAATAG AAGTACC | gap | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P97443 ZINC-FINGER PROTEIN BOP - MUS MUSCULUS (MOUSE), 490 aa. | 4.8E-51 | 1 |
| 5671 | cg43994444 | 1045 | GGACCTTGCACC ATCAGCTTTCTT G[G/A]GTTTCCAG CCTCCTGCCTCA CACTC | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:O75570 MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1) - Homo sapiens (Human), 445 aa. | 5.8E-51 | |
| 5672 | cg43994444 | 460 | GAAGGCAAGCTA GCAGGATGCTCC CTT/C]GAAACCTC TTTATTATGGG CCTTC | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:O75570 MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1) - Homo sapiens (Human), 445 aa. | 5.8E-51 | |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|--|---------|----|
| 5673 | cg43994384 | 449 | GTACAAATAGAA ACCACAAAAGGG TTC/TJGGATTG GGTTAAGGTGAA GAGAC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15553 PYRIN - HOMO SAPIENS (HUMAN), 781 aa. | 8E-51 | |
| 5674 | cg43999706 | 83 | GTTTATTCAACA TTATGGCATGGC [C/gap]AGTGTA TTGTTCCACAA AGGAA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD42973 PLECKSTRIN 2 - MUS MUSCULUS (MOUSE), 353 aa. | 8.2E-51 | 14 |
| 5675 | cg43916704 | 1031 | CGTGGCAGGGG CAGCTATCTGGG AG[G/A]GCTAAAC AGCCTGGAGGC TGAGTCT | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa. | 1.1E-50 | 20 |
| 5676 | cg43916704 | 2091 | TTGAAGCTGAGA GGCTGTGGATCT A/T/CJAGGAGATT CCAGCAGCATCA TGGCT | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa. | 1.1E-50 | 20 |
| 5677 | cg43916704 | 386 | CATCCAATTCCA GCATGGTCAGCA C[G/A]GAGATATT CACAGAAAGAAA CCCAG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa. | 1.1E-50 | 20 |
| 5678 | cg43916704 | 750 | GAGCTTCCCAA TCCTAGAGAATG A/C/TJGTACTTA GAAAGTTTTGTT TTGTT | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa. | 1.1E-50 | 20 |
| 5679 | cg41004313 | 161 | GGACAAAAGACA AAGAATGACACT T/TATCTCCTCTT TTGACTTTGACA CCCAA | A | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREBISIAE) HOMOLOG (SUPT6H) MUS MUSCULUS (MOUSE), 1726 aa. | 2.5E-50 | |

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|------|------------|-----|--|-----|-----|--|--|--|--------------------------|------------------|---|---------|----------|
| 5680 | cg41004313 | 499 | GTGGGGGAGAAG CTTGAGGCTGG GGC[C/gap]TCCT CACCATCATCCT CCTCTTCCA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SP TREMBL- ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREVISIAE) HOMOLOG (SUPT6H) MUS MUSCULUS (MOUSE), 1726 aa. | 2.5E-50 | |
| 5681 | cg42903672 | 129 | AGGCGGCGGGG TGGGCGGGGGG AGC[C/gap]GAGC AGTCACGTATGG GGCATCTGC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34131 CGI-136 PROTEIN - HOMO SAPIENS (HUMAN), 125 aa. | 3.5E-50 | |
| 5682 | cg43258766 | 157 | CCTGCGTGCCTC CCTGCCAGTCTT C[C/T]CCGTCTAA CCCTCAGTCCCT CTATC | C | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa. | 3.7E-50 | 7 |
| 5683 | cg43258766 | 353 | AGCAAAACAGTCC ATGCCATCCAGC CT[C]GGGAGGC TGGGGGAGAGG AAGATGA | T | C | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa. | 3.7E-50 | 7 |
| 5684 | cg43258766 | 405 | GGTGACTCCAGC ACAGCCAGCCTT G[C/gap]TCCGCA GGTGCCAGAGG CATAGGGA | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa. | 3.7E-50 | 7 |
| 5685 | cg43258766 | 409 | ACTCCAGCACAG CCAGCCTTGCTG C[G/A]CAGGTGC CAGAGGCATAG GGAGGAG | G | A | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa. | 3.7E-50 | 7 |
| 5686 | cg41568177 | 62 | GAGAAGACATT TATTGTTCTGG G[gap/GT]CTCTG GAGGCCCATTG GTGGGGCT | gap | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P31151 S100 CALCIUM-BINDING PROTEIN A7 (PSORIASIN) - Homo sapiens (Human), 100 aa. | 4.5E-50 | 1 (1q21) |

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|------|------------|------|---|---|-----|--|--|--|--------------------------|------------------|---|---------|----|
| 5687 | cg40357240 | 113 | AGAGTGAATTT TTCTTGGGACT TC/GJTITTTCTC CAGGGAAGGCT AAAAA | C | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45741 HYPOTHETICAL 112.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 1008 aa (fragment). | 5.4E-50 | |
| 5688 | cg44010855 | 1541 | CATGTTCTTTC CCTCACCACAAC AIG/TAACATGCA GTACTAAAGCAA TATAT | G | T | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa. | 5.8E-50 | 5 |
| 5689 | cg44010855 | 1749 | GCTATGTACATG TCAGAAACCATT A[G/gap]CATTGC ATGCAGGTTTCA TATCTT | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa. | 5.8E-50 | 5 |
| 5690 | cg43916819 | 497 | AAGGCATACAAC ATGAGCCTTGTC G[G/gap]CACTGC CTCACCAACCAC TGGTGGC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43182 DJ681N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa. | 6.1E-50 | 20 |
| 5691 | cg43970748 | 326 | ATAGGGGAAGAC AACAGGCCAAG GC[C/gap]ACTCT GTGTTACTTTTC CTGAAGTC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62418 DREBRIN-LIKE SH3 DOMAIN-CONTAINING PROTEIN SH3P7 - MUS MUSCULUS (MOUSE), 433 aa. | 7.4E-50 | 7 |
| 5692 | cg43970748 | 385 | TTGAGGCACACA CTGGGGCCTGC AG[G/gap]CATCG AGTGAGCCGCG TGGAGGAAC | G | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62418 DREBRIN-LIKE SH3 DOMAIN-CONTAINING PROTEIN SH3P7 - MUS MUSCULUS (MOUSE), 433 aa. | 7.4E-50 | 7 |
| 5693 | cg43970748 | 773 | TGGCAGTGGCC ACTCAGGGCTTG GC[C/gap]ACAGG CAGGGCTTGGCT CAGTATCC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62418 DREBRIN-LIKE SH3 DOMAIN-CONTAINING PROTEIN SH3P7 - MUS MUSCULUS (MOUSE), 433 aa. | 7.4E-50 | 7 |

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|------|------------|------|--|---|-----|-----|---------------|--|--------------------------|-----------------------|--|----------|---------------------|
| 5694 | cg43279836 | 464 | TGAGATTTCATAT TAAAAAGCCAC CIA/GIACATGATCA TCTGAGAAACCA ACACA | A | G | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SP TREMBL- ACC:O77836 UDP-GLCNAC:A-1,3-D- MANNOSIDE B-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4- N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa. | 7.4E-50 | |
| 5695 | cg43979181 | 139 | TTGGGAGCAGCT GGGATGATGGG GA[C/gap]CCAC ATCCATAGGGCT GGGAGGTC | C | gap | | | | SILENT- NONCODI NG | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P02818 OSTEOCALCIN PRECURSOR (GAMMA- CARBOXYGLUTAMIC ACID- CONTAINING PROTEIN) (BONE GLA- PROTEIN) (BGP) - Homo sapiens (Human), 100 aa. | 7.4E-50 | |
| 5696 | cg43298242 | 37 | GGACAAGCCTTG CTTTATTGGGA A[G/T]GGATGGG ATCACAAATAAT CTCTGC | G | T | | | | SILENT- NONCODI NG | water_ch annel | Human Gene SWISSPROT-ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa. | 1.3E-163 | |
| 5697 | cg42913771 | 348 | CATGAGGTGTCG ACTTCCAGCCAC G[T/C]AGATGCC GATTGCTTCCTG TGIGTC | T | C | Val | Ala (7868) | | CONSER VATIVE | apoptosis | Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa. | 6.2E-116 | |
| 5698 | cg43277632 | 1853 | AACTACAGATGG TACACCTACATC TIG[C]TGCAGGA AGTGGCTCCCA CACTGG | G | C | Val | Leu (7869) | | CONSER VATIVE | ATPase_ associated | Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa. | 0 | 13 (13q14.3) |

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|------|------------|------|---|---|---|-----|---------------|------------------|---------------------------|---|----------|--|
| 5699 | cg43931944 | 323 | GCACTGGTAAC CCCTCTCTGTAG A/G/CJCTTGGTCC TGGCATTATGGG AGCCA | G | C | Glu | Asp (7870) | CONSER VATIVE | ATPase_ associate d | Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa. | 0 | |
| 5700 | cg43931944 | 324 | CACTGGTAAC CCTCTCTGTAGA G/C/GJTGGTCTT GGCATTATGGGA GCCAT | C | G | Leu | Val (7871) | CONSER VATIVE | ATPase_ associate d | Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa. | 0 | |
| 5701 | cg43931944 | 688 | TTCACCATGGTG CAAGTATGGCCT GT/CJACGTCAAG TTCGACCTGTCA CTGAG | T | C | Val | Ala (7872) | CONSER VATIVE | ATPase_ associate d | Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa. | 0 | |
| 5702 | cg43251803 | 2946 | TAGCAGGACACT GCCATCTGAATC T/G/CJCTCGGTAC GCACCTCGTTTCA TGACT | G | C | Gln | Glu (7873) | CONSER VATIVE | ATPase_ associate d | Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment). | 3.1E-105 | |
| 5703 | cg43251803 | 3000 | CATCCCAGGGG GCCCCGGCTCC CCA/G/CJGCGGC CCCCGCCCCCCC ACGCGCGCCG | G | C | Leu | Val (7874) | CONSER VATIVE | ATPase_ associate d | Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment). | 3.1E-105 | |
| 5704 | cg43933735 | 444 | TGGCATTATGCA GACTCCCTCAGG C/G/AJTTGCAGTC ATCCATCAGCAA TTGAC | G | A | Arg | His (7875) | CONSER VATIVE | ATPase_ associate d | Human Gene Similar to SWISSPROT- ID:Q12697 PROBABLE CALCIUM- TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa. | 1.7E-90 | |

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|------|------------|------|---|---|---|-----|---------------|------------------|--------------------|---|----------|-----------------|
| 5705 | cg43988460 | 1624 | CCAGCCTCCAAC TGGTATCTTCAT TACJTCAACCC ATCTCGGGTCAG CTGTC | A | C | Ile | Leu (7876) | CONSER VATIVE | cadherin | Human Gene SWISSPROT-ID:P19022 NEURAL-CADHERIN PRECURSOR (N- CADHERIN) - HOMO SAPIENS (HUMAN), 906 aa. | 0 | 18 (18q11.2) |
| 5706 | cg43985533 | 328 | AATAATTACCTG ATGGAAGTCACC CIGAJCTTGCCG GATGTAACACGC CACTTC | G | A | Ala | Val (7877) | CONSER VATIVE | cathepsin | Human Gene Similar to SWISSNEW- ID:P10619 LYOSOMAL PROTECTIVE PROTEIN PRECURSOR (EC 3.4.16.5) (CATHEPSIN A) (CARBOXYPEPTIDASE C) - HOMO SAPIENS (HUMAN), 480 aa.lpcis:SWISSPROT-ID:P10619 LYOSOMAL PROTECTIVE PROTEIN PRECURSOR (EC 3.4.16.5) (CATHEPSIN A) (CARBOXYPEPTIDASE C) - HOMO SAPIENS (HUMAN), 480 aa. | 2E-52 | 7 |
| 5707 | cg43980411 | 430 | CTCTGCAATCAA TGCATCCACAGG GJAGJATTATTA CTGGAAGTGTC AATAA | A | G | Asn | Asp (7878) | CONSER VATIVE | cathepsin inhib | Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG- SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa. | 3.2E-222 | 18 (18q21.3) |
| 5708 | cg43970982 | 2132 | GGACCTCGGG AAGCGGAGGTG CCG[C/G]TGGTG CTCCTGGAGAAC GAGGCAGA | C | G | Ala | Gly (7879) | CONSER VATIVE | collagen | Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa. | 0 | 2 |
| 5709 | cg43970983 | 1219 | GCGGGTCCCTCA GTGGTGGGCC ACA[G/C]AACAG CAGGAGCTGGG CCCTGGGCA | G | C | Glu | Gln (7880) | CONSER VATIVE | collagen | Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa. | 0 | 3 (3p21.3) |
| 5710 | cg43970983 | 1668 | CTGTAACAGACC TGCAAGCCACCG A[G/C]GTGCCCG GGCAGCGGGTG CGAGTGT | G | C | Glu | Asp (7881) | CONSER VATIVE | collagen | Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa. | 0 | 3 (3p21.3) |

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|------|------------|------|--|---|---|-----|---------------|------------------|----------------|---|----------|---------------|
| 5711 | cg43970983 | 1669 | TGTAACAGACCT GCAAGCCACCG AG[G/C]TGCCCG GGCAGCGGGTG CGAGTGTC | G | C | Val | Leu (7882) | CONSER VATIVE | collagen | Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa. | 0 | 3 (3p21.3) |
| 5712 | cg43991318 | 4971 | CCGGGAGACCC CGAGGGAATACT CTA/TJCGCGTG GGCTGGGTCAC GGGGGCGCG | A | T | Tyr | Phe (7883) | CONSER VATIVE | collagen | Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa. | 1.3E-73 | 1 (1p34) |
| 5713 | cg43991318 | 5053 | GTTGCGGATCTT CTTGATGGCAGA CT/GTCTTTCATG AGGCTGAGTCG GTGGAT | T | G | Glu | Asp (7884) | CONSER VATIVE | collagen | Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa. | 1.3E-73 | 1 (1p34) |
| 5714 | cg43933757 | 1606 | TCCAGTGGGG GTGGGAGATCCT GC[A/G]TTGGAG AAACGACAGAAA GCACACA | A | G | Ile | Val (7885) | CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa. | 0 | 5 (5p13) |
| 5715 | cg43084083 | 2416 | TCTAACCCACCTG GGAAATTC AAGG C[G/A]TTGGCATT TCAAAACACTGGT ATATG | G | A | Val | Ile (7886) | CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:P01031 COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN) - HOMO SAPIENS (HUMAN), 1676 aa. | 0 | 9 (9q34.1) |
| 5716 | cg43956185 | 955 | AACATTTCTATAA GGGCTCCTACAT T[G/C]ATAACGTA CTCTCTCACCAG ATGGA | G | C | Gln | Glu (7887) | CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa. | 4.1E-190 | 1 |
| 5717 | cg43956185 | 1003 | GGATAATTTACTC ATCTGTCTCGAC A[C/G]TATATAAG CAITTTGTACTG TGCGC | C | G | Val | Leu (7888) | CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa. | 4.1E-190 | 1 |

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|------|------------|------|--|---|---|-----|---------------|------------------|----------------|---|----------|---------------|
| 5718 | cg43956185 | 591 | ATATCCACGTTT ACACACAAATTC A[G/A]CTGATTCA CCTGTTCTCAAA TAAAG | G | A | Ala | Val (7889) | CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa. | 4.1E-190 | 1 |
| 5719 | cg42542496 | 440 | CGTGACTCCCAT GTCCTTCACAGC A[G/A]ACTGAGC CAGTGCCCGAGA GGTTCAC | G | A | Arg | Lys (7890) | CONSER VATIVE | csf | Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa. | 1.2E-189 | 3 (3q26.3) |
| 5720 | cg43957094 | 2211 | AGCTTGCCCTGA TAAAAAAGCACC A[G/C]CCGGCGG AGCGGCCGCGG AGCGACC | G | C | Leu | Val (7891) | CONSER VATIVE | cyclin | Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa. | 7.9E-164 | 6 |
| 5721 | cg43242733 | 635 | GACTTGATGAGA ATGGAAAAGATT G[C/T]AATGGAGA AGGTGTTGGA AAGTC | C | T | Ala | Val (7892) | CONSER VATIVE | cyclin | Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa. | 1.3E-154 | 5 |
| 5722 | cg43986855 | 3915 | AAGTTCTCCGGG TTAGGCCCACTTC A[G/C]TGGGTCAT GATTCACAGACC ACTGG | G | C | Leu | Val (7893) | CONSER VATIVE | cyto450 | Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa. | 3.2E-293 | 2 (2p22) |
| 5723 | cg43966704 | 1275 | CGGCCCTCAAA CCCGATGCTTG A[T/C]CTGCCCA GGATCCAGTCG GGCCCC | T | C | Ile | Val (7894) | CONSER VATIVE | cytochro me | Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa. | 5.8E-184 | 11 |

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|------|------------|------|--|---|---|-----|---------------|------------------|-------------------|--|----------|----------|
| 5724 | cg43966704 | 596 | GAGGTTGTCCCA GCCGCCCGTGA CAIC/AJCCCCAG CATGCTTCTCAA TCAGTTC | C | A | Gly | Val (7895) | CONSER VATIVE | cytochro me | Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa. | 5.8E-184 | 11 |
| 5725 | cg43962888 | 447 | GCAGGGCGACTG GGTTGGAGAGG GAGI/GJTCATG CTGGCTGCAAAG AAGGGACT | A | G | Ile | Val (7896) | CONSER VATIVE | cytochro me | Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa. | 5.1E-66 | 2 (2cen) |
| 5726 | cg43962888 | 463 | GAGAGGGAGAT CATGCTGGCTGC AAI/GJGAAGGG ACTGGACCCATA CAATGTA | A | G | Lys | Arg (7897) | CONSER VATIVE | cytochro me | Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa. | 5.1E-66 | 2 (2cen) |
| 5727 | cg43962888 | 517 | GCCCCAAAGGG AGCTTCAGGCAC CAIG/AJGGAAGA CCCTAATTTAGT CCCGTCC | G | A | Arg | Lys (7898) | CONSER VATIVE | cytochro me | Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa. | 5.1E-66 | 2 (2cen) |
| 5728 | cg43962888 | 546 | AGACCCCTAATTT AGTCCCCTCCAT CTI/AJCCAACAAG AGAATAGTAGGC TGCAT | T | A | Ser | Thr (7899) | CONSER VATIVE | cytochro me | Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa. | 5.1E-66 | 2 (2cen) |
| 5729 | cg43962888 | 621 | CGTCTGGTTTTG GCTGCACAAAGG CIG/CJAGGCCCA GCGATGCCCCG GCTGTGG | G | C | Glu | Gln (7900) | CONSER VATIVE | cytochro me | Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa. | 5.1E-66 | 2 (2cen) |
| 5730 | cg34396112 | 3497 | ACTTGCTTCCCA GCAAACCAAGCG CAIG/CJCTGCTC CAGGACCCCTCT GAACACC | G | C | Leu | Val (7901) | CONSER VATIVE | dehydrog enase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |

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|------|------------|-------|--|---|---|-----|---------------|------------------|-------------------|--|----------|----------|
| 5731 | cg44033747 | 1337 | TTGGCGAATATG GCTGCCATGTT G/GCJAATCTACC ATGGTTCCCATG GGCTG | G | C | Gly | Ala (7902) | CONSER VATIVE | dehydrog enase | Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa. | 0 | 9 (9p22) |
| 5732 | cg43057018 | 1597 | TGACCTAATGAA CCAAGGAAAAAG C/GJTCGGAACA ATCCTCATCTTT GAAG | A | G | Ile | Val (7903) | CONSER VATIVE | dehydrog enase | Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.jpds:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa. | 1.3E-209 | 4 (4q22) |
| 5733 | cg43973273 | 1476 | CAGCCTTCTCTT GGACAGCGACAT A/C/GJATCCCTTT CTGGGGCATGA GTTTC | C | G | Val | Leu (7904) | CONSER VATIVE | dna_ma_ bind | Human Gene Homologous to SPTREMBL-ID:Q13097 DNA/RNA- BINDING PROTEIN - HOMO SAPIENS (HUMAN), 363 aa (fragment). | 2E-112 | |
| 5734 | cg43327854 | 1114 | TCAAAGTGGAGGA TGATGGGGATG GC/G/AJATTACAT GTCTGAGCCTGA GGCTGT | G | A | Asp | Asn (7905) | CONSER VATIVE | dna_ma_ bind | Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa. | 5.5E-57 | 1 |
| 5735 | cg43958856 | 568 | AACCGGCATGG CCAAAGCCCGC GCG/A/GJTCGGC ATCGACCTGGGC ACCACCTA | A | G | Ile | Val (7906) | CONSER VATIVE | eph | Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa. | 0 | 6 |
| 5736 | cg44017749 | 12288 | GCGCCTCCTACC ACTTCCAACCGC C/G/AJCCGGCGA CAGATTGACCGG GGTGTC | G | A | Arg | His (7907) | CONSER VATIVE | eph | Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa. | 0 | 12 |

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|------|------------|------|---|---|---|-----|---------------|------------------|----------|--|----------|-----------------|
| 5737 | cg43950268 | 2136 | GCTCCCGGCTG AGGTTACAGGG AATG/CJTCCTCA CTGTCCACCACA CCTCGGA | G | C | Asp | Glu (7908) | CONSER VATIVE | eph | Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa. | 0 | 16 |
| 5738 | cg43982507 | 637 | CATGGCACGTC CGCGCTCTGGG CGC/GJCTGGC TGCTGCTCGCG TGIGCTG | C | G | Leu | Val (7909) | CONSER VATIVE | eph | Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa. | 0 | 9 (9p24) |
| 5739 | cg43949555 | 1239 | AATCTGATGGAT GACATAGAAAAG G/C/TAAGTAGAC GATGGTGTAAAT ACTTTC | C | T | Ala | Val (7910) | CONSER VATIVE | eph | Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCUS SP. (STRAIN SY), 545 aa. lpcis:SPTREMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa. | 6.7E-80 | 21 |
| 5740 | cg44011461 | 2430 | GATGAGGGCATA GATGCTGCTGAA G/C/JTGAGGT GTCAGTCAAGTA GTATTT | G | C | Thr | Ser (7911) | CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa. | 0 | 16 (16q24.1) |
| 5741 | cg43942273 | 1775 | CCTCAGGGGTC CAAGAGGCGGC TTG/CJCAAAAG GGATTCCAGGA AAATGGC | G | C | Ala | Gly (7912) | CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P23141 LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE) - HOMO SAPIENS (HUMAN), 567 aa. | 2.2e-310 | 16 |

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|------|------------|------|---|---|---|-----|---------------|------------------|----------|---|----------|----|
| 5742 | cg43942273 | 335 | TACTTCTTTGTC CTTCAGCTTCTG G[G/C]CCGCCTG GGTGTGGCACC AATCTG | G | C | Ala | Gly (7913) | CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P23141 LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE) - HOMO SAPIENS (HUMAN), 567 aa. | 2.2e-310 | 16 |
| 5743 | cg43957743 | 1066 | TGGCATACCTGG ATATTTTAAATCCA [G/C]TGGAGATAA AAGACAGCCAC TAGG | G | C | Thr | Ser (7914) | CONSER VATIVE | esterase | Human Gene SWISSNEW-ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment). pcls:SWISSPROT-ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment). | 1.9E-178 | |
| 5744 | cg43286057 | 1921 | GGACCCAGCAG GACGGGATATCT CC[A/C]TCCGCC CTCTCCTGGAGC ACTGTGA | A | C | Ile | Leu (7915) | CONSER VATIVE | gaba | Human Gene Homologous to SPTREMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa. | 1.9E-121 | 9 |
| 5745 | cg43286057 | 1925 | CCAGCAGGACG GGATATCTCCAT CC[G/A]CCCTCTC CTGGAGCACTGT GAGAAC | G | A | Arg | His (7916) | CONSER VATIVE | gaba | Human Gene Homologous to SPTREMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa. | 1.9E-121 | 9 |

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| 5746 | cg43969014 | 618 | GTCTGCTGCGTA GGTGGAGTTGGT C/A/CJCAAAGGTC ACAGGCTGGGA GGGGTC | A | C | Val | Gly (7917) | CONSER VATIVE | glucuronidase | Human Gene Similar to SWISSPROT- ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa. | 7.4E-80 | 5 |
| 5747 | cg43943531 | 2148 | TTTGAGCTTGAT GTCCTGGAGGAA G/C/GIATATACCA CAGAACATTGGC TGGTC | C | G | Ala | Gly (7918) | CONSER VATIVE | glycoprotein | Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa. | 0 (11q23.3) | 11 |
| 5748 | cg43943531 | 915 | GTCCTTTTCATCA GAGCACATGGCA G/C/GJCTTTGGG GTCCTTGGTCTC TGCCAG | C | G | Ala | Gly (7919) | CONSER VATIVE | glycoprotein | Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa. | 0 (11q23.3) | 11 |
| 5749 | cg43065549 | 1676 | GGTCAGAGCAGT CAAGGAGGGGA CG/C/GJTGCGGC TGACCCCGAGCAG TGTCAGA | C | G | Leu | Val (7920) | CONSER VATIVE | glycoprotein | Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa. | 0 (15q15) | 15 |
| 5750 | cg44034764 | 282 | CTCGGAGGTGT GGAGGGCTGTG AGT/G/JTCGTGA GAGTCCTGGGG GCTGGGCT | G | T | Asp | Glu (7921) | CONSER VATIVE | glycoprotein | Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa. | 0 (Xp21.2) | 7 |
| 5751 | cg44004239 | 177 | GACACCAAGAGG GGCTTAGGCTTC TT[G/CJATCCACA GCAGAGTTTCT GGGATT | G | C | Gln | Glu (7922) | CONSER VATIVE | glycoprotein | Human Gene SWISSPROT-ID:Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN-DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa. | 0 | |
| 5752 | cg43094362 | 292 | AGACGTGGACCA CTGGCTCACGAC A/C/TJGAGGCTG CCTCCTGGAATG GCTTGG | C | T | Arg | His (7923) | CONSER VATIVE | glycoprotein | Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa. | 9.7E-230 | 7 |

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|------|------------|------|--|---|---|-----|---------------|------------------|------------------|---|---------------------------|--|
| 5753 | cg43987514 | 964 | TAGCGCAGAGA GTTTCGTGGCCG CTGIC/GITTCGG CTGGCCCCCAGT GCCCCAGG | C | G | Ser | Thr (7924) | CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa. | 3.2E-215 | |
| 5754 | cg43958628 | 520 | TATTACTTAATTG GTGAAAAAATTG C/TATATTGTGAA CTTAAAGGATCA GTA | C | T | Ala | Val (7925) | CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa. | 8.6E-206 | |
| 5755 | cg43059879 | 369 | ACCACAGTGGCT TTTTTCACAGGT A/A/CJTITACAAAG ATGCTTTACAAC TTGGC | A | C | Leu | Val (7926) | CONSER VATIVE | glycoprot ein | Human Gene SWISSNEW-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa. Jcds:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa. Jcds:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa. | 6.6E-199 (17q23) | |
| 5756 | cg42845511 | 1726 | AAGATCTCGTAC GCTCAGTATGAG A/A/GJTACCTGA AGTCAGACAACA TGATC | A | G | Lys | Arg (7927) | CONSER VATIVE | glycoprot ein | Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa. | 2.9E-86 (20q12) | |
| 5757 | cg43054905 | 1258 | GTAGTCATAACC ATCCACATTAAAC C/G/AJCCGGCAT AACATAGAAATC CACAAG | G | A | Ala | Val (7928) | CONSER VATIVE | glycoprot ein | Human Gene Similar to SWISSPROT- ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa. | 2.6E-85 (13q14.1 1) | |

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| 5758 | cg44021513 | 1357 | TCTGGCCCTGCT GGTACGCGGG GCIG/CJTCTGCG CTCCTGCTGAAC TTCACTC | G | C | Asp | Glu (7929) | CONSER VATIVE | glycoprot ein | Human Gene Similar to SWISSPROT- ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa. | 8E-84 | 1 (1q22) |
| 5759 | cg43965366 | 1819 | TCITTTAAAGGA TTGGTAAACTGA AIC/TJTGTCACAG TCATGTCAGAAC CAACT | C | T | Val | Ile (7930) | CONSER VATIVE | glycoprot ein | Human Gene Similar to SWISSPROT- ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa. | 8.9E-61 | 6 (6p25) |
| 5760 | cg42713500 | 1094 | GAGGCCCGAGG CCGGGCCCTGC AGGIC/GJCGCG TAGCCAAACGAC GAGTGCTG | C | G | Gly | Ala (7931) | CONSER VATIVE | homeobo x | Human Gene SWISSPROT-ID:P78337 PITUITARY HOMEOBOX 1 (HINDLIMB EXPRESSED HOMEOBOX PROTEIN BACKFOOT) - HOMO SAPIENS (HUMAN), 314 aa. pcis:SPTREMBL- ID:P78337 HINDLIMB EXPRESSED HOMEOBOX PROTEIN BACKFOOT - HOMO SAPIENS (HUMAN), 314 aa. | 2.5E-174 | |
| 5761 | cg43928699 | 378 | GGTGAACGACTA CAGCAGCGCCCT CIC/GJTCCGCCA CGACCCCTGG GCAAACC | C | G | Leu | Val (7932) | CONSER VATIVE | homeobo x | Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa. | 3.8E-148 | 10 |
| 5762 | cg42908326 | 924 | AGCAGCCGCCA AGACCACCAGCA AGIAGJACTCCA GCATCGCCGATC TCAGACT | A | G | Asn | Asp (7933) | CONSER VATIVE | homeobo x | Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEOBOX PROTEIN - MUS MUSCULUS (MOUSE), 331 aa. | 5.8E-136 | 3 |
| 5763 | cg43285385 | 434 | TTCAATTAACAAAA AACTCTGCTAAA TIAJAAAATGCGG TTTTCACAGCAT TAGG | T | A | Tyr | Phe (7934) | CONSER VATIVE | hydrolas e | Human Gene TREMBLNEW- ID:G2951931 HUMAN GAMMA- GLUTAMYL HYDROLASE (EC 3.4.22.12) - HOMO SAPIENS (HUMAN), 318 aa. | 4.8E-173 | 8 |

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| 5764 | cg43929210 | 956 | ACTGGTTTGCA AAACGAGCCTTA A/C/TJTGCCCTTGA ATCTTGACACAT CATT A | C | T | Val | Ile (7935) | CONSER VATIVE | hydroxyst eroid | Human Gene SWISSPROT-ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17- BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa. | 0 | 5 |
| 5765 | cg44014662 | 1207 | TCTCGAGCAAGA CGTTCAGTCCTG T/C/TJCATATA GTCCATGAGGAA TAAAC | C | T | Asp | Asn (7936) | CONSER VATIVE | hypoxanthine | Human Gene Homologous to SWISSPROT-ID:P00492 HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) (HGPRT) (HGPRTASE) - HOMO SAPIENS (HUMAN), 217 aa. | 9.1E-115 X (Xq26) | |
| 5766 | cg43925670 | 312 | TTTAGAAGAAA AAGTCTGGTGAA G/T/AJTCCATAC TTGAATCAGGAT TGAGT | T | A | Thr | Ser (7937) | CONSER VATIVE | interferon | Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 . aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0 | 1 |
| 5767 | cg42862121 | 1623 | TCATGTGGGG CCAGACTGCAC GC/A/CJTCTGTGA GGCTCAGGCTTG GCAACA | A | C | Asp | Glu (7938) | CONSER VATIVE | interferon | Human Gene SWISSPROT-ID:Q13568 INTERFERON REGULATORY FACTOR 5 (IRF-5) - HOMO SAPIENS (HUMAN), 504 aa. | 4.2E-284 | 7 |
| 5768 | cg43510640 | 257 | GCCTGGACGAC CAACACTGGGAT GAT/CJGATGAG CAGAATGGTCAT GAAGATG | T | C | Ile | Val (7939) | CONSER VATIVE | interferon | Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa. | 1.2E-62 | |

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| 5769 | cg44339782 | 257 | GCCTGGACGAC CAACACTGGGAT GA[T]CGATGAG CAGAATGGTCAT GAAGATG | T | C | Ile | Val (7940) | CONSER VATIVE | interferon | Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa. | 1.2E-62 | |
| 5770 | cg43951261 | 4481 | TTTTACCCAGGC AAATCAAAAGCC A[C]GJTCCAGAAA AATCTTTGCATG ACAAA | C | G | Thr | Ser (7941) | CONSER VATIVE | isomeras e | Human Gene SWISSPROT-ID:Q02880 DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1626 aa. | 0 | 3 (3p) |
| 5771 | cg43989064 | 841 | AATGCTTTGGTA TTTGATGGGTCT A[G]JTTCAGAG CCTCTAAACAAC TGTC A | G | T | Leu | Ile (7942) | CONSER VATIVE | isomeras e | Human Gene SWISSPROT-ID:Q08752 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-40) (CYP- 40) (CYCLOPHILIN-RELATED PROTEIN) - HOMO SAPIENS (HUMAN), 370 aa. | 1.3E-200 | 4 |
| 5772 | cg44001328 | 901 | GGGGTTGAAATA GCGCAGCAGCA CT[G]A[CGTTCCA AGTCTTGCTGCTG CTGGCA | G | A | Ala | Val (7943) | CONSER VATIVE | isomeras e | Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa. lpcis:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa. | 9.9E-189 | 1 |
| 5773 | cg43961450 | 1230 | TCAGACTCAAGT CCAAGTCCTTTA A[G]T[CAGCAGT GCGTAGAACTGG GGTCT | G | T | Leu | Ile (7944) | CONSER VATIVE | isomeras e | Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-) - RATTUS NORVEGICUS (RAT), 361 aa. | 1.8E-117 | 5 |

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|------|------------|------|---|---|---|-----|---------------|------------------|--------|--|----------------|---------------|
| 5774 | cg43145505 | 314 | AGAATGCCTCCG TGAGGCTACATT A/A/GTAAACCAT AAGCATGAACCTA TTTAA | A | G | Ile | Val (7945) | CONSER VATIVE | kinase | Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa. pcsl:SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa. | 0 | 3 |
| 5775 | cg43019995 | 1904 | CCCCCAAACCTGC CCCCCGAGCTTC TTTAA/CCCCCATCA CCGTGCGCTGTT GCGAT | T | A | Phe | Tyr (7946) | CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P53667 LIM DOMAIN KINASE 1 (EC 2.7.1.-) (LIMK-1) - HOMO SAPIENS (HUMAN), 647 aa. | 0 (7q11.23) | 7 |
| 5776 | cg43947829 | 1855 | ACAAGCTTTTGT GCTTGCAAAGGA A/C/TJGCGCTGG GAAGAATTGGAA GGACAC | C | T | Val | Ile (7947) | CONSER VATIVE | kinase | Human Gene TREMBLNEW- ID:G2979628 AURORE RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa. | 1.5E-217 | |
| 5777 | cg43917871 | 1684 | CCCAAGATATCA TTGAAACGTGGA TIC/TJTAATTCAA TGTTGTATTTGT CAATA | C | T | Asp | Asn (7948) | CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa. | 2E-215 | 11 (20p13) |
| 5778 | cg43981459 | 1050 | ATTGTTTCCTGG TACAGACCATAT TIG/AJATCAGTTG AAGCTCATTTTA AGACT | G | A | Asp | Asn (7949) | CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:Q16539 MITOGEN-ACTIVATED PROTEIN KINASE P38 (EC 2.7.1.-) (MAP KINASE P38) (CYTOKINE SUPPRESSIVE ANTI- INFLAMMATORY DRUG BINDING PROTEIN) (CSAID BINDING PROTEIN) (CSBP) (MAX-INTERACTING PROTEIN 2) (MAP KINASE MXI2) - HOMO SAPIENS (HUMAN), 360 aa. | 3.1E-194 | 6 |

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|------|------------|------|--|---|---|---------------|------------------|--------------------|---|----------|----|
| 5779 | cg43987006 | 452 | GGAGAACTTGAG GGGGCTGACGG GG[G/A]CCCGGG GGCTACTGTTGA GGCGCCT | G | A | Ala (7950) | CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P21425 RIBOSOMAL PROTEIN S6 KINASE I (EC 2.7.1.-) (S6K) (P70-S6K) - RATTUS NORVEGICUS (RAT), AND ORYCTOLAGUS CUNICULUS (RABBIT), 502 aa. | 3.1E-176 | 11 |
| 5780 | cg44918533 | 870 | GGAAGTCAAGTA GGTGGAGCACA CA[G/A]CCTTGA GACGTGGCTGG CTGAACC | G | A | Ala (7951) | CONSER VATIVE | kinase | Human Gene Similar to SPTREMBL- ID:Q19632 SIMILAR TO SERINE/THREONINE PROTEIN KINASE. NCBI GI: 1086650 - CAENORHABDITIS ELEGANS, 821 aa. | 1.2E-70 | |
| 5781 | cg43991478 | 1274 | CTTTTCAAATAG CGCTTGTTGAAA [A/G]CAGTAGGT CCGACGGCCGG TGAGTC | A | G | Ala (7952) | CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa. | 0 | |
| 5782 | cg43991478 | 1275 | TTTTTCAAATAGC GCTTGTTGAAAA [C/T]AGTAGGTCC GACGGCCGGTG AGTCC | C | T | Ile (7953) | CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa. | 0 | |
| 5783 | cg43991478 | 1341 | ACGTCAGCAAGA TTGTGGGGCTGC A[G/C]CCGGGTG AGGTCACGCAG GATGGTG | G | C | Leu (7954) | CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa. | 0 | |
| 5784 | cg43920644 | 1423 | GTTCTGCAGGCG CTGCCCATGTGCG A[T/G]CATCTTGA TGACATCATCAG CAGAG | T | G | Leu (7955) | CONSER VATIVE | kinesin | Human Gene SPTREMBL-ID:Q99661 MITOTIC CENTROMERE-ASSOCIATED KINESIN - HOMO SAPIENS (HUMAN), 725 aa. | 0 | 1 |
| 5785 | cg42918454 | 2315 | CAGATGCAGCTG AGCCTGGCAGAA A[G/C]TGAAGCTT CCTTGGGAAACA CTAAC | G | C | Thr (7956) | CONSER VATIVE | laminin | Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa. | 0 | 1 |

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|------|------------|------|---|---|---|-----|---------------|------------------|------------------|---|----------|-----------------|
| 5786 | cg43983535 | 4190 | TCAACAGCCTCC TTCTTTTCTCCA [C/A]TGCAGTCAT GTTTTCTGATTT ACT | C | A | Val | Leu (7957) | CONSER VATIVE | laminin | Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa. | 0 | 6 (6q22) |
| 5787 | cg42536982 | 7508 | TCTGCATTGAGC GTTCTAATGCGT T[G/C]CAAGCGA AGGCGAATATAT CGTGCA | G | C | Gln | Glu (7958) | CONSER VATIVE | laminin | Human Gene SWISSPROT-ID:P25391 LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) - HOMO SAPIENS (HUMAN), 3075 aa. | 0 | |
| 5788 | cg42930646 | 1216 | CGTCAATGTTAC TGATGCGGATAG C[G/C]TATGGATG GAAATGGACGAT GAGGA | G | C | Val | Leu (7959) | CONSER VATIVE | laminin | Human Gene SWISSPROT-ID:P07221 CALSEQUESTIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ-BINDING PROTEIN) - ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa. | 1.8E-198 | 1 |
| 5789 | cg43966144 | 718 | AAGCTTGTGTCATG CCTCACAGCAGT G[C/T]GCACAAG ACTGCCCCAGCCCC AATGGA | C | T | Ala | Val (7960) | CONSER VATIVE | MHC | Human Gene Homologous to SWISSPROT-ID:P28068 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa. | 9.1E-147 | 6 (6p21.3) |
| 5780 | cg43111577 | 1089 | GCTTATGAAGAA GAGAACAAAGCT G[G/T]GGAGAAG ATGCCCGAGAGAG CTGTCC | G | T | Gly | Val (7961) | CONSER VATIVE | misc_cha nnel | Human Gene TREMBLNEW- ID:G1518639 CGMP-GATED CATION CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 1251 aa. | 0 | 16 (16q13) |
| 5791 | cg44019843 | 483 | GCCAGACCATCT CTGTGCACCCCTG G[T/C]GCCCTCTG GGCCCTGAGTG CTTGCGC | T | C | Val | Ala (7962) | CONSER VATIVE | misc_cha nnel | Human Gene SPTREMBL-ID:Q15478 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1836 aa. | 0 | 17 (17q23.1) |
| 5792 | cg40367355 | 1058 | CGGATTCTCCTC AACCAAGCCACT G[C/T]CAAAATTC ACGTGGACTCCT CCTCT | C | T | Ala | Val (7963) | CONSER VATIVE | misc_cha nnel | Human Gene SPTREMBL-ID:O00564 INWARDLY RECTIFYING K+ CHANNEL HOMO SAPIENS (HUMAN), 375 aa. | 4.1E-199 | 21 |

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|------|------------|------|--|---|---|-----|---------------|------------------|---------------|--|----------|---------------|
| 5793 | cg44929972 | 1149 | GTGACTTTTITTA TGAAGACATGGA [G/T]TCCTTGACG CAGATGCTTAGG GCCT | G | T | Glu | Asp (7964) | CONSER VATIVE | ngf | Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa. | 4.7E-214 | 7 |
| 5794 | cg43979114 | 287 | CCTGCAGGACAC ACCATCCCCAA GT/C]CCACTGG ACTAAACTCAG CATTCC | T | C | Val | Ala (7965) | CONSER VATIVE | ngf | Human Gene Homologous to TREMBLNEW-ID:G387171 NERVE GROWTH FACTOR - MUS MUSCULUS (MOUSE), 307 aa. | 1.5E-130 | 1 (1p13.1) |
| 5795 | cg43924936 | 3009 | CTCTTACTTCA GCCTCCTCTTCT TG/C]CAATTTCT TTTTCGTTGCAA TGTC | G | C | Gln | Glu (7966) | CONSER VATIVE | nuc_rec pt | Human Gene TREMBLNEW- ID:G2655006 THYROID HORMONE RECEPTOR COACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 920 aa. | 0 | 5 |
| 5796 | cg30421838 | 2486 | GCCAGCGCCTTT GCCCCGCCGCG GA[G/C]TTCACCC TGTGCGCTCGTCC ACCCCG | G | C | Glu | Asp (7967) | CONSER VATIVE | nuc_rec pt | Human Gene SWISSNEW-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa. [pcds:SWISSPROT-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa. | 0 | 11 (11q22) |
| 5797 | cg43315956 | 2799 | ACTTTCCCTTCA CTCTGCCAGCTG G[G/C]TAAATACA CCACGAAATCCA GTGCT | G | C | Gly | Ala (7968) | CONSER VATIVE | nuc_rec pt | Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa. | 2.3E-244 | 3 |
| 5798 | cg43315956 | 3542 | CAGTGGGTCA GTCAGTCACCCAC TC[G/C]TGCAATA AGACATTTTCTA GCTACT | G | C | Val | Leu (7969) | CONSER VATIVE | nuc_rec pt | Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa. | 2.3E-244 | 3 |
| 5799 | cg43972383 | 1195 | ATCTCTCTAAAAT AATGAAACTTGA A/C]AATGAAAAT AAAGCCTTGGAT AGCC | A | C | Glu | Asp (7970) | CONSER VATIVE | nuclease | Human Gene Homologous to SWISSPROT-ID:P12753 DNA REPAIR PROTEIN RAD50 (153 KD PROTEIN) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1312 aa. | 1.6E-149 | 5 |

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|------|------------|------|--|---|---|-----|---------------|------------------|------------------|--|----------|-----------------|
| 5800 | cg43947341 | 270 | CCAACTCCTTGG GTTCTTTCCCAG A/G/C CTCTTACT TTCTGAGGGCCC AGGCC | G | C | Ala | Gly (7971) | CONSER VATIVE | nuclease | Human Gene Homologous to SWISSPROT-ID:P07992 DNA EXCISION REPAIR PROTEIN ERCC-1 - HOMO SAPIENS (HUMAN), 297 aa. | 1.1E-115 | |
| 5801 | cg43951535 | 1535 | GGTGAACACAG CGAGTAGCTTTT A/G/C CCCTTTGC TTGGGCAACCT GCTGA | G | C | Ser | Thr (7972) | CONSER VATIVE | nuclease nhib | Human Gene SPTREMBL-ID:Q13181 RNASE L INHIBITOR - HOMO SAPIENS (HUMAN), 599 aa. | 2.5e-315 | 4 (4q31) |
| 5802 | cg44012756 | 2324 | ACCTGCAAAAGAC ATGACCAGTGGC T/A TCGTGTGCA CCTGCCGGGAG GGCTTC | A | T | Tyr | Phe (7973) | CONSER VATIVE | oncogen e | Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa. | 0 | |
| 5803 | cg43297056 | 2389 | CACCTGCTTCCCC AGCCGGCCCTTC A/C G GCGCTTG GCAATCAGTGTC CACTGC | C | G | Val | Leu (7974) | CONSER VATIVE | oncogen e | Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa. | 1.9E-103 | 20 (20q13.1) |
| 5804 | cg42849556 | 1051 | CTCCTAGTTCC AAAGCCCTTGA A/G A ACCCAG CTGTCACCCAGGC CAGAAA | G | A | Arg | Lys (7975) | CONSER VATIVE | oxidase | Human Gene SWISSPROT-ID:P19878 NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) (NEUTROPHIL NADPH OXIDASE FACTOR 2) (P67-PHOX) - HOMO SAPIENS (HUMAN), 526 aa. | 2.8E-287 | 1 (1q25) |
| 5805 | cg43999400 | 1236 | GATGTGACATGG GCAACACAAGAA A/A G AATTTCTT TGCAGTGGCTCA GGAGG | A | G | Lys | Arg (7976) | CONSER VATIVE | peptidas e | Human Gene SWISSPROT-ID:P27487 DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN- 2) (ADABP) - HOMO SAPIENS (HUMAN), 766 aa. | 0 | 2 (2q23) |
| 5806 | cg41626506 | 634 | AGCCAGCGACAT GGAGATCCAAGT C/A G CCCGAGG GAGCCTCCCGG AGTCTAC | A | G | Val | Ala (7977) | CONSER VATIVE | peroxida se | Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa. | 0 | 3 (3q26.3) |

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| 5807 | cg42691989 | 825 | CCGGGTGGTTGT GCCTCAGAGCG AA[G/C]CCACATT CTCAATCAGCAC GGCCCT | G | C | Ala | Gly (7978) | CONSER VATIVE | peroxidase | Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa. | 8.9E-101 | 14 (14q24.1) |
| 5808 | cg43956369 | 5054 | AGTTGAGCAAAA TTGGACACACCG GT[A]ACCTCGTT CTGACTGAGTTA CACAG | T | A | Thr | Ser (7979) | CONSER VATIVE | phosphatase | Human Gene SWISSNEW-ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R- PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa. pcis:SWISSPROT- ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa. | 0 | 6 |
| 5809 | cg43321833 | 2339 | CTCACGTTCCACC ATCAATCTCCTG G[G/T]GGTGATG CTCACCATCAAA AGGAGA | G | T | Gly | Val (7980) | CONSER VATIVE | phosphatase | Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment). | 0 | 20 |
| 5810 | cg43956187 | 390 | TACAGTAATAGA TTTTGGAGGAT G[A/G]TATGGA GTATAATGTTGT GATCAT | A | G | Ile | Val (7981) | CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:Q05209 PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.48) (PTPG1) - HOMO SAPIENS (HUMAN), 780 aa. | 0 | 7 (7q11.23) |
| 5811 | cg36899343 | 3058 | TGTTGGAAGCCG CAAATCTGCATT T[G/A]ATCCCTG CAGCTGAAGGCT TTCCC | G | A | Asp | Asn (7982) | CONSER VATIVE | phosphatase | Human Gene SPTREMBL-ID:Q13187 INOSITOL POLYPHOSPHATE 4- PHOSPHATASE - HOMO SAPIENS (HUMAN), 938 aa. | 0 | |

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| 5812 | cg43928335 | 3498 | CAGCAAGAGCTA ATAGTACCTCAT CTTATCATCATATA AATTGTATCTGT AAGAA | A | Glu | Asp (7983) | CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:P54613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS SCROFA (PIG), 602 aa (fragment). | 3.2E-302 | 11 (11q22) |
| 5813 | cg43984117 | 823 | GGTGACGTCAG GCCCAAACACTGAC AGG/CJTCACGC CCCGCTTGCTGA TCGAGCG | C | Thr | Ser (7984) | CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa. | 2.1E-273 | |
| 5814 | cg43988365 | 2812 | ACAGTGCAAGGC CATGAAGTGCGG CTT/CJTGCTGTG TGCACGACCTGG TAAAA | C | Lys | Arg (7985) | CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:Q14642 TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 412 aa. lpcis:SPTREMBL-ID:Q14642 INOSITOL 1,4,5-TRIPHOSPHATE 5- PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa. | 2.6E-227 | 10 |
| 5815 | cg42688448 | 1803 | GGTTCAGGAC GAGGCGCCCATG GTA[G/C]TCTGAG GCTGGGCATGG GCATGGGC | C | Thr | Ser (7986) | CONSER VATIVE | polymrase | Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIID - HOMO SAPIENS (HUMAN), 1083 aa. | 0 | 20 |
| 5816 | cg43968623 | 836 | GGCACCATTGAA GTGTCAAAGGTG G[G/T]TACGGGG ACTGTCCTGGCT GTGTGG | T | Gly | Val (7987) | CONSER VATIVE | polymrase | Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa. lpcis:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa. | 7E-199 | |
| 5817 | cg42937321 | 354 | GCGCGTGGTCAT CAACATCTCCGG G[C/G]TGCGCTT CGAGACGCAGC TGAAGAC | G | Leu | Val (7988) | CONSER VATIVE | potassium channel | Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa. | 5.4E-284 | 1 (1p21) |

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| 5818 | cg43331104 | 330 | GCGCGTGGTGA TCAACATCTCCG GG[G/C]TGCCT TCGAGACGCAG CTCAAGAC | G | C | Val | Leu (7989) | CONSER VATIVE | potassiu m_chann el | Human Gene SWISSPROT-ID:Q09470 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUKI) (HBK1) - HOMO SAPIENS (HUMAN), 495 aa. | 5.6E-266 | 12 |
| 5819 | cg43262191 | 773 | GGCTTTCGGGTA CCTGCTGGGCTC T[G/A]TCATGCTG CAGATCTTTGTG GACTA | G | A | Val | Ile (7990) | CONSER VATIVE | prostagla ndin | Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa. | 0 | 3 |
| 5820 | cg43923853 | 1874 | TGGAGTATGCAT ACAAGAAGTCGG C[C/A]TCCACTGG TATTTATGACAC GCCA | C | A | Glu | Asp (7991) | CONSER VATIVE | protease | Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa.lpcis:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa. | 2E-149 | 4 |

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|------|------------|------|---|---|-----|---------------|------------------|----------|---|----------|-----------------|
| 5821 | cg42918089 | 408 | CCTATAACTGGA ATGTTAAACTCC C[G/A]CGTCATAG AAATAATGCAGA AGCCC | A | Arg | His (7992) | CONSER VATIVE | protease | Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. | 2.4E-146 | 11 (11q21) |
| 5822 | cg43310246 | 1169 | GCAAGACAGTG GATGGGCCCG GGA[G/C]GTCAC GCTGCAGGCCAT GGCCGATG | C | Glu | Asp (7993) | CONSER VATIVE | protease | Human Gene Homologous to SWISSPROT-ID:P21662 NEUROENDOCRINE CONVERTASE 1 PRECURSOR (EC 3.4.21.93) (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) (PROPROTEIN CONVERTASE 1) (PC3) (FURIN HOMOLOG) (PROPEPTIDE PROCESSING PROTEASE) - MUS MUSCULUS (MOUSE), AND MUS COCKII, 753 aa. | 1.1E-141 | 20 (20p11.2) |
| 5823 | cg43310246 | 1170 | CAAGACAGTGGA TGGGCCCGGG AG[G/C]TCACGC TGCAGGCCATG GCCGATGG | C | Val | Leu (7994) | CONSER VATIVE | protease | Human Gene Homologous to SWISSPROT-ID:P21662 NEUROENDOCRINE CONVERTASE 1 PRECURSOR (EC 3.4.21.93) (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) (PROPROTEIN CONVERTASE 1) (PC3) (FURIN HOMOLOG) (PROPEPTIDE PROCESSING PROTEASE) - MUS MUSCULUS (MOUSE), AND MUS COCKII, 753 aa. | 1.1E-141 | 20 (20p11.2) |

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|------|------------|------|---|---|---|-----|---------------|------------------|------------------|--|----------|-----------------|
| 5824 | cg43074055 | 536 | CGACGCGGAGA ACAAACTGAACG ACjAGjTTCCT CATCCAGCTGAG CAGCCC | A | G | Ile | Val (7995) | CONSER VATIVE | protease | Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa. | 5.7E-138 | 19 (19p13.3) |
| 5825 | cg42309989 | 317 | GTTAACGCCTT ACTGACTGACTG AIGjACTATAGGC GAGGTGAAGGC TGGTCC | G | A | Ala | Val (7996) | CONSER VATIVE | protease | Human Gene Similar to SWISSNEW- ID:P31795 POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)] - RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN), 581 aa (fragment). pcIs:SWISSPROT- ID:P31795 POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)) - RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN), 581 aa (fragment). | 8.3E-82 | |
| 5826 | cg43979831 | 1345 | GGCACCGAGGC TGCAGCAGCCAC CAjGjCTTCGC GATCAAATTCTT CTCTGCC | G | C | Ser | Thr (7997) | CONSER VATIVE | protease nhib | Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa. | 1.1E-228 | 14 |
| 5827 | cg43268468 | 1183 | CGGTGAATGATG GATTCTGTTCGC TIGjCTCCGCTC CCAGCGAGAGG GCCGAG | G | C | Gln | Glu (7998) | CONSER VATIVE | protease nhib | Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa. | 2.6E-188 | 17 (17p13.3) |
| 5828 | cg43268468 | 1184 | GGTGAATGATGG ATTCTGTTCGCT GjGjTCCGCTC CCAGCGAGAGG GCCGAGA | C | G | Glu | Asp (7999) | CONSER VATIVE | protease nhib | Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa. | 2.6E-188 | 17 (17p13.3) |

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|------|------------|------|--|---|---|-----|---------------|------------------|------------------|---|----------|---------------------|
| 5829 | cg43268468 | 286 | GCCCCTGTGTCT GTGTCCCTCAGT A[C/T]GAAGATGA AAGGCTGGTTAA GGTGA | C | T | Val | Ile (8000) | CONSER VATIVE | protease nhib | Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa. | 2.6E-188 | 17 (17p13.3) |
| 5830 | cg43060292 | 907 | AGGGAAGTTGT GGGTCTAATTCA A[A/G]ACCTCAAG CCAAACACCATC ATGGT | A | G | Asn | Asp (8001) | CONSER VATIVE | protease nhib | Human Gene Similar to SWISSPROT- ID:P09008 CONTRAPSIN-LIKE PROTEASE INHIBITOR 6 PRECURSOR (CPI-26) (SERINE PROTEASE INHIBITOR 3) (SPI-3) (SPI-2.2) - RATTUS NORVEGICUS (RAT), 418 aa. | 2.2E-83 | X (Xq22.2) |
| 5831 | cg43938319 | 6705 | CAACAAGTATGG GGTCAGCCTCAT C[G/A]ATCCCAA ACGAAGGATATC CTCAC | G | A | Asp | Asn (8002) | CONSER VATIVE | struct | Human Gene SP TREMBL-ID:Q13402 MYOSIN VIIA - HOMO SAPIENS (HUMAN), 2215 aa. | 0 | 11 (11q13.5) |
| 5832 | cg44033566 | 3186 | GGACTCGCACC CTGAGCAGAAG GAG[A/G]ATATTG GTCAGCGGCAAA AACACTT | A | G | Asn | Asp (8003) | CONSER VATIVE | struct | Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.lpcis:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa. | 0 | 14 (14q22) |
| 5833 | cg43957486 | 2089 | ATCTGCGGGCC CGACTCGGCCCT TG[C/T]CGCCA CATTGGCACCGA CTGTGAC | C | T | Ala | Val (8004) | CONSER VATIVE | struct | Human Gene SWISSPROT-ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa. | 0 | 20 (20p11.2) |
| 5834 | cg43916919 | 230 | AAATTGCTTGAA GATGGGACTCTC A[C/T]GGCCCTG AGGCAGAAATCTC CACCTG | C | T | Arg | His (8005) | CONSER VATIVE | struct | Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.lpcis:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa. | 4.3E-188 | 2 (2cen) |

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|------|------------|------|---|---|---|-----|---------------|------------------|----------|--|-------------------------|----|
| 5835 | cg43918346 | 706 | GTGGCACCCGCC GGGATGGAAAGT GGC/GJAGAATG TTCATTTTCATCG CTCGGG | C | G | Gln | Glu (8006) | CONSER VATIVE | struct | Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa. | 2.4E-130 | |
| 5836 | cg43973395 | 262 | AGCAGCCGGAA GAGGAGGCTGC GGA/GCJGAGGA GGAGGAAGCCC CCGAAGAGC | G | C | Glu | Asp (8007) | CONSER VATIVE | struct | Human Gene Homologous to SWISSNEW-ID:P13805 TROPONIN T, SLOW SKELETAL MUSCLE ISOFORMS - HOMO SAPIENS (HUMAN), 277 aa.pcls:SWISSPROT-ID:P13805 TROPONIN T, SLOW SKELETAL MUSCLE ISOFORMS - HOMO SAPIENS (HUMAN), 277 aa. | 2E-114 (19q13.4) | 19 |
| 5837 | cg43961212 | 2158 | GATCTGGAAGCC GGACATCCTCTG A/GCJCAAGTCG ACTGATCCGCTG GCGAAC | G | C | Ala | Gly (8008) | CONSER VATIVE | struct | Human Gene Homologous to TREMBLNEW-ID:G1703715 PANTOPHYSIN=SYNAPTOPHYSIN HOMOLOG - MUS SP, 261 aa. | 2.4E-114 | 7 |
| 5838 | cg42522566 | 273 | GGCCAGGTGCA CAGGTGTACAGA GA/GA/GTCTACA GGCCTTGCACTG GCAGCC | G | A | Arg | Lys (8009) | CONSER VATIVE | struct | Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa. | 6E-55 | |
| 5839 | cg43977322 | 1441 | CTTCGGGTCTCC AGCTGCAGGTTT T/GCJCCCTCTCCA GCTGTAATTGT GGTTC | G | C | Gln | Glu (8010) | CONSER VATIVE | struct | Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa. | 1.5E-52 | 16 |
| 5840 | cg40388639 | 4912 | ATTTTGGAGTC ACCCTGCGAACG T/A/TJCGAAGTGA CCAACCGCCTTA GATCT | A | T | Tyr | Phe (8011) | CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa. | 0 (12q24.2) | 12 |

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|------|------------|------|---|---|---|-----|---------------|------------------|----------|--|---------|----------------|
| 5841 | cg43987111 | 1818 | GGAGTCTGAGAA CTTCGTGTATTT GIC/GJCCACAAG GGCAATAGAGCA GGTCTC | C | G | Gly | Ala (8012) | CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa. | 0 | 18 (1p34.1) |
| 5842 | cg43124627 | 1841 | ATTATTCAAGA GCTGCCAAAGAC TTA/GJTCAGTGG GAAGACAAAAG AAATGA | A | G | Ile | Val (8013) | CONSER VATIVE | synthase | Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. Jcds:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. | 7.7E-79 | 16 |
| 5843 | cg43124627 | 846 | ATCATGGCCATA TTCTTTACCAGT GIG/CJAACAAGT GGATATCCGAAA ATGACT | G | C | Gly | Ala (8014) | CONSER VATIVE | synthase | Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. Jcds:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. | 7.7E-79 | 16 |
| 5844 | cg43933068 | 580 | AGGTGGATGCC GAAGAAAAAGAA GAT/GJGTGAAAT CTTGTGCTGAGT GGGTGT | T | G | Asp | Glu (8015) | CONSER VATIVE | synthase | Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa. | 1.9E-75 | 12 |

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|------|------------|------|--|---|---|-----|---------------|------------------|----------|--|----------|-----------------|
| 5845 | cg42711317 | 1131 | TAAAGATGTGGG ATTGAAAAAAGA A/GA/JATATTGCA ATGTGGGAAGTA AATGA | G | A | Asp | Asn (8016) | CONSER VATIVE | thiolase | Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa. | 2.9E-221 | 11 (11q22.3) |
| 5846 | cg43278427 | 1120 | CTTGATGTGTAA TGAGAGCAGTAT G/C/GJAGAGCTT GCCCCAGAGAA AATCTGT | C | G | Gln | Glu (8017) | CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa. | 0 | 14 (14q31) |
| 5847 | cg43278427 | 1124 | ATGTGTAATGAG AGCAGTATGCAG A/G/CJCTTGCGC CAGAGAAATCT GTGAAT | G | C | Ser | Thr (8018) | CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa. | 0 | 14 (14q31) |
| 5848 | cg43306266 | 315 | CCTACACAGGCA TGTTGGCGCCCC GA/G/CJCGTTCC GCCGAGGCGCG GGGCAACC | G | C | Glu | Asp (8019) | CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa. | 4.8E-212 | 1 (1p31.2) |
| 5849 | cg42704646 | 311 | CCTACACAGGCA TGTTGGCGCCCC GA/G/CJCGTTCC GCCGAGGCGCG GGGCAACC | G | C | Glu | Asp (8020) | CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa. | 3.1E-194 | 1 (1p31.2) |
| 5850 | cg2514276 | 646 | TACGTCACCATC TTCTACGCCCTG G/G/CJCTACCCAC CACATCATGACG GCGAGG | G | C | Gly | Ala (8021) | CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P33032 MELANOCORTIN-5 RECEPTOR (MC5- R) (MC-2) - HOMO SAPIENS (HUMAN), 325 aa. | 7E-172 | |

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|------|------------|------|---|---|---|-----|---------------|------------------|----------------------|---|----------|----------|
| 5851 | cg40245117 | 1509 | TGCTCTGTCTATG GCTGCCCTTTATC TTA/CITCATCAAC TGCATCATCTAC TTTAA | A | C | Ile | Leu (8022) | CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P33765 ADENOSINE A3 RECEPTOR - HOMO SAPIENS (HUMAN), 318 aa. | 1.5E-167 | 1 (1p21) |
| 5852 | cg32423505 | 737 | CACATCAGAAGG AAGACTACCAT ATT/CJGGCAAAA CAAGCTTGAAAA GGCTA | T | C | Ile | Val (8023) | CONSER VATIVE | tm7 | Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa. | 1.2E-55 | 3 (3q21) |
| 5853 | cg43335562 | 339 | CAAGACCTAGCT CCCCAGCAGAG AGT/CJGGCCCC ACAACAAAAGAG GTCCAGC | T | C | Val | Ala (8024) | CONSER VATIVE | tm7 or | Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa. | 2.3E-55 | 8 |
| 5854 | cg43948839 | 798 | TCCCAGCGCGT GGGCCGCGGCT CCA/CJGTCCG CCACCGCGCCT CCTTTGCCA | C | G | Val | Leu (8025) | CONSER VATIVE | transcript factor | Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.lpcis:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa. | 0 | 17 |

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|------|------------|------|--|---|---|-----|---------------|------------------|----------------------|---|---------------------------|----|
| 5855 | cg43948839 | 799 | CCACAGCGCGTG GGCCGCGGCTC CACjGjCjTCCGC CACCGCGCCTC CTTTGCCAC | G | C | Asp | Glu (8026) | CONSER VATIVE | transcript factor | Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.lpcis:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa. | 0 | 17 |
| 5856 | cg43936136 | 2321 | TCTCCCAATTAT CTCGTTCACATC AIA/TATAAAGTG ATGTCGGGAGAG CCAAAT | A | T | Phe | Tyr (8027) | CONSER VATIVE | transcript factor | Human Gene SPTREMBL-ID:Q99840 TRANSCRIPTION FACTOR NFATX2 - HOMO SAPIENS (HUMAN), 1068 aa. | 0 | |
| 5857 | cg44130900 | 1488 | AGAAACAATTTA GCACACTGGTCG AIG/TJCAACAGC AACTGCTGGAAA AAAAA | G | T | Glu | Asp (8028) | CONSER VATIVE | transcript factor | Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment). | 7.5e-310 | 2 |
| 5858 | cg43920700 | 1055 | GCCCCAAGTCCA TCGATGACAGTG AIG/TJATGGAGA GCCCTGTTGATG ACGTGT | G | T | Glu | Asp (8029) | CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:Q14938 NUCLEAR FACTOR 1X (NF1-X) (NF-1/X) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGCA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 441 aa. | 2.1E-243 (19p13.3) | 19 |
| 5859 | cg43255478 | 667 | CGGCTGCAGGC GGCGCACCACG GGGjGjTGGACG CGGGCATGGGT GACAGCCTC | G | T | Gly | Val (8030) | CONSER VATIVE | transcript factor | Human Gene SPTREMBL-ID:Q92481 AP 2 BETA TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 449 aa. | 5.4E-236 | |

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|------|------------|------|---|---|---|-----|---------------|------------------|----------------------|---|----------|---------|
| 5860 | cg44012546 | 1960 | ATCCGGAGGGC CGGTGGTCCGG GCG[C]/TGGGGA TCCTCTCCAGC GGTTCCTC | C | T | Arg | His (8031) | CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:P70459 ETS-DOMAIN TRANSCRIPTION FACTOR ERF - MUS MUSCULUS (MOUSE), 551 aa. pcis:SPTREMBL- ID:P70459 ETS-DOMAIN TRANSCRIPTION FACTOR ERF (ERF) - MUS MUSCULUS (MOUSE), 551 aa. | 8E-199 | 19 |
| 5861 | cg43947199 | 2208 | CTTGGTGCCCGA GGAAAGGATGAA A[C/G]ATAAGTAT CTCGAGCATTTG TCTCA | C | G | Val | Leu (8032) | CONSER VATIVE | transcript factor | Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa. pcis:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa. | 4.2E-158 | 8 |
| 5862 | cg43982109 | 1818 | CTCTGCTCCAGA CCTTCCCAGGGC A[C/G]TCAGCAC GCCCCACATGCT TCGGAG | C | G | Ser | Thr (8033) | CONSER VATIVE | transcript factor | Human Gene Homologous to SWISSPROT-ID:Q00059 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1) - HOMO SAPIENS (HUMAN), 246 aa. | 5.6E-131 | 10 (7p) |
| 5863 | cg43918185 | 141 | AGAGCCCGGCC CGACGCCGCCA TGA[G/C]CGCCG CGCTCTCAGCC TGGACGGC | G | C | Ser | Thr (8034) | CONSER VATIVE | transcript factor | Human Gene Homologous to SWISSPROT-ID:Q03484 CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (TRANSCRIPTION FACTOR CELF) - RATTUS NORVEGICUS (RAT), 268 aa. | 2.1E-122 | 8 |
| 5864 | cg43918209 | 1269 | GTTGGGAAAGG CGCCCTCCGCTT GC[G/C]CCGGAG GGGGCTGCAGG CGATCGGC | G | C | Ala | Gly (8035) | CONSER VATIVE | transcript factor | Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa. | 2.7E-115 | 19 |

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|------|------------|------|---|---|---|-----|---------------|------------------|----------------------|---|---------|---------------|
| 5865 | cg44910798 | 258 | TGATGCCTAGTG AGACTTTGGCCT G/C/TJGGAAATC TCTATCACATATA ATTA | C | T | Arg | His (8036) | CONSER VATIVE | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 3.7E-89 | |
| 5866 | cg42849540 | 1841 | TCCAGAAAGAGC TCTGCAGGCGG AG/C/GJAAAGGC AGGCAGCCCG AAAGCAGA | C | G | Ala | Gly (8037) | CONSER VATIVE | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 2E-88 | 20 (20q13) |
| 5867 | cg42532030 | 318 | TATAAATGTGAT GAGTGTGGGAAA G/C/GJCTTCAGTC AGAGCTCAGATC TTATT | C | G | Ala | Gly (8038) | CONSER VATIVE | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 1.9E-57 | |
| 5868 | cg43984952 | 620 | CTGCTGCAGGAC AGCGACTGCAAG G/C/TJGTCTCCG GAGGGCCCGCA GGCCAC | C | T | Ala | Val (8039) | CONSER VATIVE | transcript factor | Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa. | 9.6E-53 | 12 (12q23) |
| 5869 | cg43984952 | 662 | GAGGCCACACAA CACGGCCTGGC CG/C/TJCTCAGA AGCACGAGCCG CAACGAA | C | T | Ala | Val (8040) | CONSER VATIVE | transcript factor | Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa. | 9.6E-53 | 12 (12q23) |

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|------|------------|------|--|---|---|-----|---------------|------------------|----------------------|---|---------|---------------|
| 5870 | cg43984952 | 733 | CTCGTCCCTTCAC CATTAATTCCT GIC/GJAGAACC ACCAGACGCCTT CAAGGC | C | G | Gln | Glu (8041) | CONSER VATIVE | transcript factor | Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa. | 9.6E-53 | 12 (12q23) |
| 5871 | cg43988978 | 4041 | GCGCCCTGGCA AATCCAGGAGAC AGIC/GJTCCGCC CAGCAGCTGGC CCCAGGTG | C | G | Ala | Gly (8042) | CONSER VATIVE | transport | Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa. | 0 | 16 |
| 5872 | cg43976701 | 2368 | CTCCTTTCAAAA GTCAACCCCTTCA C[G/A]CGTTCATA ATAATATGTATG CCTGG | G | A | Arg | His (8043) | CONSER VATIVE | transport | Human Gene SWISSPROT-ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa. | 0 | |
| 5873 | cg43976701 | 2370 | CCTTTCAAAAGT CAACCCCTTCACG C[G/A]TTCATAAT AATATGTATGCC TGGGG | G | A | Val | Ile (8044) | CONSER VATIVE | transport | Human Gene SWISSPROT-ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa. | 0 | |
| 5874 | cg44008864 | 1022 | GGGATGATGGTC AGCTGAGAGCG CA[G/C]GTCATG GAGGCCGATGT CTGCCACA | G | C | Leu | Val (8045) | CONSER VATIVE | transport | Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa. pcls: SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa. | 0 | |

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| 5875 | cg44008864 | 3466 | CACGTAGACCCA GAGGGTGATCA GGG/CJTCACCA GGAAGGGGCTG CACATCCA | G | C | Thr | Ser (8046) | CONSER VATIVE | transport | Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa.lcds:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa. | 0 | |
| 5876 | cg43300953 | 418 | CTGAGCAGCGC CTGGCGCAACAA CA[G/C]TGTCCC GCTGCGGCTGC GGGACGGC | G | C | Ser | Thr (8047) | CONSER VATIVE | transport | Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa. | 1.6E-261 | 5 |
| 5877 | cg42876412 | 487 | AGCATCGTGATG ACCACCTGCTCC A[G/C]CTTCTGTG CCTTGGGCATGA TGCCT | G | C | Ser | Thr (8048) | CONSER VATIVE | transport | Human Gene SWISSPROT-ID:Q14973 SODIUM/BILE ACID COTRANSPORTER (NA(+)/BILE ACID COTRANSPORTER) (NA(+)/TAUROCHOLATE TRANSPORT PROTEIN) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE) - HOMO SAPIENS (HUMAN), 349 aa. | 1.3E-184 | 14 |
| 5878 | cg42876412 | 532 | ATGCCTCTCCTC CTATACATCTAC A[G/C]CAAAGGG ATCTACGACGGA GACCTG | G | C | Ser | Thr (8049) | CONSER VATIVE | transport | Human Gene SWISSPROT-ID:Q14973 SODIUM/BILE ACID COTRANSPORTER (NA(+)/BILE ACID COTRANSPORTER) (NA(+)/TAUROCHOLATE TRANSPORT PROTEIN) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE) - HOMO SAPIENS (HUMAN), 349 aa. | 1.3E-184 | 14 |

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|------|------------|------|---|---|---|-----|---------------|------------------|------------------|---|----------|----|
| 5879 | cg43945806 | 591 | GTAGGCCCAAT CCTTCCACAGGG A/C/TGGAAATGAT GCTGCCAGTTCA CTGTC | C | T | Val | Ile (8050) | CONSER VATIVE | transport | Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa. | 2.2E-145 | 6 |
| 5880 | cg43269525 | 4020 | TCTCTTGACACC CATAATTCTCCG G/A/TJAAGAGTCT TCAAGAACAGTT GCTCG | A | T | Phe | Tyr (8051) | CONSER VATIVE | ubiquitin | Human Gene SWISSNEW-ID:Q92462 UBIQUITIN--PROTEIN LIGASE PUB1 (EC 6.3.2.-) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 767 aa. | 6.5E-163 | 15 |
| 5881 | cg43120117 | 2272 | TTC AAGGCTTTG CAAGGTTCTACA G/G/CJCGGGGCA GGGCCCCGGCT GTTCAACC | G | C | Gly | Ala (8052) | CONSER VATIVE | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN-- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa. | 7E-121 | |
| 5882 | cg43120117 | 2275 | AAGGCTTGCAA GGTCTACAGGC G/G/CJGGCAGGG CCCCGGCTGTTC ACCATC | G | C | Gly | Ala (8053) | CONSER VATIVE | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN-- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa. | 7E-121 | |
| 5883 | cg43944666 | 606 | TGTAATGAAGA AGGTATTACAGAA A/G/CJTAAAAAGA GACAACCAGGA GCATCC | G | C | Val | Leu (8054) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:O15228 DIHYDROXYACETONE PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.42) (DAP-AT) (GLYCERONE-PHOSPHATE O-ACYLTRANSFERASE) - Homo sapiens (Human), 680 aa. | 0 | 1 |
| 5884 | cg43926985 | 1454 | ACATGGATCCTC ATCCAGTTTGCA TT/GJTAGGAGGA CTGACAAATGGT AGTGG | T | G | Leu | Val (8055) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment). | 0 | 2 |
| 5885 | cg43978862 | 901 | GCACATACTCAT CCTCATAGCCTT C/T/GJTCATCAGT CTCCCCAGTGGT GGGAT | T | G | Glu | Asp (8056) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD43020 COAT PROTEIN GAMMA-COP - HOMO SAPIENS (HUMAN), 874 aa. | 0 | 3 |

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|------|------------|------|--|---|---|---------------|------------------|------------------|---|---|---|
| 5886 | cg43935402 | 1689 | AACTCTACAAAG TGCCCCCCAGCA G/C/GJAGACCTC CTCGTCTCCACC TCCACC | C | G | Gln (8057) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa. | 0 | 4 |
| 5887 | cg43964609 | 877 | CTGGGCATCCCC TTCAGGATCCAG G/A/CJCCACGGT CTGGTAAGCCCT GAAGTC | A | C | Val (8058) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P35443 THROMBOSPONDIN 4 PRECURSOR - Homo sapiens (Human), 961 aa. | 0 | 5 |
| 5888 | cg43971826 | 1014 | GATCTTACATCG AAAATGCCCTACA T/C/TJTTCACTAG CTATGATATCAA ATGTA | C | T | Asn (8059) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13576 RASGAP-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 1575 aa. | 0 | 5 |
| 5889 | cg43924112 | 4797 | ACTGGTTTAAAG GATTGAAGAATT C/A/CJCGCGTGA AGGGGAAAGTGT TCCAAA | A | C | Gly (8060) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa. | 0 | 6 |
| 5890 | cg43968933 | 1077 | TACTGTCTCAT CTTGCTAGAATG A/G/AJAATTCCTG AGACCCCTTGAAG AAGAT | G | A | Lys (8061) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB46275 SEC63 PROTEIN - HOMO SAPIENS (HUMAN), 759 aa. | 0 | 6 |
| 5891 | cg43999667 | 3945 | GTTTGTGTCAGGA CTTTTTTTTCTA C/TJAAGTTGTTTT TCTGGGATCACT GCT | C | T | Ile (8062) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment). | 0 | 6 |
| 5892 | cg43986140 | 4121 | TTGTCCTTTGGAA CTTGATATTAAGT [C/T]GACACTGCC TACAGATCCCCC CTGT | C | T | Asn (8063) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14156 HYPOTHETICAL PROTEIN KIAA0143 - Homo sapiens (Human), 885 aa (fragment). | 0 | 8 |

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|------|------------|------|--|---|---|-----|---------------|------------------|------------------|--|---|----|
| 5893 | cg43287089 | 1871 | ACTACGTTCTCA GAGTTGCTGAAT G[G/C]AATACACA ACAAAAGAGGG GACAGT | G | C | Gly | Ala (8064) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P55197 AF-10 PROTEIN - Homo sapiens (Human), 1027 aa. | 0 | 11 |
| 5894 | cg43329920 | 1862 | GTGGTCATCCTC TGATGACATCCG G[A/G]TCCTCCCA GCCAGAGGCCG GGCCCT | A | G | Ile | Val (8065) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa. | 0 | 12 |
| 5895 | cg43916884 | 732 | TTTCTGCAGCTG CTGCTTTGTCTT T[G/C]CAGCCCC CTTGGCTTTCTT GGCTGG | G | C | Ala | Gly (8066) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa. | 0 | 12 |
| 5896 | cg43924701 | 403 | AGTGGGTCCACA TAGGAGGCATCT A[T/G]TCTTTGT TACTGCTACTTT CATAA | T | G | Ile | Leu (8067) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13099 TG737 - HOMO SAPIENS (HUMAN), 824 aa. | 0 | 13 |
| 5897 | cg43924701 | 404 | GTGGGTCCACAT AGGAGGCATCTA T[T/G]TCTTTGT ACTGCTACTTTC ATAAG | T | G | Glu | Asp (8068) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13099 TG737 - HOMO SAPIENS (HUMAN), 824 aa. | 0 | 13 |
| 5898 | cg43929104 | 1023 | GCGAGGCAGGG CCAGCAGCAGG CGG[G/C]AGGGG ACGGCAAAACAG AACAGAAA | G | C | Gly | Ala (8069) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa. | 0 | 14 |
| 5899 | cg43055918 | 1732 | CCCCTATAGGTA ATCCCGAGGGG T[T/G/C]TCATCAA TGAAGCTATTCA GATGTG | G | C | Asp | Glu (8070) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa. | 0 | 17 |

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| 5900 | cg43964911 | 2446 | GAACAGGCACA GGATGTAGGG GTA[G/C]TCAGG AGTGGCGGCAG CTGGACCAG | G | C | Thr | Ser (8071) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q12767 HYPOTHETICAL PROTEIN KIAA0195 - Homo sapiens (Human), 1356 aa. | 0 | 17 |
| 5901 | cg43927434 | 239 | GGAGTCTTCATA GCATCTTCTCCA A[C/G]AGGTGCG AGGCTCTGGGG GCTCCGC | C | G | Val | Leu (8072) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa. | 0 | 19 |
| 5902 | cg43074645 | 3991 | CTGTGAGGCGCT CAGGAGAGAGA AG[G/C]AGCGAG AATTAGAACTGC AGCGTCA | G | C | Glu | Gln (8073) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O43152 KIAA0402 - HOMO SAPIENS (HUMAN), 1735 aa (fragment). | 0 | 21 |
| 5903 | cg17663981 | 395 | CAAAAACCCCTGC AGCTGCCCCAAA G[G/T]GGATGTC AACTACGCGTTT CTCCAT | G | T | Gly | Val (8074) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa. | 0 | 10 (10p11.2 3) |
| 5904 | cg43968854 | 6808 | CTTGAAAGAGCT CTCCAGACACC A[A/G]TATGCACT GACAAAGCCAC GACTCA | A | G | Ile | Val (8075) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa. | 0 | 10 (10q25) |
| 5905 | cg43968854 | 9484 | AATATCCCTGCG CTCCAGACGCCA A[A/G]ATAAGACT GAGGCAGAAC GCAAAAT | A | G | Asn | Asp (8076) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa. | 0 | 10 (10q25) |
| 5906 | cg43968854 | 9644 | AAACCCATACCT AGAGACAAAGTC A[G/C]TGAGAAC AAAGGTGCTTGA GGTCT | G | C | Ser | Thr (8077) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa. | 0 | 10 (10q25) |

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|------|------------|------|---|---|---|-----|---------------|------------------|------------------|--|---|----------------|
| 5907 | cg44026807 | 1745 | ATTGCGGGTGCTA CCCATCTCCTGC C/A/GTGTCCAG GTTGCACATGAG AAGGAA | A | G | His | Arg (8078) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14397 GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR) - Homo sapiens (Human), 625 aa. | 0 | 2 (2p23.3) |
| 5908 | cg43960198 | 1974 | GAAGAACCCACGC CAGGCAGGCGG GA/GC/JTTCGAG GTCTTGACATC AAAGCTG | G | C | Val | Leu (8079) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa. | 0 | 20 (20p13) |
| 5909 | cg43973129 | 1182 | ATAAAGGGTTAT CCAGGCGTCCA GG/GC/JCCCTGA GGACCTGGAGT GGGAGCGC | G | C | Gly | Ala (8080) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P05060 SECRETOGNANIN I PRECURSOR (SGI) (CHROMOGNANIN B) - Homo sapiens (Human), 677 aa. | 0 | 20 (20pter) |
| 5910 | cg44016815 | 1158 | AAGTTATTCTTG AACACAGGAAC [G/A]TGAAAAAGCT TCAACAAAAAGA ATTA | G | A | Arg | His (8081) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75330 INTRACELLULAR HYALURONIC ACID BINDING PROTEIN - HOMO SAPIENS (HUMAN), 724 aa. | 0 | 5 (5q33.2) |
| 5911 | cg44923983 | 299 | CGCGGCACAG CGACGAGAACG ACG/T/GJTGGC AGCCTCACAAA GGAGAAAG | T | G | Val | Gly (8082) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q09161 80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80) - Homo sapiens (Human), 790 aa. | 0 | 9 (9q22.3) |
| 5912 | cg43311566 | 932 | CACGACCTGCTC ACCACCTATGCC GT/CJTACCCACC CACAGGTGTCCT ACTGC | T | C | Val | Ala (8083) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment). | 0 | X |
| 5913 | cg43277466 | 2078 | TTCTCTCTCTTT TCCTCTCTCGCT G/CJGAGCTCTTC CAGCTCCTTTTG TTTC | G | C | Gln | Glu (8084) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa. | 0 | XY |

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| 5914 | cg43139712 | 1736 | AAGACCAGGAA AGGGGGGAGCA GG[G]TGACAAA GAGGGGCCGGG GCAAGCAC | G | T | Gly | Val (8085) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60378 F23858_1 - HOMO SAPIENS (HUMAN), 608 aa (fragment). | 0 | 0 |
| 5915 | cg43934588 | 1989 | ATGGCTAAGAGA AAAACCATTAAC A[C/G]AAATTGAA GAGTTTCTGAT GTAA | C | G | Gln | Glu (8086) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment). | 0 | 0 |
| 5916 | cg43972478 | 2072 | ACTATGTTAGGC TGGCTTTCTATC A[A/C]CGCGTGA AGGGATGGGCA AGATGCC | A | C | Leu | Val (8087) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O43284 HZW10 - HOMO SAPIENS (HUMAN), 779 aa. | 0 | 0 |
| 5917 | cg44003843 | 4744 | CCAGCTGCCCC CTGCCCTTTGT GG[C/T]CCGGGG CAGCTACAGCAG CATCGTC | C | T | Ala | Val (8088) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92545 MYELOBLAST KIA0257 - HOMO SAPIENS (HUMAN), 1805 aa (fragment). | 0 | 0 |
| 5918 | cg44015572 | 1259 | GCATTTATGCTC CAATCTGCATCA A[G/T]CAATAATT CTTCAAATACCT TCATT | G | T | Leu | Ile (8089) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q16526 PHOTOLYASE-LIKE 1 (PHOTOLYASE HOMOLOG) - HOMO SAPIENS (HUMAN), 586 aa (fragment). | 0 | 0 |
| 5919 | cg44024279 | 1902 | CAAATAACAGAG GAACAACCTTGAG G[C/G]TGTCATTG CAGATTTCTCAG GCCTG | C | G | Ala | Gly (8090) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa. | 0 | 0 |
| 5920 | cg43956210 | 1440 | CCTGTAATCCTT TCTGCTCCTTGG T[A/T]CTTAGATT TGATTAGCTATG GACAA | A | T | Tyr | Phe (8091) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa. | 3E-307 | 5 (5q13) |

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| 5921 | cg43949262 | 1762 | GTCCGTGGTGA GTCGTCCATGCA G[G/C]CCGGCAG CGCACAGTAAAT CTGGGA | G | C | Ala | Gly (8092) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa. | 9E-290 | |
| 5922 | cg43995003 | 988 | GCTGTAGAGAAA GTGAAGCGCACA A[A/G]AGATGAG CTAGAAGTCATT CATCTA | A | G | Lys | Arg (8093) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P10155 60 KD RO PROTEIN (60 KD RIBONUCLEOPROTEIN RO) (RORNP) (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) - Homo sapiens (Human), 538 aa. | 1.9E-289 | 1 |
| 5923 | cg40918088 | 1908 | AAAAGCCACAGA GGGCCGGATCA TT[A/T]CAGTGA GGATCACTACCC GCAAGG | A | T | Thr | Ser (8094) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51854 TRANSKETOLASE 2 (EC 2.2.1.1) (TK 2) (TRANSKETOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa. | 1.8E-287 X (Xq28) | |
| 5924 | cg43931056 | 1283 | GAGAGACATGGA CTTGATCATCAA G[T/C]AATTCTG TAACCTTCGAGA AAGCT | T | C | Val | Ala (8095) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15020 ORF - HOMO SAPIENS (HUMAN), 983 aa. | 4.5E-286 | 12 |
| 5925 | cg43949830 | 1073 | AGAGTCAGTCGG TTTGGACAGCAC A[C/G]TTTTCTG GATTCACCATTC AGACA | C | G | Ser | Thr (8096) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment). | 2.7E-281 | 16 |
| 5926 | cg43930921 | 535 | TGGGAGTGAAGT GCAGACACTTGG A[G/T]TCGATCCG CAGGAGCCGCTT GAGCA | G | T | Asp | Glu (8097) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q92983 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa. | 2.4E-280 | 11 |
| 5927 | cg43980328 | 717 | TTGGTTGCTTA GCCTGGATACCA G[A/T]GGAGAAG ATGTCATCCATA TCATCA | A | T | Ser | Thr (8098) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment). | 3.7E-262 | 10 |

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| 5928 | cg43254830 | 1270 | TTTAACATTCCAAAG AGCTCTGACCCA [G/C]AACAGATG CGACAGAGTTTG CTGAC | G | C | Glu | Gln (8099) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76821 KIAA0977 PROTEIN - HOMO SAPIENS (HUMAN), 1166 aa. | 1.3E-251 | 2 |
| 5929 | cg43962278 | 331 | TTATGGCTTAGA C GAAGGGAACAG CT[C/G]AAAGAAG CCCTTGAAGAGG GTGAGG | C | G | Glu | Gln (8100) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD01211 ASPARTYL AMINOPEPTIDASE - HOMO SAPIENS (HUMAN), 472 aa. | 1.5E-250 | 2 |
| 5930 | cg43973393 | 856 | AAGGAATGTGCC A ATATATACAAAC A[A/G]AGCTCTCT GTTACTTGAAGC TGIGC | A | G | Lys | Arg (8101) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q07617 INFERTILITY-RELATED SPERM PROTEIN - HOMO SAPIENS (HUMAN), 528 aa (fragment). | 1.5E-241 | |
| 5931 | cg43928134 | 1540 | TTCAGATGGAGA C GTACTTCTGAAT T[C/T]TACTATCA GAAATCCACAA AGATT | C | T | Arg | Lys (8102) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa. | 5.8E-240 | 8 |
| 5932 | cg44013460 | 1020 | CACTGAGTTGAA C AAAGCTGGACTT C[C/G]CAGCTCC AATTGGACCCAG CAGCAG | C | G | Gly | Ala (8103) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa. | 2.6E-237 | 1 |
| 5933 | cg43962127 | 788 | CGGCAAAAATCC C AACGTTGGGTGG A[C/T]AGAGGCG TCGATCATAAAG CACACA | C | T | Val | Ile (8104) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa. | 1.1E-233 | 7 |
| 5934 | cg43916785 | 3427 | CATTTCTCTTCTT C CTTTCTTCTTCTT C/T]TTTCAGCTTC TTTCTCATATTCC CG | C | T | Arg | Lys (8105) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment). | 2.5E-230 | 14 |

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| 5935 | cg43994204 | 1312 | GAGGCTCTGCTG CAGCTGTGCGAG G[C/T]CCTAAGCC TGATGGAACCTG TCAAG | C | T | Ala | Val (8106) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa. | 5.4E-221 | 19 |
| 5936 | cg43994204 | 654 | CTCCACCAAGGA GAGCTACCCGCA C[G/A]TCAAGACT GTCTGGGACGCA GCAGA | G | A | Val | Ile (8107) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa. | 5.4E-221 | 19 |
| 5937 | cg43989168 | 308 | CACCTCATTAC TCGTTTAGCTTT G[G/C]CTTCAATC CTCTGGCCACTT CCAAAT | G | C | Ala | Gly (8108) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P70541 TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP- GTP EXCHANGE FACTOR) - Rattus norvegicus (Rat), 452 aa. | 2.2E-215 | 1 |
| 5938 | cg43062448 | 1357 | TAAAGGAATCC ATAAAATGGTGA A[G/C]TCCCAGG AGCTCCACAAAT GTAGCC | G | C | Leu | Val (8109) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa. | 9.9E-213 (3q21.3) | 3 |
| 5939 | cg43049457 | 176 | CTGAGCCGACAT CTTCACTCATCA AT[C/G]TCATTCT TGCTCTCTCTCC CCTCC | T | C | Ile | Val (8110) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa. | 5.5E-212 | 2 |
| 5940 | cg44021565 | 1285 | ACGCTGACCCAT GGAGGCTGCAA AGT[A/G]ATCACT GCCTTTGTGGTG TCCACT | T | A | Thr | Ser (8111) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa. | 1E-203 | 1 |
| 5941 | cg44021565 | 388 | CCAGAAATCCAAA GAGATTCTTAAA T[C/T]CCACTTTT TCCTTCTTTTCAG TTCT | C | T | Asp | Asn (8112) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa. | 1E-203 | 1 |

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| 5942 | cg44128902 | 964 | AAGATGGAGTCA GCAGATCAGGC CGT/CJTGCTGA GCTCAACGGGA CCCAGGTG | T | C | Val | Ala (8113) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa. | 1E-201 | 1 (1p36.2) |
| 5943 | cg43967823 | 1057 | GAGGACATGCTG GCTATGCCCAAG GIC/TJGGCGCTG CTCAACGACTGC GTGTGC | C | T | Ala | Val (8114) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P54826 GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1) - Homo sapiens (Human), 345 aa. | 1.9E-193 | 9 (9q21.3) |
| 5944 | cg43944615 | 1568 | AGCTCACACTCT TTTCGGGTTTGT TIC/TJCTTCTGG GCACTCCTAGTT TTAAT | C | T | Arg | Lys (8115) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14877 FRPHE - HOMO SAPIENS (HUMAN), 346 aa. | 1.3E-192 | |
| 5945 | cg43973314 | 1045 | GCATTGCAAG CTCCCCCAAT GIC/TJCTTGAGAA TTTCAAAAGAGG TAATC | C | T | Ala | Val (8116) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:O75521 DBI-RELATED PROTEIN 1 (DRS-1) - Homo sapiens (Human), 364 aa. | 3.6E-192 | 6 |
| 5946 | cg43968431 | 492 | ATTCACCAACCCA CTTGGGTAAGGA GIC/GJCTTTGGG GTCCACCTGGG CCAGGTA | C | G | Gly | Ala (8117) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa. | 1E-191 | 11 |
| 5947 | cg42374050 | 580 | GGCTGGGTCAG AACCTGTTTAAAT GGT/CJGGCCAG CTTCTTGACC TCTTGGT | T | C | His | Arg (8118) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O15335 CHONDROADHERIN - HOMO SAPIENS (HUMAN), 359 aa. | 4.1E-191 | |
| 5948 | cg43119894 | 1986 | ACGGTCAGGGT CCACATAATGCA TTTC/TJTTTCAT GTCACATTCTTC AGCAGT | C | T | Arg | Lys (8119) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAA75235 LACTOSYLCEAMIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.9) - MUS MUSCULUS (MOUSE), 387 aa. | 2.3E-190 | 2 |

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| 5949 | cg43926852 | 1689 | AGTTCGGGAGG CCATCTGGATGG CTC/TJTGATCCA CTCTGTGCGCTC CTGGG | C | T | Arg | Lys (8120) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P08567 PLECKSTRIN (PLATELET P47 PROTEIN) - Homo sapiens (Human), 350 aa. | 2.9E-190 | 2 |
| 5950 | cg43996402 | 1313 | TGCAAAACCCACT GTTTCTCATCTC C[G/C]CTATTAGC TCCGAGGGGTG CATCGA | G | C | Ala | Gly (8121) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |
| 5951 | cg43996402 | 653 | TGCTTGTAAC ACCAGGACTTCT G[C/G]TCCGGCT TCTCCGGCTCCT TTCCTC | C | G | Ser | Thr (8122) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |
| 5952 | cg43996402 | 854 | CTGGCTTTTC CCGGTTATGGTG A[C/G]TGCTAGAA AGTTCTTCATGA AGCTT | C | G | Ser | Thr (8123) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |
| 5953 | cg43249389 | 1134 | AGAAGTGGATCC ATTGCTTCGAGG A[C/A]GTCACGG CCATCATTTTCT GTGTCG | C | A | Asp | Glu (8124) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa. | 1.4E-188 | 15 |
| 5954 | cg43965001 | 785 | AATGTGTCGCAG TTGGCTATTGGG A[A/G]CGTCCTTC ACAAAAATCCAG CTGAC | A | G | Val | Ala (8125) | CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD42861 NY-REN-2 ANTIGEN - HOMO SAPIENS (HUMAN), 570 aa. | 1E-178 | 14 |
| 5955 | cg43919917 | 1069 | TGACTCAGAGCA GGTGCCCCCAGG CA[C/A]TCCGCC GGCTCCGCCCG CGCACCCCG | C | A | Leu | Ile (8126) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60808 BK833B7.1 - HOMO SAPIENS (HUMAN), 339 aa. | 3.5E-178 | 22 |

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| 5956 | cg43989723 | 422 | CGGAGCTGCG GGCCGGAGCG AGGIC/TJTGAGAT CCGGGTCTTCCT CCAGCAG | C | T | Ala | Val (8127) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa. | 1.5E-175 | |
| 5957 | cg43989723 | 595 | GATAACAGGGCC ACTGGAAGAAGC CIG/CJTGGCAGT GGCTTCTCGCA GGTGCT | G | C | Val | Leu (8128) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa. | 1.5E-175 | |
| 5958 | cg43926685 | 490 | GTTCACTACAAT TCTAAATACAAG AIG/CJCTATGATA TAGCCCAAGATG CGCCG | G | C | Ser | Thr (8129) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa. | 2.5E-168 (1p36.33) | |
| 5959 | cg43329903 | 854 | GTGGTCATCCTC TGATGACATCCG GIA/GJTCCTCCCA GCCCAGAGCCG AGCCCT | A | G | Ile | Val (8130) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa. | 5.9E-167 | 12 |
| 5960 | cg43315424 | 213 | ATCATCAGGGAT GCTGGAGTCTG GCIC/GJCCCCC CACACCACCGA GCTGAAG | C | G | Gly | Ala (8131) | CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q60525 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA 5 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 538 aa. | 8.8E-158 | |
| 5961 | cg43990820 | 411 | GGCCCCAGGCT TTCTTCTTG CAIG/CJAACACTC TGCAAGGAGGC ATGCAGT | G | C | Leu | Val (8132) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 3.3E-150 | 3 |
| 5962 | cg42929454 | 414 | AAAGTCAGTGGT GTTCTTTTGAA CIG/CJCCAAGGC TAGAACACATTT TAAGCC | G | C | Ala | Gly (8133) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P78345 RNASEP PROTEIN P38 - HOMO SAPIENS (HUMAN), 283 aa. | 1.1E-144 | 10 |

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| 5963 | cg42706411 | 220 | CATCAGGTGGAGC GAGATTAGAAAC ATC/GTATTGATA AAATAACTCAAT ATGTT | G | Thr | Ser (8134) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P32856 EPIIMORPHIN (SYNTAXIN 2) - Homo sapiens (Human), 288 aa. | 3.8E-140 | 7 |
| 5964 | cg43260991 | 315 | GCGCCACACAGG GAGCCAGGAGC CTGT/GGCGCA GGCCCATGCGC AAGTCCTTC | G | Val | Gly (8135) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q60949 TBC1 - MUS MUSCULUS (MOUSE), 1141 aa. | 6.2E-140 | |
| 5965 | cg43303845 | 863 | AGAACAGCAACG GCAAAAGGAGCT G/C/GJAGCGGA AAGGCTGGAGC GAGAAAG | G | Gln | Glu (8136) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa. | 1.9E-138 | |
| 5966 | cg43952219 | 1066 | TGCCACTCGCCA GTTTGCCAAAGA G/C/ATCTACCAG ATTTTTTGGAG GCATA | A | Glu | Asp (8137) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa. | 2.5E-136 | X |
| 5967 | cg43984220 | 226 | GGTCAGCGGG CACCAGGTGCT CT/G/CJGAAGAG CTTGAGGATGTG GTTCTCG | C | Gln | Glu (8138) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa. | 5.8E-135 | 19 |
| 5968 | cg43950180 | 577 | TATGGAATCACA GTTATCTCCTTG C/C/TJTGATTCA ATTTGGTTGAG AAGTG | T | Arg | Lys (8139) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q09996 PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS) - Caenorhabditis elegans, 1198 aa. | 3E-131 | 5 |
| 5969 | cg43918152 | 369 | AACAGACAGTTA CGCAGCCATTTC A/G/CJAAAGTGGAT CGATTGCAGTCA GAGCC | C | Glu | Gln (8140) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa. | 5E-131 | 9 (12q23) |

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| 5970 | cg43928955 | 175 | GCCTAGTACTCT TATGTGAAGTCT A/C/GCAAGCTTG TGCTCAAGGGAA CCAAG | C | G | Thr | Ser (8141) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa. | 1.3E-129 | |
| 5971 | cg43917824 | 646 | CCAGTGCCCAAC ATGACACCTTCA G/G/CJAGTCGGC CGGAGAGAGCA CTCGTGT | G | C | Gly | Ala (8142) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:000236 KIAA0251 - HOMO SAPIENS (HUMAN), 820 aa (fragment). | 1.3E-128 | 16 |
| 5972 | cg43931286 | 511 | GTGTTTGAAGAC CCAGTCATCAGT A/A/GJATTCACCA ACATGATGATGA TAGGA | A | G | Lys | Arg (8143) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD2775 30S RIBOSOMAL PROTEIN S7 HOMOLOG - HOMO SAPIENS (HUMAN), 242 aa. | 1.4E-128 | 17 |
| 5973 | cg43307940 | 438 | TACATCCCCTGG AGATGGCCCCACC T/T/CJCTTTTGG TCAGTTGGCAAA CCAGC | T | C | Lys | Arg (8144) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa. | 8.1E-125 | 15 |
| 5974 | cg43067745 | 160 | CACAGAAAGAGA TCACAGACTCCC T/A/GJCCCTTAGAA GAAGGGAGGTG GTAGAT | A | G | Val | Ala (8145) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |
| 5975 | cg43926002 | 390 | CGGGCACAGAA ACACAGCAGCG GGA/G/CJGAGCA ACACCAGCACTG CCAACAGA | G | C | Ser | Thr (8146) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa. | 1.6E-116 | 10 |
| 5976 | cg41045063 | 611 | AGCTTCCACCAA GGTTGTACCAATT G/C/TJCTCCAG CGCCTGACGCC CCTGGCC | C | T | Ala | Val (8147) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P32970 CD27 LIGAND (CD27-L) (CD70 ANTIGEN) - Homo sapiens (Human), 193 aa. | 3.3E-102 | 19 (19p13) |

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| 5977 | cg43980312 | 2657 | AACAGTATCTTT GGAAGTGGTCG AGATJTGTGTG AGCTCTGGACTC TCTACA | A | T | Ser | Thr (8148) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa. | 7.9E-101 | 8 (8q22) |
| 5978 | cg43252708 | 534 | CCTTGCCGAGAG ATTGACGTGTC C[G]ATTTGCATC CTGGGCTCCCT CGCTT | G | A | Val | Ile (8149) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75679 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa. | 2.1E-100 | |
| 5979 | cg43927693 | 713 | GTATGGCGGGA CAACCATGGCTG GC[G]ATGGGG ACGGCGGCTGC CAGAGTGA | G | A | Arg | His (8150) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa. | 5.3E-95 | 22 |
| 5980 | cg42835634 | 532 | TACTGTGACTTC TTCTACTTGAT G[G]TGACCAA GGTAGGTCCTG GGATGAC | G | T | Gly | Val (8151) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43731 ER LUMEN PROTEIN RETAINING RECEPTOR - HOMO SAPIENS (HUMAN), 214 aa. | 3E-92 | 22 |
| 5981 | cg43921592 | 453 | CCCGGATGTG GATACCTATAAG GA[G]ATTTCAT ATTTGTTGCGG AGTTCA | G | T | Glu | Asp (8152) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16548 BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC- SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) - Homo sapiens (Human), 175 aa. | 4.9E-92 | 15 |
| 5982 | cg43978148 | 536 | GGAGAATTGCCA GACTTGTTGTAC C[AG]ATTATATC ATCTCAGTCTTG AATT | A | G | Asn | Asp (8153) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment). | 4E-90 | 16 |

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| 5983 | cg43978148 | 690 | GAAAAAGAGGTT GTTGCTGTAGCC C[A/G]TGCTGTT ATCAAGCAATGC TCAGC | A | G | His | Arg (8154) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment). | 4E-90 | 16 |
| 5984 | cg43059113 | 456 | GCACTCAGCAGT GCGTGCTTTTTC TTTCTGGGAAA GGCAGGACAAC CAGCTT | T | C | Lys | Arg (8155) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa. | 7.4E-89 | 3 |
| 5985 | cg43960450 | 1409 | CTTTCTCCTGCAG ACGTTCAATAAT A[G/C]CAGCTAG ATTAGCCTCAG GTTTT | G | C | Ala | Gly (8156) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa. | 8.5E-88 | 8 |
| 5986 | cg43960450 | 1544 | TTCTCGCTCGTG TCCCTCTTCTC T[G/A]CCAATTGT TTCAGCACCTGG GCCTC | G | A | Ala | Val (8157) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa. | 8.5E-88 | 8 |
| 5987 | cg43955651 | 519 | GCCACACTCTCT GTGCATCGGCTT G[C/T]GCGTGT CGGGTGAAGG AGTTGAA | C | T | Arg | His (8158) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa. | 1.1E-87 | 2 |
| 5988 | cg43922714 | 227 | GAACTAGGAGAA ACATTAAATTTA [A/G]AGAAGCTGT TGTTTTAGGGAG CACG | A | G | Lys | Arg (8159) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34141 CGI-146 PROTEIN - HOMO SAPIENS (HUMAN), 193 aa. | 9.8E-87 | 19 |
| 5989 | cg43996941 | 481 | TGAAGAAACTC AGCTAAATTTCC T[G/A]TAGGAAG GAGAGATTTGA CATGCT | G | A | Val | Ile (8160) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q16044 PREPRO-MELANIN- CONCENTRATING HORMONE - HOMO SAPIENS (HUMAN), 165 aa. | 3.1E-83 | 12 (12q23) |

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| 5990 | cg43920730 | 849 | TTTTCTCTTTG TTTGTCCACTA C/GAAGCTCACT TCTCAGAGCTAA ACTC | C | G | Val | Leu (8161) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15182 CENTRIN - HOMO SAPIENS (HUMAN), 167 aa. | 5E-83 | |
| 5991 | cg43969140 | 528 | TCGGCCCCACTC GCCAGTCACAA G/GA/CATCATTA ACACTCAGACAG GCCAC | G | A | Ala | Val (8162) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa. | 1.7E-80 | |
| 5992 | cg43969140 | 595 | GCCTTCAGAGCC TCAGCCTGCTCC A/C/A/AAACCCCTG GCAGGTGTGTCT TGGAA | C | A | Val | Leu (8163) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa. | 1.7E-80 | |
| 5993 | cg44936941 | 716 | AAAATACCAAC AGTTATTGCGTA C/C/TJTTGTAGCA TATGCTGGTTGT ACTTC | C | T | Arg | Lys (8164) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa. | 7E-77 | 1 |
| 5994 | cg44936941 | 755 | TGGTTGTACTTC ATGAGGGTTGCG A/C/TJGGTCAGAC CAGAAAAACAGC AGTCT | C | T | Arg | His (8165) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa. | 7E-77 | 1 |
| 5995 | cg38622616 | 345 | AGAATTCTTCAA TTTCACCTTCATC [G/C]TCCATGGG TTCTTCTAAACTT GGAC | G | C | Asp | Glu (8166) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD40849 SIRTUIN TYPE 1 - HOMO SAPIENS (HUMAN), 555 aa. | 6.3E-76 | |
| 5996 | cg43969639 | 959 | CCAGACCCCACTC TGCAGTAAGGTG TTT/ATCAAAACA GAAAATGCACAA ATGAA | T | A | Glu | Asp (8167) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa. | 2.3E-74 | 3 |

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|------|------------|------|---|---|---|-----|---------------|------------------|------------------|--|---------|--|
| 5997 | cg42896021 | 427 | GCATGCTTCACA CAGTGGCTGTGC C/GA/JCCTTCACA ATGAAGTGAACC GGAAG | G | A | Arg | His (8168) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa. | 1.4E-69 | |
| 5998 | cg42896021 | 481 | GGCAAGCCTGAT TTTGACTGCTCA A/GA/JAGTTGATG AGCGATGGCGT GACGGC | G | A | Arg | Lys (8169) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa. | 1.4E-69 | |
| 5999 | cg43942922 | 344 | GTACACCTCTGAG CCCACATCTCAG G/C/TJCACTAGG GGAAGAAAAAT AGGTCC | C | T | Ala | Val (8170) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.3E-68 | |
| 6000 | cg43955219 | 1361 | GCCTCATGCTCT CTGGGATTGCAG A/C/GJCATCCAG GTCTGTCTTCGC CCCTGT | C | G | Asp | Glu (8171) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P39194 III ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa. | 6.4E-68 | |
| 6001 | cg43927424 | 302 | AGCGCAGTATT CAGAGAAAAAGTA T/TJCTCTTCAG CTGAAGTACCCG CACCT | A | T | Thr | Ser (8172) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa. | 1.9E-65 | |
| 6002 | cg43927424 | 366 | GTCGGGCAGGA ACAGAAACACAC CTA/TJCTGCCA CTAGAAGTCTGT AATAIT | A | T | Tyr | Phe (8173) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa. | 1.9E-65 | |
| 6003 | cg43082068 | 765 | TTCTGGAGCTG CTGGTGAAAGAA A/C/GJCTCTGGA GGCCCGGACTC CCCGGAC | C | G | Thr | Ser (8174) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:G2352941 LEUKOCYTE- ASSOCIATED IG-LIKE RECEPTOR-1 - HOMO SAPIENS (HUMAN), 287 aa. | 2.5E-65 | |

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| 6004 | cg42381630 | 271 | TTGGCCTAGACC AAGGCGCTATGT A[C/G]AGCCTCCT GAAATGATTGGG CCTAT | C | G | Gln | Glu (8175) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SP TREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa. | 5.9E-64 | |
| 6005 | cg43950549 | 466 | TGACTGGATTAA AAGGTGTCAAGA A[C/G]TTCAGAA GGGTCAGAAATAG GAAGT | C | G | Leu | Val (8176) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa. | 1.4E-62 | |
| 6006 | cg43308257 | 839 | TCAGAGCCGGC GGTGGTGCAGA AGA[G/A]AGCCA GTGGCCAGTGA CCACACAGC | G | A | Arg | Lys (8177) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa. | 2.9E-62 | |
| 6007 | cg40968986 | 269 | TGAGCTGGAGCA GGAGCAAGAGA GA[G/C]AGGGCT CCAGAAATCATTG CCAGAA | G | C | Glu | Gln (8178) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa. | 5.1E-58 | 11 (11p15.2) |
| 6008 | cg43052776 | 401 | ACCAACAAAGAT TTCAGGGATTTT G[T/C]CAGGGAG AAAAAGTATCGG ACAGAA | T | C | Val | Ala (8179) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43247 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 323 aa (fragment). | 3.6E-57 | |
| 6009 | cg43942680 | 697 | CTCGGAGGAGA GCGCCCTCAATC AC[G/C]TGCAGC ACCCGAGCGAC GAAGCCGA | G | C | Val | Leu (8180) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD38498 T-CELL ACTIVATION PROTEIN - HOMO SAPIENS (HUMAN), 127 aa. | 1.8E-55 | 10 |
| 6010 | cg43511804 | 864 | GGGCTGATCTT CATACTCATCTT CT[T/C]TCATTGAG TACCATGACCCC TTCCA | T | C | Lys | Arg (8181) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa. | 3.1E-51 | 4 |

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| 6011 | cg44341803 | 864 | GGGCCTGATCTT CATACTCATCTT CT/CJTCATTGAG TACCATGACCCC TTCCA | T | C | Lys | Arg (8182) | CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa. | 3.1E-51 | 4 |
| 6012 | cg43291028 | 1907 | CTCTAGGCCCTT GAGCTGATACTG A[G]ATGATGGTG GCATTCTTTATCT TCAC | G | A | Thr (8183) | Ile (8183) | NON- CONSER VATIVE | angiopoietin | Human Gene SWISSNEW-ID:Q02763 ANGIOPOIETIN 1 RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR TIE-2) (TYROSINE- PROTEIN KINASE RECEPTOR TEK) (P140 TEK) (TUNICA INTERNA ENDOTHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 1124 aa.lpdls:SWISSPROT-ID:Q02763 ANGIOPOIETIN 1 RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR TIE-2) (TYROSINE- PROTEIN KINASE RECEPTOR TEK) (P140 TEK) (TUNICA INTERNA ENDOTHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 1124 aa | 0 | 9 |
| 6013 | cg43921977 | 2748 | ATTATTCATCCAA T GTTTCCATATTA T/CJCTTCAAAAAA TTCAGGGAGATC CTG | T | C | Asp (8184) | Gly (8184) | NON- CONSER VATIVE | apoptosis | Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa. | 0 | 20 |
| 6014 | cg43921977 | 2753 | TCATCCAAGTTT A CCATATTATCTTC IACJAAAAAATTCA GGGAGATCCTGA AAGT | A | C | Phe (8185) | Leu (8185) | NON- CONSER VATIVE | apoptosis | Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa. | 0 | 20 |
| 6015 | cg43921977 | 2754 | CATCCAAGTTTC A CATATTATCTTCA IACJAAAAAATTGAG GGAGATCCTGAA AGTT | A | C | Phe (8186) | Cys (8186) | NON- CONSER VATIVE | apoptosis | Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa. | 0 | 20 |

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| 6016 | cg43948568 | 2080 | CCAGAGCCTGC CCGCTGGATGTC CTTACJGATCATA TGGGGCCTGAA CAGCTCG | A | C | End | Glu (8187) | NON- CONSER VATIVE | apoptosis | Human Gene SWISSPROT-ID:P55211 CASPASE-9 PRECURSOR (EC 3.4.22.-) (CASP-9) (ICE-LIKE APOPTOTIC PROTEASE 6) (ICE-LAP6) (APOPTOTIC PROTEASE MCH-6) (APOPTOTIC PROTEASE ACTIVATING FACTOR 3) (APAF-3) - HOMO SAPIENS (HUMAN), 416 aa. | 2E-222 | 1 |
| 6017 | cg42913771 | 469 | GCTTGTTCAAAG GAGACAAGTGTC AIGCJAGCCTGG TTGGAAAACCCA AGATAT | G | C | Gln | His (8188) | NON- CONSER VATIVE | apoptosis | Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa. | 6.2E-116 | |
| 6018 | cg43277632 | 1703 | GACTGCAACAGT TCTTTATAATCCC TGTGCTGTAATTA GCCCAGAAAGAAC TCAG | T | G | Ser | Ala (8189) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa. | 0 | 13 (13q14.3) |
| 6019 | cg43277632 | 774 | AGCATGAAGGTT TCCCTGGAACAA GIGAJCAGTGCC ACTGTGAAATAT GTGCCA | G | A | Gly | Asp (8190) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa. | 0 | 13 (13q14.3) |
| 6020 | cg43252813 | 1307 | CCAGAATCCCTG AGAAAAAGCAATA GATJGGCTGTAT CACCGGGGCTAT ATAGA | A | T | Glu | Val (8191) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene SWISSNEW-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa. pcis:SWISSPROT-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa. | 0 X (Xq12) | |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|---------------------------|--|----------------|
| 6021 | cg43252813 | 3832 | CTCAAAATGCTCT TAATGCTCAGCA GIC/TATAAAGTC CTCATTGGTAAC CGGGA | C | T | His | Tyr (8192) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene SWISSNEW-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.lpcis:SWISSPROT-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa. | 0 X (Xq12) |
| 6022 | cg43931944 | 268 | ACTATTCAGGTG TATGAAGAACT TTC/GTGGTGTGT CTGTTGGAGATC CTGTA | C | G | Ser | Cys (8193) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa. | 0 |
| 6023 | cg43939527 | 1246 | AGATGACCTCTC TGGTGCTGACAT C/A/CJAGGCAATC TGTACAGAAAGCT GGTCT | A | C | Lys | Gln (8194) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene SWISSPROT-ID:P49014 26S PROTEINASE REGULATORY SUBUNIT 4 (P26S4) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 440 aa. | 14 1.5E-233 |
| 6024 | cg43958825 | 197 | GTGGGTGAGCT CCGTGGCACCC CTG/C/GJGCAGT GCGATCATGCC GCCTCCAC | C | G | Arg | Pro (8195) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa. | 11 7.8E-228 |
| 6025 | cg43958825 | 198 | TGGGTGAGCTCC GTGGCACCCCT GC/G/CJAGTGC GATCATGCCCGC CTCCACA | G | C | Arg | Gly (8196) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa. | 11 7.8E-228 |
| 6026 | cg43933600 | 304 | GCTCCAGGAGG AGGGCCGAGAA GGT[G/T]TGACC TTGTCTGCCCGC CGCACCT | G | T | Asn | Lys (8197) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa. | 19 4E-185 |

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| 6027 | cg44028571 | 415 | GGAAGTTATGGG TTTGATGCTTGG A/A/G/A/ATTTGTT GATGATTATACC GTCAG | A | G | Lys | Glu (8198) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene SPTREMBL-ID:O00487 26S PROTEASOME-ASSOCIATED PAD1 HOMOLOG - HOMO SAPIENS (HUMAN), 310 aa. | 3.8E-164 | |
| 6028 | cg43284434 | 1995 | ACTAACTTATATC GCAGAGTGGAAA [G/A]GGGGCCTC CTGGAGCACAAG ATGGG | G | A | Gly | Arg (8199) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa. | 4E-121 | 6 |
| 6029 | cg43251803 | 2910 | GGACCATCTGAG TCCACGTACTGC C[G/A]GCGTTTGA GGTAGCAGGAC ACTGCC | G | A | Arg | Trp (8200) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment). | 3.1E-105 | |
| 6030 | cg43251803 | 2981 | ATCTGAATCTGC TCGGTACGCACT C[G/A]TTTCATGA CTGAACATCCCA GGCGG | G | A | Arg | End (8201) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment). | 3.1E-105 | |
| 6031 | cg43132502 | 357 | GCTGGCCCCAG TGCAGTGGGTG GCA[C/T]CGCCG AGGCTGCTGTTA CGGCTCAT | C | T | Pro | Ser (8202) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa. | 9.4E-58 | 11 |
| 6032 | cg44000476 | 1164 | AACGGTCTCAGA GGCTGGGTAATC T/A/C]CCTGAACA GCTCCCCCATGG GCACC | A | C | • End | Glu (8203) | NON- CONSER VATIVE | ATPase_ associate d | Human Gene Similar to SPTREMBL- ID:P78344 P97 - HOMO SAPIENS (HUMAN), 907 aa. | 3.8E-53 | 3 |
| 6033 | cg43966234 | 1864 | TGGAAACATGAG CATTGAGTTTCTT [T/G]GTACAGTGT ACAAAGGTGAATA TC TT | T | G | Cys | Gly (8204) | NON- CONSER VATIVE | biotindep | Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa. | 0 | 13 (13q32) |

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| 6034 | cg43255401 | 810 | GCTGGAAGTGG AGCCCGTGGGA ATGACJCGCGT GAAGGGGACCG CGTGGAAT | A | C | Thr | Pro (8205) | NON- CONSER VATIVE | cadherin | Human Gene SWISSPROT-ID:P43121 CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELANOMA- ASSOCIATED ANTIGEN MUC18) (MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOTHELIAL- ASSOCIATED ANTIGEN) (CD146 ANTIGEN) (MELANOMA ADHESION MOLECULE) - HOMO SAPIENS (HUMAN), 646 aa. | 0 | 11 |
| 6035 | cg44026834 | 1466 | CTGCCCGATGGA GAGCGTAGAAC GTCAJATCGCTG TACATAAGGAAG CTGTGG | C | A | Asp | Tyr (8206) | NON- CONSER VATIVE | cadherin | Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa. | 0 | 17 (17q11) |
| 6036 | cg42558238 | 2115 | TGACTGGAATAA CCAAAGCCCTCCC CTTCJACCACAGC CAGAAAGCTGAGA TTGGA | T | C | Tyr | His (8207) | NON- CONSER VATIVE | cadherin | Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. cds:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. | 0 | 19 (19q13.1) |
| 6037 | cg43956560 | 1285 | CTGGCAAGGAG ATTAAAAAAGG CAJATJGAAATCC AAGAGAAAGTATG AATGAC | A | T | Lys | Met (8208) | NON- CONSER VATIVE | cadherin | Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa. | 1E-218 | 1 (1q23) |

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| 6038 | cg43956560 | 1287 | GGCAAGGAGATT AAAAAAGGCAA GATTAATCCAAG AGAGTATGAAT GACCC | A | T | Lys | End (8209) | NON- CONSER VATIVE | cadherin | Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa. | 1E-218 | 1 (1q23) |
| 6039 | cg42388009 | 378 | AAATGAAGGAGA AAACAATGAAGA AIC/TJCGAACGAA GACGAAGACTCT GAGGC | C | T | Pro | Ser (8210) | NON- CONSER VATIVE | cadherin | Human Gene SWISSPROT-ID:P21815 BONE SIALOPROTEIN II PRECURSOR (BSP II) (CELL-BINDING SIALOPROTEIN) (INTEGRIN-BINDING SIALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa. | 7E-172 | 4 |
| 6040 | cg42388009 | 379 | AATGAAGGAGAA AAACAATGAAGA CIC/TJGAACGAA GACGAAGACTCT GAGGCT | C | T | Pro | Leu (8211) | NON- CONSER VATIVE | cadherin | Human Gene SWISSPROT-ID:P21815 BONE SIALOPROTEIN II PRECURSOR (BSP II) (CELL-BINDING SIALOPROTEIN) (INTEGRIN-BINDING SIALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa. | 7E-172 | 4 |
| 6041 | cg43303099 | 965 | GAGACGGGAGG CCCGGGAGAAC TTG/C/AJCGGTCT TTAGCTTCCTAG GACCCAT | C | A | Pro | Thr (8212) | NON- CONSER VATIVE | cadherin | Human Gene SWISSPROT-ID:P32942 INTERCELLULAR ADHESION MOLECULE-3 PRECURSOR (ICAM-3) (CDW50) (CD50 ANTIGEN) (ICAM-R) - HOMO SAPIENS (HUMAN), 547 aa. | 8.7E-158 (19p13.3) | 19 |
| 6042 | cg42926989 | 269 | GCTGGCAGCAC AAAGGCTTATCG CA/C/TJGAGGAA GATGCAGCCACT CCTGCT | C | T | Val | Met (8213) | NON- CONSER VATIVE | cathepsin | Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa. | 1.7E-136 (14q11.2) | 14 |
| 6043 | cg43980411 | 1284 | TTCTTATTGCA TAAGATAACCAA C/GJTGCAATTTAT TTTTGGCAGAT TTT | C | G | Asn | Lys (8214) | NON- CONSER VATIVE | cathepsin inhib | Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG-SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa. | 3.2E-222 (18q21.3) | 18 |

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| 6044 | cg43980411 | 1310 | TGCAATTTATTTT TCGGCAGATTTT[C/G]CTCACCCCTA AAACTAAGCGTG CTGC | C | G | Ser | Cys (8215) | NON- CONSER VATIVE | cathepsin inhib | Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG- SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa. | 3.2E-222 | 18 (18q21.3) |
| 6045 | cg43971453 | 2657 | TGTCCAGCCATG AACTGTCCAAAG C[G/C]AGGGGGG AAGGTCAGCGTG GAGATG | G | C | Arg | Gly (8216) | NON- CONSER VATIVE | chloride_ channel | Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa. | 0 | 3 |
| 6046 | cg43970982 | 2131 | TGGACCTCGGG GAAGCGGAGGT GCC[G/C]CTGGT GCTCCTGGAGAA CGAGGCAG | G | C | Ala | Pro (8217) | NON- CONSER VATIVE | collagen | Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa. | 0 | 2 |
| 6047 | cg43970982 | 2222 | GGACCAAAAGGA GGAATCGGCAAC C[G/C]GGGCCCT CGTGGGGAGAC GGGAGAT | G | C | Arg | Pro (8218) | NON- CONSER VATIVE | collagen | Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa. | 0 | 2 |
| 6048 | cg43970982 | 4398 | CAGCGCCAAACT CCACTGGGAGA GG[C/G]CTGAGC CCCCCGGTCCTT ATTTTA | C | G | Pro | Ala (8219) | NON- CONSER VATIVE | collagen | Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa. | 0 | 2 |
| 6049 | cg43131198 | 5672 | GGCTCACAAACG GTGAAAGCAGAC TT[G/C]GAGTTT CCTCTGCTCCAG CACCAG | G | C | Leu | Phe (8220) | NON- CONSER VATIVE | collagen | Human Gene SWISSPROT-ID:P53420 COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1690 aa. | 0 | 2 (2q36) |
| 6050 | cg43970983 | 2792 | CTGCGCTGGGA GCCGGTGCCCA GAG[C/A]GCAGG GCTTCCTTCTGC ACTGGCAA | C | A | Ala | Glu (8221) | NON- CONSER VATIVE | collagen | Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa. | 0 | 3 (3p21.3) |

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| 6051 | cg43970983 | 9090 | ACGTCCGTTATT TCAGTGACTTGG TTCATCCGTGGG TCTAGCCTTCCC CCCTGT | C | A | Pro | Thr (8222) | NON- CONSER VATIVE | collagen | Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa. | 0 | 3 (3p21.3) |
| 6052 | cg41035069 | 1211 | AATGGAGAAAAT GGTTTGAAGGT GATCTTGGGTC CTCATGGTCCAC CTGGC | A | T | Asp | Val (8223) | NON- CONSER VATIVE | collagen | Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa. | 0 | 6 (6q12) |
| 6053 | cg41035069 | 1438 | AGGAATACACCA AACTCTGGTGG ATTGATTATAAC AAGGATAACAAG GGAAA | T | G | Tyr | Ser (8224) | NON- CONSER VATIVE | collagen | Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa. | 0 | 6 (6q12) |
| 6054 | cg41035069 | 1441 | AATACACCAAAC TCTTGGTGGATA TTTGATAACAAG GATAACAAGGGA AATGA | T | G | End | Ser (8225) | NON- CONSER VATIVE | collagen | Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa. | 0 | 6 (6q12) |
| 6055 | cg43991318 | 3625 | TGGATGCCAGG GTCTCCCTGGC TGCJGTACAGG ATCACCCAGGCTC CCCTTT | G | C | Gly | Arg (8226) | NON- CONSER VATIVE | collagen | Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa. | 1.3E-73 | 1 (1p34) |
| 6056 | cg44032748 | 1860 | ACCTCAGAAATGG AGGGGCCTCGT GTCTTCAGGGC GGAAAGTACAGA CGCAGGC | C | T | Pro | Ser (8227) | NON- CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:P07357 COMPLEMENT COMPONENT C8 ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 584 aa. | 0 | 1 (1p32) |
| 6057 | cg43281450 | 1987 | TCAGCCTGGCAG GAATGCCTGTCT TCTCTGAAGCT CATAGCCTGGAC GGCAG | C | T | Glu | Lys (8228) | NON- CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa. | 0 | 12 (12p13) |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------------|--|----------|---------------|
| 6058 | cg43281450 | 2082 | CTGGGGCTGGG GATCCTCCTCCC CTG/AJATTGCT CGGGAAGCAC ATTATC | G | A | Ser | Leu (8229) | NON- CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa. | 0 | 12 (12p13) |
| 6059 | cg43933757 | 1351 | ATGGGCTCTTGA AGAGTATCTGGA TJA/GJAATTGAC CCCTGTCATTGC CGGCC | A | G | Lys | Glu (8230) | NON- CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa. | 0 | 5 (5p13) |
| 6060 | cg43029279 | 607 | TCTCAGGATCA ATTACATGTTG CJA/GJAAATGGAT GGTCAGCACAAAC CAATT | A | G | Gln | Arg (8231) | NON- CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa. | 7.5E-191 | |
| 6061 | cg43029279 | 805 | ACATGTAGTAAT GGAGAGTGGTC GGJAC/JACCACC TAGATGCATACA TCCATGT | A | C | Glu | Ala (8232) | NON- CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa. | 7.5E-191 | |
| 6062 | cg43956185 | 1009 | TTACTCATCTGT CTCGACACTATA TJA/GJAGCATTTT GTACTGTGGGC GGATTG | A | G | Tyr | His (8233) | NON- CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa. | 4.1E-180 | 1 |
| 6063 | cg43956185 | 1266 | TGGTGACCATCC TTCTTCTGTGCA T[G/JTTATGCGA GTCCAAAATGAT TTTGA | G | T | Thr | Lys (8234) | NON- CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa. | 4.1E-190 | 1 |
| 6064 | cg43956185 | 609 | AAATTCAGCTGA TTCACCTGTTCT CJA/GJAATAAAGC TTCTGTTTGGCT GTCCA | A | G | Leu | Ser (8235) | NON- CONSER VATIVE | complem ent | Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa. | 4.1E-190 | 1 |

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|------|------------|-----|---|---|---|-----|---------------|--------------------------|---------|--|----------|---------------|
| 6065 | cg42542496 | 344 | TTGCTCCTCGTG GTCAATGCTTCTC CT/CJAACGTGCA GGCTAACGCTGT CCAGC | T | C | Leu | Pro (8236) | NON- CONSER VATIVE | csf | Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa. | 1.2E-189 | 3 (3q26.3) |
| 6066 | cg42542496 | 650 | TCATCCCTCCTG GGGCAGCTTTCT GIG/AJACAGGTC CGTCTCCTCCTT GGGGCC | G | A | Gly | Glu (8237) | NON- CONSER VATIVE | csf | Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa. | 1.2E-189 | 3 (3q26.3) |
| 6067 | cg2752665 | 551 | CCGGAAACTTCC TGTGCAACCCAG AT/CJTATCACCT TTGAAAGTTTCA AAGAG | T | C | Ile | Thr (8238) | NON- CONSER VATIVE | csf | Human Gene Similar to SWISSPROT- ID:P04141 GRANULOCYTE- MACROPHAGE COLONY- STIMULATING FACTOR PRECURSOR (GM-CSF) (COLONY-STIMULATING FACTOR) (CSF) - HOMO SAPIENS (HUMAN), 144 aa. | 5E-75 | 5 (5q31.1) |
| 6068 | cg34413296 | 435 | GCGCTACGGGG ACGTCCTGCAGA TC[C/A]GCATTGG CTCCACGCCCGT GCTGGT | C | A | Arg | Ser (8239) | NON- CONSER VATIVE | cyto450 | Human Gene SWISSNEW-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (CYP1A2) (P450-P3) (P(3)450) (P450 4) - HOMO SAPIENS (HUMAN), 515 aa.[pcls:SWISSPROT-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (P450-P3) (P450-4) - HOMO SAPIENS (HUMAN), 515 aa. | 4.6E-278 | 15 (15q22) |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------|---|----------|-----------------|
| 6069 | cg40333008 | 607 | GCTGGTGCCACT CCTTCTCATTGT G[C/A]TGCAGCG CCACAGATTGA TGATAA | C | A | Gln | His (8240) | NON- CONSER VATIVE | cyto450 | Human Gene SWISSNEW-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa. pcis:SWISSPROT-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa. | 4.9E-274 | 10 (10q24.3) |
| 6070 | cg43063374 | 1580 | TGATTGCTTCCT GATCAAAATGGA A[C/A]JAGGAAAAG CAAAACCAACAG TCTGA | A | C | Lys | Gln (8241) | NON- CONSER VATIVE | cyto450 | Human Gene SWISSNEW-ID:P33259 CYTOCHROME P450 2C17 (EC 1.14.14.1) (CYP11C17) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa. pcis:SWISSPROT-ID:P33259 CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa. | 3.2E-254 | 10 (10q24.1) |
| 6071 | cg43063374 | 1591 | TGATCAAAATGG AAAAAGGAAAAGC A[C/A]AACCAACA GTCTGAATTCAC TATTG | A | C | Gln | His (8242) | NON- CONSER VATIVE | cyto450 | Human Gene SWISSNEW-ID:P33259 CYTOCHROME P450 2C17 (EC 1.14.14.1) (CYP11C17) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa. pcis:SWISSPROT-ID:P33259 CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa. | 3.2E-254 | 10 (10q24.1) |
| 6072 | cg43966704 | 576 | CCGCCAGGGAT CACAGCAAGGA GGT[T/A]GTCCCA GCCGCCCGTGA CACCCCCCA | T | A | Asn | Tyr (8243) | NON- CONSER VATIVE | cytochrome | Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa. | 5.8E-184 | 11 |
| 6073 | cg43966704 | 597 | AGGTTGTCCAG CCGCCCGTGAC AC[C/A]CCCAGC ATGCTTCTCAAT CAGTTCT | C | A | Gly | Cys (8244) | NON- CONSER VATIVE | cytochrome | Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa. | 5.8E-184 | 11 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|---------------|---|---------|-----------------|
| 6074 | cg43962888 | 453 | GACTGGGTTGGA GAGGAGATCAT GIC/AJTGCTGC AAAGAAGGGACT GGACCC | C | A | Leu | Met (8245) | NON- CONSER VATIVE | cytochrome | Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa. | 5.1E-66 | 2 (2cen) |
| 6075 | cg43923204 | 1812 | GGTGACCGACAT CATGCAGTAGCC GIC/TJCCCGGA GTAGTCTTCACG GAGGCC | C | T | Gly | Asp (8246) | NON- CONSER VATIVE | cytochrome | Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa. | 1.7E-52 | 17 |
| 6076 | cg43923204 | 1924 | GGGCCAGCATC GAGGCTGCCCC TGGIC/TJCGCTGT CCAGCCCATGAC AGGCCGG | C | T | Ala | Thr (8247) | NON- CONSER VATIVE | cytochrome | Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa. | 1.7E-52 | 17 |
| 6077 | cg43967318 | 1615 | TATTTTCTTCT GGGCCCTTTGTGC IC/AJAAAGAGCA GGATGCCTTTGA AACCG | C | A | Gly | Cys (8248) | NON- CONSER VATIVE | dehydrogenase | Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa. | 0 | 17 (17p11.2) |
| 6078 | cg34396112 | 1048 | CACCCCATAGCT GAAGTAGTGGAA GIGCJGGTTCCC TGAGTTAGTCTC AAAGCT | G | C | Pro | Arg (8249) | NON- CONSER VATIVE | dehydrogenase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |
| 6079 | cg34396112 | 2946 | TCTGAAGGACTG TCAGGTAGAACT TIGCJAAGAAGAA GCTGAGGGTGA GGGTGC | G | C | Phe | Leu (8250) | NON- CONSER VATIVE | dehydrogenase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |
| 6080 | cg34396112 | 2949 | GAAGGACTGTCA GGTAGAACTTGA AIGCJAAGAAGCT GAGGGTGAGGG TGCACC | G | C | Phe | Leu (8251) | NON- CONSER VATIVE | dehydrogenase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |

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| 6081 | cg34396112 | 2952 | GGACTGTCAGGT AGAACTTGAAGA A[G/C]AAGCTGA GGGTGAGGGTG CACCGBA | G | C | Phe | Leu (8252) | NON- CONSER VATIVE | dehydrog enase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |
| 6082 | cg34396112 | 3012 | TGCCACCAGGG GCATCGGGAGG CAG[A/C]TGCAG CTCCTCTGCCAG TCCTGCAC | A | C | His | Gln (8253) | NON- CONSER VATIVE | dehydrog enase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |
| 6083 | cg34396112 | 3498 | CTTGCTTCCAG CAAACACGCGCA G[C/G]TGCTCCA GGACCCCTCTGA ACACCT | C | G | Gln | His (8254) | NON- CONSER VATIVE | dehydrog enase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |
| 6084 | cg34396112 | 3721 | CTCAATGCCAAT CTCCGTGTTCCTC C[A/T]CGACCCAG CTTGGCGTCAGG GTGCTG | A | T | Val | Glu (8255) | NON- CONSER VATIVE | dehydrog enase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |
| 6085 | cg34396112 | 3806 | GCCTGTATCCAG GTCACACGCTCC C[C/T]TTCAAATC GCAGCTGCTTCC GAGGA | C | T | Gly | Arg (8256) | NON- CONSER VATIVE | dehydrog enase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |
| 6086 | cg34396112 | 3925 | CTCTGGTTTGAA TAAAGATGGCGA G[A/T]GGCTGACT GAGTGGTCTTTT TTCTG | A | T | Leu | His (8257) | NON- CONSER VATIVE | dehydrog enase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |
| 6087 | cg34396112 | 3983 | CAGCAATTGGA TTATTCCCATCT C[C/T]TCCACAGC ATCCACCATCCC TGCCA | C | T | Gly | Arg (8258) | NON- CONSER VATIVE | dehydrog enase | Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa. | 0 | 2 (2p23) |

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| 6088 | cg44033747 | 1336 | CTTGGCGAATAT GGCTGCCATGTT T[G/C]GAATCTAC CATGGTCCCAT GGGCT | G | C | Gly | Arg (8259) | NON- CONSER VATIVE | dehydrog enase | Human Gene SWISSPROT-ID:P03378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa. | 0 9 (9p22) |
| 6089 | cg43314766 | 1220 | TAGAAATACCCCA TGGTGTCGCAAT TT[C]AACAGCAT TGTCGAAGTCGG CATCA | T | C | Lys | Glu (8260) | NON- CONSER VATIVE | dehydrog enase | Human Gene SWISSPROT-ID:P00352 ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS 1) (ALDHII) (ALDH-E1) - HOMO SAPIENS (HUMAN), 500 aa. | 7.2E-273 9 (9q21) |
| 6090 | cg43996714 | 1790 | ACAGGCCGGGG ATAAGATGGTCC AG[C/A]TGTGGC CTGTAGGGGCG AAGGTGCT | C | A | Ala | Ser (8261) | NON- CONSER VATIVE | dehydrog enase | Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa. | 1.6E-266 11 |
| 6091 | cg43996714 | 2474 | CCCTTCACCAGC CCTACGCTTCGG C[G/A]GCCAGGG AAGCCCAACAAG TAAGGC | G | A | Arg | Cys (8262) | NON- CONSER VATIVE | dehydrog enase | Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa. | 1.6E-266 11 |
| 6092 | cg43330439 | 729 | GCCTAGCAGCTG TCCAAAGTACAC CT[C]GGTGGTC AGCAGGATGCA GGCCCGAG | T | C | Gln | Arg (8263) | NON- CONSER VATIVE | dehydrog enase | Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa. | 2.1E-257 |
| 6093 | cg43057018 | 1639 | CTTTGAAGATG CCAGGAGCAATT C[G/A]GAATACTA TCTGATTGAATG TGAAC | G | A | Gly | Arg (8264) | NON- CONSER VATIVE | dehydrog enase | Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.lpcis:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa. | 1.3E-209 4 (4q22) |

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| 6094 | cg44986087 | 939 | CGCCAGCTTGAA GGCATACTCGGC A/TATGCGCAG GGACTTGGCCTT GGTGAT | T | A | Asn | Ile (8265) | NON- CONSER VATIVE | dehydrog enase | Human Gene SWISSPROT-ID:P51553 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT GAMMA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 393 aa. | 9.6E-207 | X |
| 6095 | cg44917703 | 1242 | GGCTACAGCACC ACAACCGACTTC A/T/C/CAAGTCTG TCATCGGTCACC TGCAG | T | C | Ile (8266) | Thr (8266) | NON- CONSER VATIVE | dehydrog enase | Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa. | 8.8E-205 | 13 |
| 6096 | cg44917703 | 1247 | CAGCACCACAAC CGACTTCATCAA G/T/G/CTGTCTC GGTCACCTGCAG ACTAA | T | G | Ser | Ala (8267) | NON- CONSER VATIVE | dehydrog enase | Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa. | 8.8E-205 | 13 |
| 6097 | cg44917703 | 1266 | ATCAAGTCTGTC ATCGGTACCTG C/A/C/GACTAAAG GGAGCTAGAGC CCTTTA | A | C | Gln | Pro (8268) | NON- CONSER VATIVE | dehydrog enase | Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa. | 8.8E-205 | 13 |
| 6098 | cg43923979 | 864 | AAAATCTTTTGA CTGAGCTTCCGG A/G/A/GAAATTCA AAAGGAACCCCA TACAT | G | A | Pro | Leu (8269) | NON- CONSER VATIVE | dehydrog enase | Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa. | 4E-192 3 (3p13) | |
| 6099 | cg43960596 | 296 | CCTGGGCTGTAG CGGGTTCGGGG GT/G/TTCGAGCA GTCAGGGCATG CTCCAGG | G | T | His | Asn (8270) | NON- CONSER VATIVE | dehydrog enase | Human Gene SWISSPROT-ID:Q92781 11 CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa. <i>ipds</i> :SWISSPROT-ID:Q92781 11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa. | 4.4E-170 | 12 |

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| 6100 | cg43960596 | 857 | TCCACCCACTTG GCTGCCTGCTG GA[A/C]GCTCTG GGGATCAGTGAT ATCCAAC | A | C | Phe | Val (8271) | NON- CONSER VATIVE | dehydrog enase | Human Gene SWISSNEW-ID:Q92781 11 CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa. pcis:SWISSPROT-ID:Q92781 11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa. | 4.4E-170 | 12 |
| 6101 | cg43969759 | 919 | AGAAATCTGCTCC GTGAAGGCTCCT G[C/T]GATGGCA GCAACACCTATG ATGGCT | C | T | Ala | Thr (8272) | NON- CONSER VATIVE | dehydrog enase | Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa. | 1.8E-109 | 11 |
| 6102 | cg43969759 | 1199 | CAAAACACGTGAT TGGAAGGCTTGT T[G/C]TTGGTGAT TCGCAGAGCAG CCAAGA | G | C | Asn | Lys (8273) | NON- CONSER VATIVE | dehydrog enase | Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa. | 1.8E-109 | 11 |
| 6103 | cg43969759 | 431 | GTGTAAGGAGT CATAGTCTGGAG T[G/T]TAGACCAG GGATCTTACAAA AGCCT | G | T | Tyr | End (8274) | NON- CONSER VATIVE | dehydrog enase | Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa. | 1.8E-109 | 11 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|-----------------|--|---|---------------------|
| 6104 | cg43248620 | 1748 | AGGCCCCCTTCC TGCCGCCCGG GG[A/T]TCGGGA CCCCCGTTTGAA GACCACT | A | T | Ile | Asn (8275) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene SPTREMBL-ID:Q14550 ZINC-FINGER DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 1482 aa. | 0 | 1 |
| 6105 | cg40993080 | 3300 | TGGGCGTGCC CTCTCTCTCCC CTT[G/C]ACGCGT TTTTCTGCCAT TTCTTG | T | G | Lys | Gln (8276) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa. | 0 | 6 |
| 6106 | cg40993080 | 3302 | GGCGTGCCCT CTCTCTCTCCC TC[A/T]CGCGTTT TTCTGCCATTT CTTGTA | A | T | Val | Glu (8277) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa. | 0 | 6 |
| 6107 | cg40993080 | 3306 | TGCCCCCTCTCTC CTCCCCCTCACG C[G/T]TTTTCTC GCCATTTCTTGT ACTCA | G | T | Arg | Ser (8278) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa. | 0 | 6 |
| 6108 | cg40993080 | 3307 | GCCCCCTCTCTCC TCCCCCTTCACGC G[T/G]TTTTCTG CCATTCTTGT CTCAT | T | G | Lys | Asn (8279) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa. | 0 | 6 |
| 6109 | cg42913756 | 366 | GGCAGCCAGCT CCAATCCCAAAG GG[G/T]CCCAGA TGCAGCCGATCT CCCTCCC | G | T | Ala | Ser (8280) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene SWISSPROT-ID:P48378 DNA BINDING PROTEIN RFX2 - HOMO SAPIENS (HUMAN), 723 aa. | 0 | 19 (19p13.3) |

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|------|------------|-----|--|---|-----|---------------|--------------------------|-----------------|---|----------|----|
| 6110 | cg43988954 | 670 | CCGGTTTCGAAG ACCATCCAGGCG GG/AJAGCCAC ACCAATGGAGAA GTGGTC | A | Ser | Phe (8281) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene SWISSNEW-ID:Q15633 TAR RNA BINDING PROTEIN (TRANS- ACTIVATION RESPONSIVE RNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 366 aa. pcis:SWISSPROT- ID:Q15633 TAR RNA BINDING PROTEIN (TRANS-ACTIVATION RESPONSIVE RNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 366 aa. pcis:SPTREMBL-ID:Q12878 TAR RNA BINDING PROTEIN 2 - HOMO SAPIENS (HUMAN), 366 aa. | 6.4E-194 | 12 |
| 6111 | cg43955901 | 755 | CTGCAAAAGCATT GTGAGCTGCATC A/C/TJTTGTGCA TTGCCACAGGAG ATACC | T | Ser | Asn (8282) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene Similar to SWISSNEW- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SWISSPROT- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. | 9.4E-97 | 2 |
| 6112 | cg43955901 | 770 | AGCTGCATCACT TTGTGCATTGCC A/C/AJAGGAGATA CCGGAGCCCATG ACAGAC | A | Cys | Phe (8283) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene Similar to SWISSNEW- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SWISSPROT- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. | 9.4E-97 | 2 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|-----------------|---|----------|---------------|
| 6113 | cg43130017 | 338 | TGAAGCGATGCG AGATACCTGAAG GTTC/TTTCCAC ACTGCTTGCATT CATAC | T | C | Thr | Ala (8284) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa. | 2.9E-95 | |
| 6114 | cg43918693 | 4135 | AGCTTCTTGTCG TTCATCAGCTGC AIGTTCAGGTAAT CTGGGGTGGGC TTCGGC | G | T | Leu | Met (8285) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene Similar to SPTREMBL- ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa. | 3.6E-74 | 6 |
| 6115 | cg43327954 | 1115 | CAAGTGGAGGAT GATGGGGATGG CGA/GJTTACATG TCTGAGCCTGAG GCTGTG | A | G | Asp | Gly (8286) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa. | 5.5E-57 | 1 |
| 6116 | cg43327954 | 1434 | GCATGAACCGCT CGGAACAGGTCT TTC/AJACGTGCTC TGTGTGCCAGGA GACAT | C | A | Phe | Leu (8287) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa. | 5.5E-57 | 1 |
| 6117 | cg43327954 | 1435 | CATGAACCGCTC GGAACAGGTCTT CJA/CJGTGCTCT GTGTGCCAGGA GACATT | A | C | Thr | Pro (8288) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa. | 5.5E-57 | 1 |
| 6118 | cg43946971 | 1232 | TCACCGAGTACT CGAGCTTGTTATA A[G/C]GACCCAG TGGTGCACACAC ACTGCA | G | C | Lys | Asn (8289) | NON- CONSER VATIVE | dna_ma_ bind | Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa. | 4.9E-52 | 6 (6p21.3) |
| 6119 | cg43269465 | 324 | AGGAGCTGGTC GAACCAAGCTGC GGTCA/JCTCCTC ATTCACCAGTCG GTCCCGG | C | A | Asp | Tyr (8290) | NON- CONSER VATIVE | dynein | Human Gene Homologous to SPTREMBL-ID:Q27810 DYNEIN HEAVY CHAIN ISOTYPE 6 (EC 3.6.1.3) (ADENOSINETRIPHOSPHATASE) (ADENYLPHOSPHATASE) (ATP MONOPHOSPHATASE) (TRIPHOSPHATASE) (ATPASE) - TRIPNEUSTES GRATILLA (HAWAIIAN SEA URCHIN), 1125 aa (fragment). | 9.7E-111 | |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|-----|--|----------|---------------|
| 6120 | cg43950268 | 2402 | TAGAACTCCTCA TGTTGCCACTCA C[G/C]GACATCCT TGGGTCCATCA TCCAG | G | C | Arg | Gly (8291) | NON- CONSER VATIVE | eph | Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa. | 0 | 16 |
| 6121 | cg43982507 | 2645 | GCCAAATAATTC ACTGGATCAGAG CTT/AJAGCCACTC TAGTCAACAACC TGAAT | T | A | Leu | Gln (8292) | NON- CONSER VATIVE | eph | Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa. | 0 | 9 (9p24) |
| 6122 | cg43945212 | 1793 | GTTGCGCGCGG AGCCCTATCCCA CGT/CJCGCGCT TCGGCAGCCAAT GCATGCA | T | C | Ser | Pro (8293) | NON- CONSER VATIVE | eph | Human Gene SWISSPROT-ID:P43135 APOLIPOPROTEIN A1 REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa. | 5.8E-232 | 7 |
| 6123 | cg41554010 | 1092 | GGTGACGACGAT GGAACAGCTCAG G[C/A]JAGAACTG GGCCCCCATGC GGGGGA | C | A | Gln | Lys (8294) | NON- CONSER VATIVE | eph | Human Gene SWISSNEW-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa. pcds:SWISSPROT-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa. | 1.8E-203 | 11 (11q23) |
| 6124 | cg41554010 | 1083 | GTGCAGCAGATG GAACAGCTCAGG C[A/C]GAAACTG GGCCCCCATGC GGGGGAC | A | C | Gln | Pro (8295) | NON- CONSER VATIVE | eph | Human Gene SWISSNEW-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa. pcds:SWISSPROT-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa. | 1.8E-203 | 11 (11q23) |
| 6125 | cg43985169 | 958 | ACTGCTAAATTC AGTTTACGAGAG G[C/A]ATTGTGTG GCTGCTCAATTA ATGTA | C | A | Ala | Glu (8296) | NON- CONSER VATIVE | eph | Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa. | 2.4E-123 | |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|----------|--|---------|----|
| 6126 | cg43949555 | 217 | CCACTCGTACAG CATATGGACCAA ATTAJGGAATGAA CAAAATGGTTAT CAACC | T | A | Asn | Lys (8297) | NON- CONSER VATIVE | eph | Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCLUS SP. (STRAIN SY), 545 aa. pcis:SPTREMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa. | 6.7E-80 | 21 |
| 6127 | cg43949555 | 858 | ACAGTGTGATA AAGAAATGCTGAA ATTAJATTGATGA ATTTAGTAAGG GAGAA | T | A | Ile | Lys (8298) | NON- CONSER VATIVE | eph | Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCLUS SP. (STRAIN SY), 545 aa. pcis:SPTREMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa. | 6.7E-80 | 21 |
| 6128 | cg43984905 | 1866 | GGGCCAGAGAT GGACGTGTACCA GGAGJCCGCTT CCAGGACAACG GGGCCTGT | A | G | Asp | Gly (8299) | NON- CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa. | 0 | 3 |
| 6129 | cg43984905 | 2088 | ACAGTGGAGATC CATGGCGTGAG CC[G]AGGACGT GGCCAGCCGCC AGACTGCT | G | A | Arg | Gln (8300) | NON- CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa. | 0 | 3 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|----------|--|---|---------------------|
| 6130 | cg43984905 | 2262 | TTCATTGGCCAG AGTACCATCCCC TTT/GJGAACAGCC TCAAGCAAGGAT ACCGC | T | G | Leu | Trp (8301) | NON- CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa. | 0 | 3 |
| 6131 | cg43984905 | 884 | TGAGCGCTACGA GCCCCAGCGAGA CTG/AJCCAAGG CGCAGCGGCAG ATGACCAA | G | A | Ala | Thr (8302) | NON- CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa. | 0 | 3 |
| 6132 | cg44011461 | 2013 | GTAGAGGGAGTT A TATATCTCTTCC [A/G]TATTGTAGC GCTCCAGGAGCT CGGG | A | G | Met | Thr (8303) | NON- CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa. | 0 | 16 (16q24.1) |
| 6133 | cg44011461 | 2420 | GGTAGTGCTGGA G TGAGGGCATAGA TTG/CJTGCTGAA GGTGAGGTTGTC AGTCA | G | C | Ser | Arg (8304) | NON- CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa. | 0 | 16 (16q24.1) |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|----------|--|----------|-----------------|
| 6134 | cg44011461 | 2423 | AGTGCTGGATGA GGGCATAGATGC TIG/CJCTGAAGGT GAGGTTGTCACT CAAGT | G | C | Ser | Arg (8305) | NON- CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa. | 0 | 16 (16q24.1) |
| 6135 | cg44011461 | 963 | AACCGTCGTCCT GAACCTGTTGTT G[C]TCATACTCG GCTCCACAGATC TCCAC | C | T | Gly | Asp (8306) | NON- CONSER VATIVE | esterase | Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa. | 0 | 16 (16q24.1) |
| 6136 | cg42031001 | 362 | CCCGCTGCCACT GATAGGAACCT A[G]TAGGCTCCA GCAGCAGACAG AGCAGC | G | T | Arg | Ile (8307) | NON- CONSER VATIVE | fgf | Human Gene Homologous to SWISSPROT-ID:P12034 FIBROBLAST GROWTH FACTOR-5 PRECURSOR (FGF-5) (HBGF-5) - HOMO SAPIENS (HUMAN), 268 aa. | 6.1E-141 | 4 |
| 6137 | cg43320667 | 824 | TTGCTGGTGGAG CTGCCCGCCTG GG[G/C]CTGCTC AGGACCAATTCTC TGGCGGA | G | C | Pro | Ala (8308) | NON- CONSER VATIVE | gaba | Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa. | 0 | 3 (3p25) |
| 6138 | cg43320667 | 825 | TGCTGGTGGAG CTGCCCGCCTG GG[G/C]GTGCTC AGGACCAATTCTC TGGCGGA | C | G | Gln | His (8309) | NON- CONSER VATIVE | gaba | Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa. | 0 | 3 (3p25) |
| 6139 | cg43320667 | 853 | CTCAGGACCATT CTCTGGGCGAAC G[A/G]TGCTCTCG CTGGGCTGGAC CATGAC | A | G | Ile | Thr (8310) | NON- CONSER VATIVE | gaba | Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa. | 0 | 3 (3p25) |

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|------|------------|-------|--|---|---|-----|---------------|--------------------------|---------------|---|----------------|---|
| 6140 | cg43286057 | 1828 | GGGGGGCATGC TGCTAATCGACC TGT/GIGTATCCT GATCTACTGGCA GGGTGT | T | G | Cys | Gly (8311) | NON- CONSER VATIVE | gaba | Human Gene Homologous to SPTREMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa. | 1.9E-121 | 9 |
| 6141 | cg43286057 | 1841 | CTAATCGACCTG TGATCCTGATC TIA/GICTGGCAG GGTGTGGAACC CCTGCGA | A | G | Tyr | Cys (8312) | NON- CONSER VATIVE | gaba | Human Gene Homologous to SPTREMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa. | 1.9E-121 | 9 |
| 6142 | cg43969076 | 1020 | ACACATCTGCAT CACTTCCTCTGC A/G/TAGGGGTA GTGGCTGGTAC GGAAAGC | G | T | Ser | Tyr (8313) | NON- CONSER VATIVE | glucuronidase | Human Gene SWISSPROT-ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa. | 0 (7q21.11) | 7 |
| 6143 | cg43969076 | 237 | TGGTATCAGTCT TGCTCAAGTAAA C/G/AJGGCTGTTT TCCAAACATTGT GACTT | G | A | Pro | Leu (8314) | NON- CONSER VATIVE | glucuronidase | Human Gene SWISSPROT-ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa. | 0 (7q21.11) | 7 |
| 6144 | cg43969014 | 688 | ATCACCATCCTC CCACGAGTACAG G/T/GJAGGCGGG GTGTTCTGTGCAT CAGGTA | T | G | Tyr | Ser (8315) | NON- CONSER VATIVE | glucuronidase | Human Gene Similar to SWISSPROT- ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa. | 7.4E-80 | 5 |
| 6145 | cg43285373 | 12871 | TCTGCCTGGATG AATGGAGAGGAC C/G/CJCAACATCC TGGTTTTCGAGG ACCTT | G | C | Arg | Pro (8316) | NON- CONSER VATIVE | glycoprotein | Human Gene SWISSPROT-ID:P98164 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 (MEGALIN) (GLYCOPROTEIN 330) - HOMO SAPIENS (HUMAN), 1751 aa (fragment). | 0 | 2 |

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|------|------------|------|--|---|-----|---------------|----------------------------------|------------------|--|---|---------------------|
| 6146 | cg43286488 | 1356 | CTCCAGGTAAGT A ATGAGTGACCCAC A[A]GJGTGCCCG AGAGATCAGGGT TCCACT | G | Leu | Pro (8317) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa. pcls:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa. | 0 | 12 |
| 6147 | cg43943531 | 1467 | CAGGATTCCACC A TACCCTATTAAAG A[A]TJTGAAAGTG CAAGTGGGATGA TACTG | T | Asn | Ile (8318) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa. | 0 | 11 (11q23.3) |
| 6148 | cg43943531 | 504 | TCCTTCACGCC A ATCGTCACGTAC C[A]TJCCTTACCA AAGAGCTCAAGG ATGCA | T | His | Leu (8319) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa. | 0 | 11 (11q23.3) |
| 6149 | cg43943531 | 861 | TACTGCCTGGGC T ACTATACTTTCTA [T]/GJGCAGATCTC CTTTGTGGGTTT CCAG | G | Met | Arg (8320) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa. | 0 | 11 (11q23.3) |
| 6150 | cg43065490 | 1172 | ACTATAATGAGG G AGGGACTTCAGA A[G]CJGGAGAAG GCCAGAGAGGC AGAATCT | C | Lys | Asn (8321) | NON- CONSER VATIVE 1096 | glycoprot ein | Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa. | 0 | 15 (15q15) |

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| 6151 | cg43065549 | 1598 | GGTTATGATGG ATGGCAGATTCT C[G/C]ACCCAAG TGCTCCTAATGG AGGTGG | G | C | Asp | His (8322) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa. | 0 | 15 (15q15) |
| 6152 | cg43065549 | 1738 | CCATAAATGCCT CATGTGTGGTCT G[G/A]AAGTGCT GTGAGGATGGG ACACTGG | G | A | Trp | End (8323) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa. | 0 | 15 (15q15) |
| 6153 | cg44034764 | 1079 | GTGCTCGGGCC AAAGGCCTCAGG AA[A/C]AAACAAA GCCGCCAGCGT GGGCTCG | A | C | Phe | Val (8324) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa. | 0 | 7 (Xp21.2) |
| 6154 | cg44034764 | 266 | CTGAGGGGCC GTGGACTCGGA GGT[G/T]TGGAG GGCTGTGAGTGT CGTGAGAG | G | T | His | Asn (8325) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa. | 0 | 7 (Xp21.2) |
| 6155 | cg43997653 | 1941 | CAAGCGCCATGT CTTCCACTTCGG C[A/G]CCGTGAG CCCCCAGAGCCTC CCAGGC | A | G | Thr | Ala (8326) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P50895 LUTHERAN BLOOD GROUP GLYCOPROTEIN PRECURSOR (B-CAM CELL SURFACE GLYCOPROTEIN) (AUBERGER B ANTIGEN) (F8/G253 ANTIGEN) - HOMO SAPIENS (HUMAN), 628 aa. | 0 | |
| 6156 | cg44004239 | 391 | GAAGACCCCAAGT TACCCATCCTGG G[G/C]TGAGTGC CCACCTCAGAAG TCAAAAT | G | C | His | Gln (8327) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN-DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa. | 0 | |

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| 6157 | cg43010733 | 1380 | GAGCCCTTCGCC TTCCACATGCCG A/A/C/GTCGCTCT ACGGCTTCTTCT GGAAG | A | C | Lys | Thr (8328) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:Q09327 BETA-1,4-MANNOSYL-GLYCOPROTEIN BETA-1,4-N-ACETYLGLUCOSAMINYL- TRANSFERASE (EC 2.4.1.144) (N- GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E III) (N- ACETYLGLUCOSAMINYLTRANSFERAS E III) (GNT-III) (GLCNAC-T III) - HOMO SAPIENS (HUMAN), 531 aa. | 5E-304 | |
| 6158 | cg43094362 | 191 | CCCACTGCTCTA CTTCATGGTCAC C/A/C/CTCCTGTC CAGGAAGATCAG TGGCC | A | C | Ser | Arg (8329) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa. | 9.7E-230 | 7 |
| 6159 | cg43094362 | 271 | ATGCCTGCGGTT ACGGGAAGCAG AC/G/CTGGACC ACTGGCTCACGA CACGAGG | G | C | Thr | Arg (8330) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa. | 9.7E-230 | 7 |
| 6160 | cg43094362 | 287 | GAAGCAGACGT GGACCACTGGCT CA/C/T/GACACGA GGCTGCCTCCTG GAATGG | C | T | Val | Met (8331) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa. | 9.7E-230 | 7 |
| 6161 | cg43987514 | 963 | CTAGCGCAGAGA GTTCTGGCCG CT/G/C/CTTCCGC TGGCCCCCAGT GCCCCAG | G | C | Ser | Arg (8332) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa. | 3.2E-215 | |

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| 6162 | cg43301245 | 866 | GGCATAGGGGA CCTGCTGGCCG AGG(A/G)TTCAT GGACTGTGGCTC CGCGGAG | A | G | Ile | Thr (8333) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa. | 3E-210 | 1 |
| 6163 | cg43074195 | 2209 | GACCCCAAGCA GCACCACCACAA CTC(A/JAAATTAC CAAGACTGTAA AGGTGG | C | A | Gln | Lys (8334) | NON- CONSER VATIVE | glycoprot ein | Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.4E-197 | 1 |
| 6164 | cg43988092 | 2155 | AGGCGGGAAT GTGGAAGAA TTT(C/JAACAAA TAATGTAGCACC AGAAGA | T | C | Lys | Glu (8335) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa. | 4E-192 | 8 |
| 6165 | cg42671047 | 1163 | ATCATCCTCTAC TGGGGACACCA CTT(C/JTTCATG AATTGGATTGCC TTGGTA | T | C | Phe | Ser (8336) | NON- CONSER VATIVE | glycoprot ein | Human Gene SWISSNEW-ID:P29017 T- CELL SURFACE GLYCOPROTEIN CD1C PRECURSOR (CD1C ANTIGEN) - HOMO SAPIENS (HUMAN), 333 aa.lpcis:SWISSPROT-ID:P29017 T-CELL SURFACE GLYCOPROTEIN CD1C PRECURSOR (CD1C ANTIGEN) - HOMO SAPIENS (HUMAN), 333 aa. | 2.8E-184 | 1 (1q21) |
| 6166 | cg43991224 | 193 | AGGCAGGTGATC AGGATGCCCTTC TTC(G/JTCATCTGT CTACCTACAGCC TGGTT | C | G | Ser | Cys (8337) | NON- CONSER VATIVE | glycoprot ein | Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa (fragment). | 1.5E-139 | |

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| 6167 | cg43991224 | 297 | GGATGAAAGAGAC GCAGCTGTACAC A/C/A/CTGCTTCC TTAAATGCTCT CTGCA | A | Pro | Thr (8338) | NON- CONSER VATIVE | glycoprot ein | Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa (fragment). | 1.5E-139 | |
| 6168 | cg43076975 | 1728 | TAACAATGCATT TCAGCTCGTCAG C/A/T/TGGGAAG CTGTCCATTGAA AAGGC | T | Ile | Phe (8339) | NON- CONSER VATIVE | glycoprot ein | Human Gene Homologous to SWISSNEW-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa. lpcis:SWISSPROT-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa. | 3.4E-120 | 5 |
| 6169 | cg43924574 | 470 | TAGGGAACCTGC TGATCCTGGAGC C/G/A/CGTGATCT TGGCTCCTTTCA GGAAC | A | Arg | Trp (8340) | NON- CONSER VATIVE | glycoprot ein | Human Gene Homologous to SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP- 39) (39 KD SYNOVIAL PROTEIN) (YKL- 40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa. lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa. | 1E-106 | 1 |

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| 6170 | cg44929742 | 869 | CAGGGTCAGCC GGTACATCTGGG CC[T/G]GGGCAT TGGGCTCCAGC CGAAGCAG | T | G | Gln | Pro (8341) | NON- CONSER VATIVE | glycoprot ein | Human Gene Similar to SWISSNEW- ID:P17426 ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) MUS MUSCULUS (MOUSE), 977 aa. pcis:SWISSPROT-ID:P17426 ALPHA ADAPTIN (A) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) - MUS MUSCULUS (MOUSE), 977 aa. | 5.4E-94 | 19 |
| 6171 | cg44021513 | 1356 | TTCTGGCCCTGC TGGTACGCGGG GG[C/G]GTCTGC GCTCCTGCTGAA CTTCACT | C | G | Ala | Pro (8342) | NON- CONSER VATIVE | glycoprot ein | Human Gene Similar to SWISSPROT- ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa. | 8E-84 | 1 (1q22) |
| 6172 | cg43983795 | 1531 | TACGGCCCTCG GGCCCGTAGAAT T[C/T]GCGGCCTT TGGTCACATCGA ACACC | C | T | Glu | Lys (8343) | NON- CONSER VATIVE | glycoprot ein | Human Gene Similar to SPTREMBL- ID:Q96250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa. | 1.2E-74 | X |
| 6173 | cg41568631 | 1756 | GCACCCAGAAG GCTCAGACGCA GAG[C/G]GGAAG GCAGTAGAGACA GCAGCAGC | C | G | Arg | Gly (8344) | NON- CONSER VATIVE | glycoprot ein | Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa. | 9.9E-70 | 14 (14q11.2) |

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| 6174 | cg41568631 | 1757 | CACCCAGAAGG CTCAGACGCAGA GC[G/C]GAAGGC AGTAGAGACAGC AGCAGCC | G | C | Arg | Pro (8345) | NON- CONSER VATIVE | glycoprot ein | Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa. | 9.9E-70 | 14 (14q11.2) |
| 6175 | cg42659724 | 773 | ACTTTACTAAAA GCTTATTTCTGT C[AT]ATATCAT TTTGTAGAAATC ATCCA | A | T | Gln | Leu (8346) | NON- CONSER VATIVE | glycoprot ein | Human Gene Similar to SWISSNEW- ID:P26717 NKG2-C TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 231 aa.lcds:SWISSPROT-ID:P26717 NKG2- C TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 231 aa. | 1.8E-69 | |
| 6176 | cg43918233 | 1027 | TCTTCAGAGCCT ACTGAGGATGTG G[AG/G]GCCCAAA GAGGCTGAAGAT GATGAT | A | G | Glu | Gly (8347) | NON- CONSER VATIVE | glycoprot ein | Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa. | 7.6E-67 | 2 |
| 6177 | cg43918233 | 534 | CAGCCCCAACAG GTCGGGTGCGG AG[G/C]CAAAGA CCCAAAAAGACA GCCCTAG | G | C | Ala | Pro (8348) | NON- CONSER VATIVE | glycoprot ein | Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa. | 7.6E-67 | 2 |
| 6178 | cg43078615 | 248 | CTGTCCGGCGCT GCCTGCCCTCT G[G/C]GCCCTAA CACTGGAAGCAG CTCTCA | G | C | Trp | Cys (8349) | NON- CONSER VATIVE | glycoprot ein | Human Gene Similar to TREMBLNEW- ID:G2909819 ERYTHROCYTE MEMBRANE GLYCOPROTEIN RH50 - HOMO SAPIENS (HUMAN), 409 aa. | 7.1E-60 | 1 (1p36.2) |
| 6179 | cg44913214 | 2075 | AAGCTGTTGAAT TTGGAGGGCTTT C[CT/AT]CAGGGA GCCAGTCACGAT TGTCAT | C | T | Pro | Leu (8350) | NON- CONSER VATIVE | helicase | Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa. | 0 | 10 |

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| 6180 | cg43956596 | 3949 | CCGGAAGAGC AAGGGAGCCC ATG A G CCCCCTC GCCGCACGCCA GCCCCGCTT | A | G | Thr | Ala (8351) | NON- CONSER VATIVE | helicase | Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa. pcis:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa. | 0 | 16 |
| 6181 | cg43916626 | 2264 | CTCTCTGTGAAT CTGGCTGGCAA GT A T GTCGTGT TGGTGATATAAT CAGGGC | A | T | Leu | Gln (8352) | NON- CONSER VATIVE | helicase | Human Gene Homologous to SWISSPROT-ID:P45818 ATP- DEPENDENT RNA HELICASE ROK1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 564 aa. | 4.8E-103 | 17 |
| 6182 | cg43971940 | 930 | GATTGTGTAGCC ACCTCCTCCAAG CT A T CAGTAAT GGTAAGTTAAA GTTT | T | A | Lys | Met (8353) | NON- CONSER VATIVE | histone | Human Gene SWISSPROT-ID:Q92769 HISTONE DEACETYLASE 2 (HD2) - HOMO SAPIENS (HUMAN), 488 aa. | 2.5E-176 | 6 |
| 6183 | cg42341753 | 1486 | GGCGAGAAGCC ATCAGGTGGAGC CC C T GGCTGC GGATGGCGAGC AGGACGAG | C | T | Pro | Leu (8354) | NON- CONSER VATIVE | homeobo x | Human Gene SWISSPROT-ID:Q14774 HOMEBOX PROTEIN HLX1 (HOMEBOX PROTEIN HB24) - HOMO SAPIENS (HUMAN), 488 aa. | 5.2E-263 | 1 |
| 6184 | cg43332152 | 982 | CCTGGCGGCCA AGCGGCGGGGA CCG C G GCACC ACCATCAAAGCC AAGCAGCT | C | G | Arg | Gly (8355) | NON- CONSER VATIVE | homeobo x | Human Gene SWISSPROT-ID:P36199 HOMEBOX PROTEIN LIM-1 (HOMEBOX PROTEIN LMX-2) - MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND MESOCRICETUS, 406 aa. | 3.4E-227 | 17 |
| 6185 | cg41637704 | 1202 | GGAGCTGCTGG GGCCGCCAGCG CCG C G GAGAC AAGGCGAGCGG ACCGCCTGC | C | G | Arg | Gly (8356) | NON- CONSER VATIVE | homeobo x | Human Gene SWISSPROT-ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa. | 1.2E-224 | 7 |

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| 6186 | cg43143467 | 630 | CTTGCCCAACGTA CCAGCTGTGCGA G/A/C/JCCTCTTAC CAGCCCACATCT ATTCC | A | C | Thr | Pro (8357) | NON- CONSER VATIVE | homeobo x | Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment). | 2.1E-179 | 2 (2q35) |
| 6187 | cg43143467 | 631 | TTGCCAACGTAC CAGCTGTGCGA G/A/C/JCCTCTTAC CAGCCCACATCT ATTCCA | C | A | Thr | Asn (8358) | NON- CONSER VATIVE | homeobo x | Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment). | 2.1E-179 | 2 (2q35) |
| 6188 | cg42721526 | 769 | GGGTCTCTTGCC CATCTCTCCGGC C/G/A/JCCCCGCC AGGAAACGACGA GAAGGC | G | A | Ala | Thr (8359) | NON- CONSER VATIVE | homeobo x | Human Gene Homologous to TREMBLNEW-ID:G2822175 HXA1_HUMAN HOMEOBOX PROTEIN HOX-A1 - HOMO SAPIENS (HUMAN), 335 aa. | 6.9E-144 | 7 |
| 6189 | cg42359655 | 4927 | CCTATTTTCAAG AATGGAGATTAC A/G/A/JTGAGGTG ATGAAGACGCG GATCCGT | G | A | Ser | Asn (8360) | NON- CONSER VATIVE | hydrolas e | Human Gene SWISSPROT-ID:P09848 LACTASE-PHLOIRIZIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE- GLYCOSYLCERAMIDASE) - HOMO SAPIENS (HUMAN), 1927 aa. | 0 | 2 (2q21) |
| 6190 | cg43296921 | 553 | AGCCGCCCTGGC TCATTCCTTCTC CT/T/G/JTCAGGTT AACAGAGAGGTT GATGTC | T | G | Lys | Thr (8361) | NON- CONSER VATIVE | hydrolas e | Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa. | 3.3E-238 | 15 (15q23) |
| 6191 | cg43927025 | 192 | GTTGGTGGTCTG TTTGGTTCTCTG G/A/C/JCCCTGCAT TCTGAGGGGTCT GGAGG | A | C | Thr | Pro (8362) | NON- CONSER VATIVE | hydrolas e | Human Gene SWISSPROT-ID:P38571 LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTERYL ESTERASE) - HOMO SAPIENS (HUMAN), 399 aa. | 5.1E-224 | 10 (10q24) |

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| 6192 | cg43927025 | 213 | CTGGACCCTGCA TTCTGAGGGTC T[G]A[GAGGGAA ACTGACAGCTGT GGATCC | G | A | Gly | Arg (8363) | NON- CONSER VATIVE | hydrolas e | Human Gene SWISSPROT-ID:P38571 LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTERYL ESTERASE) - HOMO SAPIENS (HUMAN), 399 aa. | 5.1E-224 | 10 (10q24) |
| 6193 | cg43285385 | 621 | ACATTGAAAAAC TTCITTAACITTT IC/TATTCATTGT AAAATTCCTCAC GGAG | C | T | Glu | Lys (8364) | NON- CONSER VATIVE | hydrolas e | Human Gene TREMBLNEW- ID:G2951931 HUMAN GAMMA- GLUTAMYL HYDROLASE (EC 3.4.22.12) - HOMO SAPIENS (HUMAN), 318 aa. | 4.8E-173 | 8 |
| 6194 | cg43925670 | 1254 | GCCTCTGAAGGA TATGGAAGCTGA CT/GICTGTTCCT GGGTAGCTTCA TGCTC | T | G | Ser | Arg (8365) | NON- CONSER VATIVE | interferon | Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. Jcds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0 | 1 |

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| 6195 | cg43925670 | 438 | CCACTTTTCGGT GCCAATTCAAAG C A T GGTGAGTT TCAGTTTATCTC CTTCC | A | T | Cys | Ser (8366) | NON- CONSER VATIVE | interferon | Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0 | 1 |
| 6196 | cg43925670 | 479 | ATCTCCTTCCTC ACAGTTGATTGT G G T TCAGTCGT CCATGCACCACC ACTTC | G | T | Thr | Asn (8367) | NON- CONSER VATIVE | interferon | Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment) | 0 | 1 |
| 6197 | cg43082514 | 349 | AAAAGATGCACC ACTCTTTAGAAA C T C GGGCAAT CCATACAGGAAA GCATCA | T | C | Trp | Arg (8368) | NON- CONSER VATIVE | interferon | Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa. | 5.5E-188 | 4 (4q35.1) |
| 6198 | cg43925658 | 578 | TGAAATTCCTGA AACCAGACCATAG T G A GAAATGTA TGTCCTGCATTG TTTCT | G | A | His | Tyr (8369) | NON- CONSER VATIVE | interferon | Human Gene Homologous to SPTREMBL-ID:Q13325 RETINOIC ACID- AND INTERFERON-INDUCIBLE 58K PROTEIN RI58 - HOMO SAPIENS (HUMAN), 482 aa. | 4.8E-141 | 10 (10q23) |

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| 6199 | cg43972852 | 849 | TTCACATCTCAC TAACAAGTTTGA G[G]TACAAGACT GTGGCATATACA GAGCA | G | T | Asp | Tyr (8370) | NON- CONSER VATIVE | isomerase | Human Gene SWISSPROT-ID:P30101 PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (GRP58) (ERP57) - HOMO SAPIENS (HUMAN), 505 aa. | 3.8E-274 | |
| 6200 | cg44929725 | 2694 | ATTGAGAAAGAG AGATTCTATGAA A[A]GJCCGGTGC AGCCAGTGACA CCATCA | A | G | Asn | Ser (8371) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa. | 0 | 1 (1p31.3) |
| 6201 | cg42859664 | 747 | GGTCCACTTCAC GGGACTTGCTCT G[A]GJGGCCCC TGAGGCTGCATA GACCCC | A | G | Leu | Pro (8372) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P07332 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FES/FPs (EC 2.7.1.112) (C-FES) - HOMO SAPIENS (HUMAN), 822 aa. | 0 | 15 (15q26.1) |
| 6202 | cg42859664 | 748 | GTCCACTTCACG GGGACTTGCTCTG A[G]AIGCCCCCT GAGGCTGCATAG ACCCCA | G | A | Leu | Phe (8373) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P07332 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FES/FPs (EC 2.7.1.112) (C-FES) - HOMO SAPIENS (HUMAN), 822 aa. | 0 | 15 (15q26.1) |
| 6203 | cg43917392 | 3326 | ATTGTGCTCACT GGGTACTAACAG A[C]TJTAAGGAT AGAGCGTAGTGA CTAAT | C | T | Ser | Asn (8374) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P34925 TYROSINE-PROTEIN KINASE RYK PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 604 aa. | 4.0e-315 | |
| 6204 | cg43957153 | 329 | TGAGGAGGGGG AGCTGAGAGATC AC[C]TJGCATGGA GATCACAAATAAG GAAGTC | C | T | Arg | Cys (8375) | NON- CONSER VATIVE | kinase | Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa. | 1.2E-304 | 4 (1p36) |
| 6205 | cg43952792 | 1126 | CCGCGAGAGTG AAACCACCAAAG GT[G]TCCTATTC ACTTCTATCCG TGATTG | G | T | Ala | Ser (8376) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P08241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa. | 4.3E-300 | 6 (6q21) |

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| 6206 | cg43965549 | 1355 | GCCAGAGAGG ATCAGCCACGCT GTTC/AJAGAGTCT GGACTCTGCCCT CTTGGA | C | A | Gln | Lys (8377) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE - SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa. | 2.3E-253 | 10 (10p11.2) |
| 6207 | cg43965549 | 1356 | CCCAGAGAGGAT CAGCCACGCTGT CTAC/GAGTCTG GACTCTGCCCTC TTGGAG | A | C | Gln | Pro (8378) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa. | 2.3E-253 | 10 (10p11.2) |
| 6208 | cg43967889 | 1158 | GAATTACGGGAC CCAAATGTCAAA CTT/AJACCAATG GGCGAGACACA CCTGCA | T | A | Leu | Gln (8379) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P49841 GLYCOGEN SYNTHASE KINASE-3 BETA (EC 2.7.1.37) (GSK-3 BETA) - HOMO SAPIENS (HUMAN), 420 aa. | 1.9E-226 | 3 |
| 6209 | cg43967889 | 663 | ATCTGCCATCGG GATATTAAACCG CTAG/GAACCTCT TGTTGGATCCTG ATACT | A | G | Gln | Arg (8380) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P49841 GLYCOGEN SYNTHASE KINASE-3 BETA (EC 2.7.1.37) (GSK-3 BETA) - HOMO SAPIENS (HUMAN), 420 aa. | 1.9E-226 | 3 |
| 6210 | cg43963232 | 2187 | AGTACTGTCCCC GCGAGCATCGA GG/GC/ATTCTA CTGCACCATCT CTTCCA | G | C | Ile | Met (8381) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P31323 CAMP-DEPENDENT PROTEIN KINASE TYPE II-BETA REGULATORY CHAIN - HOMO SAPIENS (HUMAN), 417 aa. | 4.6E-223 | 7 (7q22) |
| 6211 | cg43947829 | 1933 | ACAGGTAATGGA TTCTGACAAGGA ATT/ATTGCTGAG TCACGAGAACAC GTTTT | T | A | Ile | Phe (8382) | NON- CONSER VATIVE | kinase | Human Gene TREMBLNEW- ID:G2979628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa. | 1.5E-217 | |

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| 6212 | cg38438124 | 850 | ATGGGATCACCC TTCAACCCAGT TIG/CIGTGGCA TGTACCGGCTTA ATGTTG | G | C | Leu | Phe (8383) | NON- CONSER VATIVE | kinase | Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII-ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P-5- KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa. | 2.8E-216 | 10 |
| 6213 | cg43917871 | 1966 | TCAGCCAAACCC CAGTCTATTAGT CIG/ATAGCTTTC TGTGCTCATGAT CAATC | G | A | Arg | End (8384) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa. | 2E-215 | 11 (20p13) |
| 6214 | cg43933472 | 2482 | TTTCATTGCTC GATGGTTGGTGC TTC/TGAATAATG TCATTGATTCCA ATGAT | C | T | Arg | Gln (8385) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL- REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa. | 5.4E-197 | 22 |
| 6215 | cg38309035 | 487 | TGCAGGGACTC GAAGTAGGGATG GG[C/A]CAGCGC CTCGCCTGCCGT CACCCGC | C | A | Ala | Ser (8386) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P53778 EXTRACELLULAR SIGNAL- REGULATED KINASE 6 (EC 2.7.1.-) (ERK6) (ERK5) (STRESS-ACTIVATED PROTEIN KINASE-3) (MITOGEN- ACTIVATED PROTEIN KINASE P38 GAMMA) (MAP KINASE P38 GAMMA) - HOMO SAPIENS (HUMAN), 367 aa. pcis:SPTREMBL-ID:Q99588 STRESS-ACTIVATED PROTEIN KINASE-3 - HOMO SAPIENS (HUMAN), 367 aa. | 2.9E-195 | |

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| 6216 | cg43929069 | 347 | AGTAATCTTTTG GCTGGATCATAC TTCJCCAACATTT TCTGAATGAGGT CAAA | T | C | Glu | Gly (8387) | NON- CONSER VATIVE | kinase | Human Gene SWISSNEW-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa. Jcds:SWISSPROT-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa. | 1.6E-192 | |
| 6217 | cg43007055 | 693 | CGGAGCGGGG CGCGTCGCCC TCCGTCGCGCC GAGAAAGGTGA GCCGGCCGC | G | T | Ala | Ser (8388) | NON- CONSER VATIVE | kinase | Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa. | 1.7E-168 | 6 (6q22.2) |
| 6218 | cg43007055 | 798 | AGCGAGGCTG CCGAGCCCGGC TCGTCGJCCACG GCCGCGGAGGG AGAGGCCGC | C | G | Pro | Ala (8389) | NON- CONSER VATIVE | kinase | Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa. | 1.7E-168 | 6 (6q22.2) |
| 6219 | cg43982923 | 912 | AGTTGCAATGGT GACCTCGATCCT GATJGATTGTAA AGTCATTCTCT TCCAG | A | T | Glu | Val (8390) | NON- CONSER VATIVE | kinase | Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa. | 3.6E-159 | 19 |
| 6220 | cg43969473 | 2576 | GCCTCCCAGCAT TGGCAAATCGAA CIGATJGGACAG ACGTCAGGCAGA AATTGG | G | A | Val | Met (8391) | NON- CONSER VATIVE | kinase | Human Gene SPTREMBL-ID:Q27467 SIMILARITY TO TYROSINE-PROTEIN KINASE - CAENORHABDITIS ELEGANS, 1280 aa. | 2.1E-154 | 11 |
| 6221 | cg44016530 | 539 | ATGCTGAACATG CTTCGTGGGGCT ATATCTTTTGT TTCTCTGTAGTC TCITT | T | A | Asp | Val (8392) | NON- CONSER VATIVE | kinase | Human Gene Homologous to SPTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment). | 1.7E-129 | 12 |

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| 6222 | cg43286014 | 257 | GAGCGAGGGCG TGACGCTCGTCG TGTTGACAGATA AGCTTGTTCTGG TGTTGGC | T | G | Tyr | Asp (8393) | NON- CONSER VATIVE | kinase | Human Gene Similar to SWISSPROT- ID:P23919 THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE) - HOMO SAPIENS (HUMAN), 212 aa. | 1E-87 | |
| 6223 | cg43984445 | 308 | TTACCTCTCTCA TGAGGTCTTCTT GT/ATTTGGTTAC TTCCTCAGAAAA ATCAT | T | A | Lys | Asn (8394) | NON- CONSER VATIVE | kinase | Human Gene Similar to SWISSPROT- ID:Q16854 DEOXYGUANOSINE KINASE PRECURSOR (EC 2.7.1.13) (DGUOK) - HOMO SAPIENS (HUMAN), 277 aa. pcds:SPTREMBL-ID:Q16854 DEOXYGUANOSINE KINASE (EC 2.7.1.13) - HOMO SAPIENS (HUMAN), 277 aa. | 8.7E-73 | 2 |
| 6224 | cg43985883 | 186 | AGTCACAAGCGG AAGAGGAGATCT C/G/AJAGGAGC ACACAAGAGAAC AGGAAT | G | A | Arg | Gln (8395) | NON- CONSER VATIVE | kinase | Human Gene Similar to SWISSNEW- ID:O35493 PROTEIN KINASE CLK4 (EC 2.7.1.-) - MUS MUSCULUS (MOUSE), 481 aa. | 1.2E-64 | |
| 6225 | cg43985883 | 226 | AGAACAGGAATT GTATACCCACATC A/G/CJGTGTTTAA ACAATCTGATTG TGCTC | G | C | Gln | His (8396) | NON- CONSER VATIVE | kinase | Human Gene Similar to SWISSNEW- ID:O35493 PROTEIN KINASE CLK4 (EC 2.7.1.-) - MUS MUSCULUS (MOUSE), 481 aa. | 1.2E-64 | |
| 6226 | cg43982810 | 227 | GGACCCAAACAT CATCCATCTATT A/G/TJCTGTGTGT ATCACTGATGAC CCTCT | G | T | Ala | Ser (8397) | NON- CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:Q16832 RECEPTOR PROTEIN-TYROSINE KINASE TKT PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE TYRO 10) (NEUROTROPHIC TYROSINE KINASE, RECEPTOR- RELATED 3) - HOMO SAPIENS (HUMAN), 855 aa. | 0 | 1 |

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| 6227 | cg14396889 | 1094 | CAATCAGCTTTG GTTACCATCGTA GIA/GJAAAGGGA TTTATAAATGCTA CCAAT | A | G | Glu | Gly (8398) | NON- CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:P36888 FL CYTOKINE RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR FLT3) (STEM CELL TYROSINE KINASE 1) (STK-1) (CD135 ANTIGEN) - HOMO SAPIENS (HUMAN), 993 aa. | 0 | 13 |
| 6228 | cg44021449 | 2713 | GAAGATCTACAG TGGGGACTACTA TTC/TGTCAAGGC TGTGCCTCCAAA CTGCC | C | T | Arg | Cys (8399) | NON- CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:Q08418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa. | 0 | 15 |
| 6229 | cg43322545 | 1212 | GGAGGGAGTGC CCCTGGGCCCC CCT[GIA/JAGAACA TTAGTGCTACGC GGAATGG | G | A | Glu | Lys (8400) | NON- CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. pcds:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. | 0 | 19 (19q13.1) |
| 6230 | cg43991478 | 1301 | AGTAGGTCCGAC GGCCGGTGAGT CC[G/C]GGTTCA CAGTCAAGACGT CAGCAAG | G | C | Pro | Arg (8401) | NON- CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa. | 0 | |
| 6231 | cg43991478 | 1895 | GTGCTCCACGTA CTCTGTCAACCAT G[A/C]TATTTTCA GGGCCGCGCAC ACAGAC | A | C | Ile | Ser (8402) | NON- CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa. | 0 | |

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| 6232 | cg43991478 | 894 | GCGGCTAGGTCT CGGTGGATGTAG TIGCJCTGCCG TGCAGATAGGCC ATGCCC | G | C | His | Asp (8403) | NON- CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa. | 0 | 0 |
| 6233 | cg43991478 | 895 | CGGCTAGGTCTC GGTGGATGTAGT GIC/GJTGCCGCT GCAGATAGGCCA TGCCCT | C | G | Gln | His (8404) | NON- CONSER VATIVE | kinaserec eptor | Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa. | 0 | 0 |
| 6234 | cg43920644 | 2056 | TGACATTCCAAA GTAGCCCGAAAT TIT/CJTITTAATCA TTCGGGCAAAAT CCCAG | T | C | Lys | Glu (8405) | NON- CONSER VATIVE | kinesin | Human Gene SPTREMBL-ID:Q98661 MITOTIC CENTROMERE-ASSOCIATED KINESIN - HOMO SAPIENS (HUMAN), 725 aa. | 0 | 1 |
| 6235 | cg43942537 | 1165 | CACGTGCTCTTC CAAACCCCTTCAC GIC/TJCTGTCTT GCTTGTTCTCGT CTATC | C | T | Gly | Asp (8406) | NON- CONSER VATIVE | kinesin | Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa. pcls:SWISSPROT-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa. | 0 | 10 |
| 6236 | cg43942537 | 1250 | TTTTCCTGATCT GTGGCTTTCAAC TIC/TJCTCATGTT CTACTCTTAGAC GTTCC | C | T | Glu | Lys (8407) | NON- CONSER VATIVE | kinesin | Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa. pcls:SWISSPROT-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa. | 0 | 10 |
| 6237 | cg43964874 | 3378 | ACCAGTGCCACT GTGATCCAAGCA GIG/TJGGGCAGT GCCCATGCCTCC CCAATG | G | T | Arg | Ser (8408) | NON- CONSER VATIVE | laminin | Human Gene SWISSNEW-ID:P55288 LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) - HOMO SAPIENS (HUMAN), 1798 aa. pcls:SWISSPROT- ID:P55288 LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) - HOMO SAPIENS (HUMAN), 1798 aa. | 0 | 3 (3p21) |

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| 6238 | cg43983535 | 2722 | TTTGTGTCAAA GTATGTTCTCC C[C]ATGTCAGCC AGTGAATGTAAT CACACG | C | A | Arg | Met (8409) | NON- CONSER VATIVE | laminin | Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa. | 0 | 6 (6q22) |
| 6239 | cg42536982 | 7509 | CTGCATTGAGCG TTCTAATGCGTT G[C/G]AAGCGAA GGCGAATATATC GTGCAG | C | G | Leu | Phe (8410) | NON- CONSER VATIVE | laminin | Human Gene SWISSPROT-ID:P25391 LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) - HOMO SAPIENS (HUMAN), 3075 aa. | 0 | |
| 6240 | cg44009224 | 64 | GGTCAGCTGCA GCATGGGATGG CTG[A/T]GGATCT TTGGGGCAGCC CTGGGGCA | A | T | Arg | Trp (8411) | NON- CONSER VATIVE | laminin | Human Gene SWISSPROT-ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa. | 0 | |
| 6241 | cg42930646 | 1215 | TCGTCAATGTTA CTGATCGGATA G[C/G]GTATGGA TGGAAATGGACG ATGAGG | C | G | Ser | Arg (8412) | NON- CONSER VATIVE | laminin | Human Gene SWISSPROT-ID:P07221 CALSEQUESTIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ-BINDING PROTEIN) - ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa. | 1.8E-198 | 1 |

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| 6242 | cg43958558 | 451 | TGAAGTGGTCAGT GTTCAACCAGTA CTTATGTATTTT GAATGGTTTCCC ACTTT | A | Gln | His (9413) | NON- CONSER VATIVE | laminin | Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.lpcis:SWISSPROT-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE- BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa. | 3.9E-139 | 14 (14q21) |
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| 6243 | cg43958558 | 762 | GGCCAGTGGC AGGCTAGGCTC CGG/GTGGCAC TTGGCTGTCCAG AAGATGGG | G | T | Pro | Thr (8414) | NON- CONSER VATIVE | laminin | Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa. pcis:SWISSPROT-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE- BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa. | 3.9E-139 | 14 (14q21) |
| 6244 | cg43931460 | 732 | AGGTCAGGATTT TGCAGGTCCACT G[A/C]CAGGTGA AGGCGAGTCCG GCCATTA | A | C | Ser | Ala (8415) | NON- CONSER VATIVE | MHC | Human Gene Similar to SWISSPROT- ID:P25963 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN MAD3 - HOMO SAPIENS (HUMAN), 317 aa. | 7.6E-69 | 14 |
| 6245 | cg43111577 | 1062 | AGCCACAGGG TACAGAGGTGGT TC[G/C]AGCTTAT GAAGAAGAGAAC AAAGCT | G | C | Arg | Pro (8416) | NON- CONSER VATIVE | misc_cha nnel | Human Gene TREMBLNEW- ID:G1518639 CGMP-GATED CATION CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 1251 aa. | 0 | 16 (16q13) |
| 6246 | cg40367355 | 647 | TTTATTCATGGG GACTTAGAACCC G[G/A]TGAGCCC ATTCAAAATCATA CCCCC | G | A | Gly | Asp (8417) | NON- CONSER VATIVE | misc_cha nnel | Human Gene SPTREMBL-ID:O00564 INWARDLY RECTIFYING K+ CHANNEL HOMO SAPIENS (HUMAN), 375 aa. | 4.1E-199 | 21 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|---------------|---|----------|----|
| 6247 | cg44929972 | 1119 | TTCTCTTTGAATT GGCCAGAGGAA TTA/GGAGAGTG ACTTTTTTATGA AGACA | A | G | Ile | Met (8418) | NON- CONSER VATIVE | ngf | Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa. | 4.7E-214 | 7 |
| 6248 | cg39307062 | 350 | GCAAGATCGACA AGACGCAGCGC AA/GC/GCTGT CCCTTCTGCCGC TTCCAGA | G | C | Lys | Asn (8419) | NON- CONSER VATIVE | nuc_rec pt | Human Gene SWISSPROT-ID:Q13285 STEROID HORMONE RECEPTOR AD4BP (STEROIDGENIC FACTOR 1) (STF-1) (SF-1) (FUSHI TARAZU FACTOR HOMOLOG 1) - HOMO SAPIENS (HUMAN), 461 aa. | 7.2E-257 | |
| 6249 | cg43315956 | 3132 | GTGTTACACCTTT GCCAACCAGCTC C/T/A/GCCTTTGG AAATGGATGACA CAGAA | T | A | Leu | Gln (8420) | NON- CONSER VATIVE | nuc_rec pt | Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa. | 2.3E-244 | 3 |
| 6250 | cg43315956 | 3422 | AATGCCACCTCT CATTCAAGAAAT G/C/A/TGGAGAAT TCTGAAGGACAT GAACC | C | A | Leu | Met (8421) | NON- CONSER VATIVE | nuc_rec pt | Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa. | 2.3E-244 | 3 |
| 6251 | cg43935583 | 1345 | TCAGTATGGCTC TTTTCCAGGTGG C/T/C/JTTCCTGGG GGAATGCCTGGT AATT | T | C | Phe | Leu (8422) | NON- CONSER VATIVE | nuc_rec pt | Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa. | 1.3E-195 | 22 |
| 6252 | cg43935583 | 1383 | TGCCTGGTAATT TTCCCGGAGGAA TTG/AJCTCTGGAAT GGAGGGGGCA TGCCTG | G | A | Met | Ile (8423) | NON- CONSER VATIVE | nuc_rec pt | Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa. | 1.3E-195 | 22 |
| 6253 | cg43935583 | 1411 | TGGAATGGGAG GGGGCATGCCT GGA/A/GTGGCT GGAATGCCTGGA CTCAATGA | A | G | Met | Val (8424) | NON- CONSER VATIVE | nuc_rec pt | Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa. | 1.3E-195 | 22 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|---------------|--|----------|----|
| 6254 | cg43935583 | 1527 | ATGTGGCTCAGAG ACCCAGCAAATA T[G/A]TCAAAATA CCAGAGCAACCC AAAGG | G | A | Met | Ile (8425) | NON- CONSER VATIVE | nud_rec pt | Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa. | 1.3E-195 | 22 |
| 6255 | cg43935583 | 1577 | GTTATGAATCTC ATCAGTAAATTG T[C/G]AGCCAAAT TTGGAGGTC AAG CGTAA | C | G | Ser | End (8426) | NON- CONSER VATIVE | nud_rec pt | Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa. | 1.3E-195 | 22 |
| 6256 | cg43949686 | 1320 | CCGCGCCCAACC CACCATCTCCAA CC[A/C]GCGCTCA CCTCATCTCCTC TGCCAAG | A | C | Gln | Pro (8427) | NON- CONSER VATIVE | nud_rec pt | Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa. | 2.4E-167 | |
| 6257 | cg44926604 | 811 | TCTAGTGGGCGC TCAGCTCACAGC T[G/T]CTCAAATG GGAACAGATGG GAAGCT | G | T | Gln | Lys (8428) | NON- CONSER VATIVE | nuclease | Human Gene SWISSPROT-ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) HOMO SAPIENS (HUMAN), 939 aa. | 0 | 3 |
| 6258 | cg43952559 | 268 | AGCCAGGATTGC CTTCTCCTGCTA T[G/A]ATTCCAAA AAATTGGCCTTT AATAG | G | A | Met | Ile (8429) | NON- CONSER VATIVE | nuclease | Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcls: SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 7.8E-156 | |

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|------|------------|------|--|---|---|-----|----------------|--------------------------|-------------------|---|----------|----------|
| 6259 | cg43952559 | 765 | CAAAATTACTA GGGACATTAAAT TTAGGATATGAC CTGCTCTAGGCA TTCCT | A | G | End | Trp (8430) | NON- CONSER VATIVE | nuclease | Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.lpcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 7.8E-156 | |
| 6260 | cg44130572 | 604 | TAATGAGAACAA AGTTACAACATA CTTCJAGAGCCTC TGGACATAGCTA AGACA | T | C | End | Gln (8431) | NON- CONSER VATIVE | nuclease | Human Gene Similar to SWISSNEW- ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - MUS MUSCULUS (MOUSE), 1300 aa.lpcis:SWISSPROT-ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - MUS MUSCULUS (MOUSE), 1300 aa. | 2.4E-53 | |
| 6261 | cg43951535 | 1536 | GTGAACTACAGC GAGTAGCTTTTA G[C/G]CCTTTGCT TGGGCAAAACCTG CTGAT | C | G | Ser | Arg. (8432) | NON- CONSER VATIVE | nuclease inhib | Human Gene SPTREMBL-ID:Q13181 RNASE L INHIBITOR - HOMO SAPIENS (HUMAN), 599 aa. | 2.5e-315 | 4 (4q31) |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|--------------|--|---|---------------------|
| 6262 | cg43988571 | 2468 | GCCTCTTGACCT CACTTGCAGCAC C/A/TJAGGTGAAG ACCTTGCTGCTA AATGC | A | T | Lys | End (8433) | NON- CONSER VATIVE | oncogen e | Human Gene SWISSNEW-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT- 10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa.jpds:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa. | 0 | 10 (10q24) |
| 6263 | cg43988571 | 2469 | CCTCTTGACCTC ACTTGCAGCACC A/A/TJGGTGAAGA CCTTGCTGCTAA ATGCT | A | T | Lys | Met (8434) | NON- CONSER VATIVE | oncogen e | Human Gene SWISSNEW-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT- 10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa.jpds:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa. | 0 | 10 (10q24) |
| 6264 | cg36524555 | 192 | AAGAGCTCTGGG GCCGGGGCGG CA/G/CJGGGCTC CGGGGGCTCGG GTTCCGGT | G | C | Arg | Thr (8435) | NON- CONSER VATIVE | oncogen e | Human Gene SWISSPROT-ID:P22681. PROTO-ONCOGENE C-CBL - HOMO SAPIENS (HUMAN), 906 aa. | 0 | 11 (11q23.3) |
| 6265 | cg36524555 | 600 | GAGAAITCTCAG CCTAGGCGAAAC C/C/TJAACCAAC TGCCCTCATCT TCAGC | C | T | Pro | Leu (8436) | NON- CONSER VATIVE | oncogen e | Human Gene SWISSPROT-ID:P22681 PROTO-ONCOGENE C-CBL - HOMO SAPIENS (HUMAN), 906 aa. | 0 | 11 (11q23.3) |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|--------------|---|----------|---------------------|
| 6266 | cg36524555 | 663 | GAACTAAAAGGA ATCTTTCCAAGT G/A/GJACTCTTTC AGGAGACACAT TTCGG | A | G | Glu | Gly (8437) | NON- CONSER VATIVE | oncogen e | Human Gene SWISSPROT-ID:P22681 PROTO-ONCOGENE C-CBL - HOMO SAPIENS (HUMAN), 906 aa. | 0 | 11 (11q23.3) |
| 6267 | cg44012756 | 2030 | GGCTACACAGG GAGCATGTGTAA CA/T/GJCAACATC GATGAGTGTGCG GGCAAC | T | G | Ile | Ser (8438) | NON- CONSER VATIVE | oncogen e | Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa. | 0 | |
| 6268 | cg44012756 | 2323 | CACCTGCAAAGA CATGACCAGTGG C/T/AJACGTGTGC ACCTGCCGGGA GGGCTT | T | A | Tyr | Asn (8439) | NON- CONSER VATIVE | oncogen e | Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa. | 0 | |
| 6269 | cg44012756 | 559 | TGTCACACGAGTG TGGCCAGAAGC CC[G/A]GGCTTT GCCGCCACGGA GGCACCTG | G | A | Gly | Arg (8440) | NON- CONSER VATIVE | oncogen e | Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa. | 0 | |
| 6270 | cg43966629 | 5250 | AAC TTCGGGATC CTGCAGAGGTTT G/G/TTCCTGTG ATGCGTTGTGGA GGTGG | G | T | Thr | Asn (8441) | NON- CONSER VATIVE | oncogen e | Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa. | 1.3E-123 | 1 |
| 6271 | cg43966629 | 5251 | ACTTCGGGATCC TGCAGAGGTTTG G/T/GJTCCTGTGA TGCCTTGTGGAG GTGGT | T | G | Thr | Pro (8442) | NON- CONSER VATIVE | oncogen e | Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa. | 1.3E-123 | 1 |
| 6272 | cg43297056 | 944 | GGCAGTGTGGA CATCATCAGCTT CA/C/TJATCCTCA TCCACAATGTCA AGAGCC | C | T | Val | Met (8443) | NON- CONSER VATIVE | oncogen e | Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa. | 1.9E-103 | 20 (20q13.1) |

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|------|------------|-----|---|---|---|-----|---------------|--------------------------|---------------|---|---------------------------|----------|
| 6273 | cg42904626 | 196 | GTGCCTTGACGA TACAGCTAATTC A/GCJAATCATTT TGTGGACGAATA TGATC | G | C | Gln | His (8444) | NON- CONSER VATIVE | oncogen e | Human Gene Similar to SWISSPROT- ID:P01118 TRANSFORMING PROTEIN P21/K-RAS 2B - HOMO SAPIENS (HUMAN), 188 aa. | 1.1E-97 | 12 |
| 6274 | cg44028217 | 428 | AACTGCTCAAAG ACCACGGGCGG GTG/CJCCAGGG GTCGTTCTGGTG GTAGATG | G | C | His | Asp (8445) | NON- CONSER VATIVE | oxidase | Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa. | 0 7 (7q31) | 7 (7q31) |
| 6275 | cg44028217 | 569 | GGCAGCACCTG GTCGGCCATGG AGT/A/GJGATCTG CAGGCGGTACT GCGCTTGT | A | G | Tyr | His (8446) | NON- CONSER VATIVE | oxidase | Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa. | 0 7 (7q31) | 7 (7q31) |
| 6276 | cg44028217 | 691 | GCCTGGCGCTC CCAGGAGTACTG CGT/CJCTGCTCC AGAGTTGGCTGG ACCACG | T | C | Thr | Ala (8447) | NON- CONSER VATIVE | oxidase | Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa. | 0 7 (7q31) | 7 (7q31) |
| 6277 | cg43972840 | 945 | GAGGGCAGCAG CTGTCCCTTCGG AA/CJAAGCTATG GCTGTGCTGAG GAAGCCC | C | A | Thr | Lys (8448) | NON- CONSER VATIVE | oxygenas e | Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa. | 4.6E-168 (16p13.3) | 16 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|-----------------|--|-----------------------|----|
| 6278 | cg43948682 | 1212 | AAGTCCTCTATTC GTCTCAGGGACT G[A/G]CGCGTAG TGAATGATGGCG CCGTG | A | G | Ser | Pro (8449) | NON- CONSER VATIVE | peptidas e | Human Gene Similar to TREMBL-NEW- ID:G2687937 PEPTIDASE, PUTATIVE - BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE), 592 aa. | 5E-75 | 10 |
| 6279 | cg42347730 | 1427 | TAGTCCCTAAAG GTGATAATCTGC A[C/T]GAAGGCTC CCAGGATTTTCC GGGCT | C | T | Val | Met (8450) | NON- CONSER VATIVE | peroxida se | Human Gene SPTREMBL-ID:Q13408 SALIVARY PEROXIDASE - HOMO SAPIENS (HUMAN), 712 aa. | 0 | 17 |
| 6280 | cg41626506 | 1001 | CTCCAGGCCTCC AGGTTTCATGCCA G[T/G]GATGCTGT CACAAAGACTCAA AGTCT | T | G | Thr | Pro (8451) | NON- CONSER VATIVE | peroxida se | Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa. | 0 (3q26.3) | 3 |
| 6281 | cg41626506 | 2405 | TTCTCACAAGTC ATCTGGCAGTCA G[C/A]CCCTCCC CCGAAGGCAGC TTTGCTG | C | A | Ala | Ser (8452) | NON- CONSER VATIVE | peroxida se | Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa. | 0 (3q26.3) | 3 |
| 6282 | cg42691989 | 826 | CGGGTGGTTGT GCCTCAGAGCG AAG[C/G]CACATT CTCAATCAGCAC GGCCCTG | C | G | Ala | Pro (8453) | NON- CONSER VATIVE | peroxida se | Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa. | 8.9E-101 (14q24.1) | 14 |
| 6283 | cg42535091 | 1803 | GCAGGATTGAAG AAGAGCAGAAAA G[C/G]AAGAGGA AAGGGCACGAAT ATACAA | C | G | Ser | Arg (8454) | NON- CONSER VATIVE | phosphat ase | Human Gene SWISSPROT-ID:Q06124 PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (PTP-1D) (SH PTP3) (SH-PTP2) - HOMO SAPIENS (HUMAN), 593 aa. | 0 | 12 |
| 6284 | cg42535091 | 1840 | GCACGAATATAC AAATATTAAAGTAT [T/C]CTCTAGCGG ACCAGACGAGTG GAGA | T | C | Ser | Pro (8455) | NON- CONSER VATIVE | phosphat ase | Human Gene SWISSPROT-ID:Q06124 PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (PTP-1D) (SH PTP3) (SH-PTP2) - HOMO SAPIENS (HUMAN), 593 aa. | 0 | 12 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|-----------------|--|---|---------------|
| 6285 | cg43920534 | 4693 | GGCTGTTGGCC CACTTGTGGAC C[G/A]TCTCCATA TCACACAGATTG TCCAC | G | A | Thr | Met (8456) | NON- CONSER VATIVE | phosphat ase | Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa. | 0 | 12 |
| 6286 | cg43920534 | 4727 | TCACACAGATTG TCCACTAAATC C[G/A]GACATGCTT CTTCTTTACCCC AGTGA | A | G | Trp | Arg (8457) | NON- CONSER VATIVE | phosphat ase | Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa. | 0 | 12 |
| 6287 | cg43321833 | 2318 | ACTGACGTGATC GCTGGCCTCCTC A[C/T]GTTACCA TCAATCTCCTGG GGGTG | C | T | Thr | Met (8456) | NON- CONSER VATIVE | phosphat ase | Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment). | 0 | 20 |
| 6288 | cg43321833 | 2324 | GTGATCGTGGC CTCCTCACGTTT A[C/T]CATCAATC TCCTGGGGGTG ATGCTC | C | T | Thr | Ile (8459) | NON- CONSER VATIVE | phosphat ase | Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment). | 0 | 20 |
| 6289 | cg43321833 | 2330 | GCTGGCCTCCTC ACGTTACCCATC A[A/T]TCTCCTGG GGGTGATGCTCA CCATC | A | T | Asn | Ile (8460) | NON- CONSER VATIVE | phosphat ase | Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment). | 0 | 20 |
| 6290 | cg42460457 | 1437 | GGTCACGTCTAG TGTCAGCTGTGG G[G/A]GCCGTCA CCAGTCTCCTAT TGACAT | G | A | Gly | Ser (8461) | NON- CONSER VATIVE | phosphat ase | Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa. | 0 | 3 (3p14.2) |
| 6291 | cg42460457 | 1473 | GTCTCCTATTGA CATTTTAGACCA GT/CATGCGCG TGTTGGGAAGA ATACCA | T | C | Tyr | His (8462) | NON- CONSER VATIVE | phosphat ase | Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa. | 0 | 3 (3p14.2) |

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| 6292 | cg42460457 | 3466 | ACCTTCGTGTGC CTCATCCTTCTC ATTCGTGTGTGC TCGTTACTGGA GAGGG | T | C | Ile | Thr (8463) | NON- CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa. | 0 | 3 (3p14.2) |
| 6293 | cg42460457 | 5419 | CAATACCAGTTC ATCTATAAGCA AIGTGTCTTAGCT TGGTCAGCACTA AAGAA | G | T | Arg | Met (8464) | NON- CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa. | 0 | 3 (3p14.2) |
| 6294 | cg43928335 | 3499 | AGCAAGAGCTAA TAGTACCTCATC TTTATCATCATAA ATTGTATCTGTA AGAAA | T | A | Glu | Val (8465) | NON- CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:P54613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS SCROFA (PIG), 602 aa (fragment). | 3.2E-302 | 11 (11q22) |
| 6295 | cg43988365 | 2003 | AACGAGATGTCC AGTTCATACAGT CCTGTCCTTAA AGACAGACAAC CCTTG | C | T | Gly | Arg (8466) | NON- CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:Q14642 TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 412 aa. Ids: SPTREMBL-ID:Q14642 INOSITOL 1,4,5-TRIPHOSPHATE 5- PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa. | 2.6E-227 | 10 |
| 6296 | cg43307302 | 1279 | TTGGTTGGCGCT TTTGTGGCTGG ATC/GACTGTTT TTCAGCAAAATG CCCTA | C | G | Thr | Arg (8467) | NON- CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:P17706 T- CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) (TCPTP) - HOMO SAPIENS (HUMAN), 415 aa. | 8.7E-218 | 18 (18p11.3) |
| 6297 | cg44004203 | 3233 | TCCATTGTTGCT GATCTGGAACCT CTTCCTTTTGT AGTTGCCGAAAC TTCAC | T | C | Glu | Gly (8468) | NON- CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment). | 9E-211 | |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------------------|---|----------|----|
| 6298 | cg43269274 | 1136 | TCCTCCATCCCA GTTTACAGGA T[G/T]GGCCGT TGCCACAGGGCT TCTGCT | G | T | Pro | Gln (8469) | NON- CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa. | 3.2E-151 | 10 |
| 6299 | cg43269274 | 1137 | CCTCCATCCAG TTTTAGCAGGAT G[G/T]GGCCGT GCCACAGGGCTT CTGCTG | G | T | Pro | Thr (8470) | NON- CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa. | 3.2E-151 | 10 |
| 6300 | cg43269274 | 1964 | AGCGAGTAGCG AGGTGAGGACG ACA[C/A]GCGCG GGCTCTCCTCTC GCAGCTTC | C | A | Arg | Leu (8471) | NON- CONSER VATIVE | phosphatase | Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa. | 3.2E-151 | 10 |
| 6301 | cg43301213 | 527 | CAGAAATGCATCC CTAAACTCAGC A[G/A]AGAGGCA GTAAGGAACCCA GCACAA | G | A | Glu | Lys (8472) | NON- CONSER VATIVE | phosphatase inhib | Human Gene Similar to SWISSPROT- ID:Q13522 PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (L-1) - HOMO SAPIENS (HUMAN), 171 aa. | 7.8E-70 | 12 |
| 6302 | cg44021995 | 2419 | TAAAGTAGTGGA CAGCCTGGCCC CA[T/C]CCATTAG TAATGTTTTAGT GCAGGG | T | C | Ser | Pro (8473) | NON- CONSER VATIVE | phosphorylase | Human Gene SWISSNEW-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa. pcls:SWISSPROT-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa. | 0 | 16 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|-------------------|--|----------|-----------------|
| 6303 | cg44021995 | 2429 | GACAGCCTGGC CCCATCCATTAC TAJ/CJTGTTTTA GTGCAGGGCAA ACAGGTA | A | C | Asn | Thr (8474) | NON- CONSER VATIVE | phosphor ylase | Human Gene SWISSNEW-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa. pcis:SWISSPROT-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa. | 0 | 16 |
| 6304 | cg43996195 | 1215 | TGTCACCTTCCA GAGTGGGTACC CTT/CJCATACAT GTGGAACCTGCC CTGCAT | T | C | Glu | Gly (8475) | NON- CONSER VATIVE | phosphor ylase | Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa. | 2.4E-155 | |
| 6305 | cg43996195 | 1216 | GTCACCTTCCAG AGTGGGTACCCT TTC/TATACATGT GGAACCTGCCCT GCATC | C | T | Glu | Lys (8476) | NON- CONSER VATIVE | phosphor ylase | Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa. | 2.4E-155 | |
| 6306 | cg42688448 | 1817 | GCGCCATGGTA GTCTGAGGCTG GGC/A/CJTGGC ATGGGCCTGCAT CTGGGCCA | A | C | His | Gln (8477) | NON- CONSER VATIVE | polymera se | Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa. | 0 | 20 |
| 6307 | cg42688448 | 1823 | TGGTAGTCTGAG GCTGGGCATGG GC/A/CJTGGGCC TGCATCTGGGCC AAGGCCT | A | C | His | Gln (8478) | NON- CONSER VATIVE | polymera se | Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa. | 0 | 20 |
| 6308 | cg44022214 | 2014 | TGGAAGCTCACG GCATTGAGCGTG TTA/GJGGAGCGG AGCTTGACTCC CGCAGC | A | G | Tyr | His (8479) | NON- CONSER VATIVE | polymera se | Human Gene SWISSNEW-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa. pcis:SWISSPROT- ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa. | 0 | 19 (19q13.3) |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------------|--|----------|---------------|
| 6309 | cg43958858 | 2406 | CACAGAAATCCAT CAACCGGGACA GC[G]A/JAAGAGC CCTTCTCTTCAG TTGAGAT | G | A | Glu | Lys (8480) | NON- CONSER VATIVE | polymera se | Human Gene SWISSNEW-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.lpcis:SWISSPROT- ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME- ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa. | 0 | 6 (6p12) |
| 6310 | cg44016415 | 1881 | AGGCGCATAGG CCCTCTGACTTG CA[A/G]TGAGGT TGATCCATCCTG ACAGAT | A | G | Ile | Thr (8481) | NON- CONSER VATIVE | polymera se | Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa. | 0 | X |
| 6311 | cg43993893 | 1310 | CTCAAAGTTTGC GAGTTCTGTGAG C[A/T]TGTCGGTG ATCCCCCGTTG AGAGT | A | T | Met | Lys (8482) | NON- CONSER VATIVE | polymera se | Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.lpcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa. | 5E-178 | 8 (8p11.2) |
| 6312 | cg43993893 | 680 | CATGAACCTTTGT CTCACCCCTTTGA C[A/C]GGGTATCT GTGATAAAATGA ACCTT | A | C | Leu | Arg (8483) | NON- CONSER VATIVE | polymera se | Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.lpcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa. | 5E-178 | 8 (8p11.2) |
| 6313 | cg43916712 | 3743 | TTCCTCGGGCTT GGGTACACTGT GT[G]GCCCTCAG GGCATTGTCTGG ATCGTA | T | G | His | Pro (8484) | NON- CONSER VATIVE | polymera se | Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa. | 6.2E-148 | |

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|------|------------|------|--|---|-----|---------------|--------------------------|---------------------------|---|----------|---------------|
| 6314 | cg43916712 | 3744 | TCCTCGGGCTTG GGGTACACTGTG TIGTCCCTCAGG GCATTGTCTGGA TCGTAT | T | His | Asn (8485) | NON- CONSER VATIVE | polymera se | Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa. | 6.2E-148 | |
| 6315 | cg42534568 | 911 | ATTAAAGAAGAG GAGAAGCCCCCT GCCTCCGCAA CGAGTCCAGCG CCAGGTG | T | Pro | Leu (8486) | NON- CONSER VATIVE | potassiu m_chann el | Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa. | 0 | 12 (12p13) |
| 6316 | cg43262191 | 1277 | GAAGCGCTTTGT TTTCTCTACAA [G/A]CCATTCCCC GCATAGCTACCA CCAT | A | Ala | Thr (8487) | NON- CONSER VATIVE | prostagla ndin | Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.[pcls:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa. | 0 | 3 |
| 6317 | cg42697980 | 479 | GTTGGGGGCAG GTATGTCACCGT TC[G/T]CGTGGA CCCACAGTCCTA GGACACG | T | Arg | Leu (8488) | NON- CONSER VATIVE | prostagla ndin | Human Gene SWISSNEW-ID:Q16647 PROSTACYCLIN SYNTHASE (EC 5.3.99.4) (PROSTAGLANDIN I2 SYNTHASE) - HOMO SAPIENS (HUMAN), 500 aa.[pcls:SWISSPROT- ID:Q16647 PROSTACYCLIN SYNTHASE (EC 5.3.99.4) (PROSTAGLANDIN I2 SYNTHASE) - HOMO SAPIENS (HUMAN), 500 aa. | 5.9E-262 | |
| 6318 | cg38427250 | 754 | GTTGAGCAATGT GCACCTTCACTGA A[A/G]AGAAAGAA CTGGAATTTGCG TCTGG | G | Lys | Glu (8489) | NON- CONSER VATIVE | protease | Human Gene SWISSPROT-ID:P42575 CASPASE-2 PRECURSOR (EC 3.4.22.-) (CASP-2) (ICH-1 PROTEASE) (ICH- 1L/1S) - HOMO SAPIENS (HUMAN), 435 aa. | 4.9E-226 | 7 |

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|------|------------|-----|--|---|---|-----|---------------|--------------------------|----------|--|----------|---------------------|
| 6319 | cg43306871 | 605 | GCGTATGACTTT ATTGATCCAGGA C/A/GTGTATTG CAGATCTGGGTG TAGAC | A | G | Met | Thr (8490) | NON- CONSER VATIVE | protease | Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. pcls:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa. | 3.1E-153 | 19 |
| 6320 | cg43074055 | 584 | CCCAGCCCAACCT CAGTGCCTCCGT C/G/AJCCACAGT CCAGCTGCCACA GCAGGA | G | A | Ala | Thr (8491) | NON- CONSER VATIVE | protease | Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa. | 5.7E-138 | 19 (19p13.3) |
| 6321 | cg44031287 | 393 | TGGTTTCACTG ACAGGGGAGAC AC/G/TAGAGTCA TTGTAGACATGC CAACCA | G | T | Arg | Ser (8492) | NON- CONSER VATIVE | protease | Human Gene Similar to TREMBLNEW- ID:G2736064 UBIQUITIN SPECIFIC PROTEASE 41 - GALLUS GALLUS (CHICKEN), 357 aa. | 8.1E-67 | 1 |
| 6322 | cg35817832 | 780 | AACTTCTAAGCT CACCCGTGCTGA G/G/AJCTGTTTT CCTGATGTGGAC TATGT | G | A | Ala | Thr (8493) | NON- CONSER VATIVE | protease | Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa. | 2.1E-63 | X |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|------------------|---|---------------------------|---------------|
| 6323 | cg42914280 | 434 | ATATCTAGAAA CTACTACGACCT C[G/A]AAAAAGAT GTGAAACAGTTT GTTAG | G | A | Glu | Lys (8494) | NON- CONSER VATIVE | protease | Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. | 2.3E-63 | 11 (11p23) |
| 6324 | cg43979831 | 1346 | GCACCGAGGCT GCAGCAGCCAC CAG[C/G]TTCGC GATCAAAATCTT CTCTGCC | C | G | Ser | Arg (8495) | NON- CONSER VATIVE | protease nhib | Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa. | 1.1E-228 | 14 |
| 6325 | cg43511784 | 1247 | CTATCCCCCCCG AGGTCAAGTTCA A[C/A]AAACCCCT TGCTCTCTTAAT GATTG | C | A | Asn | Lys (8496) | NON- CONSER VATIVE | protease nhib | Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1-ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa. | 9.2E-212 | |
| 6326 | cg43268468 | 1080 | GGAGGCACCTCT GAGGTTCTTCTG G[G/C]GGGCAGT GACCGTGTCAAG GAGCTC | G | C | Pro | Arg (8497) | NON- CONSER VATIVE | protease nhib | Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa. | 2.6E-188 (17p13.3) | 17 |
| 6327 | cg43268468 | 1260 | CAGGAGCACGTT GGTCGTGGGC TC[A/G]TGCTGGA TCGCACCCGGTA CAGGTC | A | G | Met | Thr (8498) | NON- CONSER VATIVE | protease nhib | Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa. | 2.6E-188 (17p13.3) | 17 |
| 6328 | cg43932980 | 261 | TGGGAAGTGGT GACACACGGTTA CT[G/T]CGGCTTG GGTGTCGGTGA CCAGCCG | G | T | Cys | Phe (8499) | NON- CONSER VATIVE | protease nhib | Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa. | 1.7E-152 | 20 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|-------------------|---|----------|---------------|
| 6329 | cg43060292 | 1245 | TACTACAGAAGG GATGGGTTGACT T[G/T]TTTGTCC AAAGTTTCCATT TCTG | G | T | Leu | Phe (8500) | NON- CONSER VATIVE | protease inhib | Human Gene Similar to SWISSPROT- ID:P09006 CONTRAPIN-LIKE PROTEASE INHIBITOR 6 PRECURSOR (CPI-26) (SERINE PROTEASE INHIBITOR 3) (SPI-3) (SPI-2.2) - RATTUS NORVEGICUS (RAT), 418 aa. | 2.2E-83 | X (Xq22.2) |
| 6330 | cg44921824 | 1452 | CAGCACCACAGC GTGGTAGGCCTC C[C/T]GCAGCTC CGGCACCGTCA CGTCCCT | C | T | Arg | Gln (8501) | NON- CONSER VATIVE | reductase | Human Gene SPTREMBL-ID:Q13716 ADRENODOXIN REDUCTASE - HOMO SAPIENS (HUMAN), 491 aa. | 3.2E-270 | |
| 6331 | cg44921824 | 1741 | TGTGTGGAGAAA TGGTGGCAGAA GCT[C/G]CGGGT GCTCCCGGGG GAGGCAGC | T | C | Ser | Gly (8502) | NON- CONSER VATIVE | reductase | Human Gene SPTREMBL-ID:Q13716 ADRENODOXIN REDUCTASE - HOMO SAPIENS (HUMAN), 491 aa. | 3.2E-270 | |
| 6332 | cg43941472 | 771 | AGGGGATGTCG CCAAAGCCTTTG GA[G/A]CTGGAG CAGATTTTGTC TGCTGGG | G | A | Ala | Thr (8503) | NON- CONSER VATIVE | reductase | Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa. | 7.4E-184 | X (Xq28) |
| 6333 | cg43941472 | 837 | TCATACGGAGTG TGCTGGAGAAAT GT[A/T]TGAGAGG AACGGACGGAA GCTCAA | T | A | Phe | Ile (8504) | NON- CONSER VATIVE | reductase | Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa. | 7.4E-184 | X (Xq28) |
| 6334 | cg43286949 | 1008 | ACGCCAACTTC CTCTCGGGCTCT GT[C/A]ATTCATCT TGGTCTCTTCCT TCGGT | T | C | Thr | Ala (8505) | NON- CONSER VATIVE | reductase | Human Gene SWISSNEW-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.[pcis:SWISSPROT-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa. | 1.3E-152 | 7 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|-----------|--|----------|---------------|
| 6335 | cg43286949 | 848 | GGAAAGAGCATCT CTCCAAAGAAAT CTTCJGCTGGACT CCATCAATGCTC CCGAG | T | C | Gln | Arg (8506) | NON- CONSER VATIVE | reductase | Human Gene SWISSNEW-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-X ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.pcds:SWISSPROT-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-X ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa. | 1.3E-152 | 7 |
| 6336 | cg43925599 | 570 | GGGTACCTGGAA GAGTGAGCCTG GTTCJAAGGTAA AGCAGCTGTTAA GTATGC | C | A | Gln | Lys (8507) | NON- CONSER VATIVE | reductase | Human Gene Homologous to TREMBLIN-NEW-ID:G2707824 ALDEHYDE REDUCTASE - HOMO SAPIENS (HUMAN), 325 aa. | 5.6E-140 | 1 |
| 6337 | cg43255045 | 5442 | CGCGAGGAGGA ACAGCTCCGCCA GGAGJAAGGGA GGAACAGCAGCT GCGCAGC | A | G | Glu | Gly (8508) | NON- CONSER VATIVE | struct | Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa. | 0 | 1 |
| 6338 | cg43255045 | 5801 | GAGGCACCGCC AAGTCGGGGAG ATAA/CJAATCCC AAGAAGGGAAG GGCCATGG | A | C | Lys | Gln (8509) | NON- CONSER VATIVE | struct | Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa. | 0 | 1 |
| 6339 | cg43957646 | 3048 | GTGTTCAATTGCT GTACGTGATAAG AAGTGGCGTGAG GGGTGGGACAT GGTGAGG | G | T | Pro | His (8510) | NON- CONSER VATIVE | struct | Human Gene SPTREMBL-ID:O00185 BETA CATENIN - HOMO SAPIENS (HUMAN), 596 aa. | 0 | 10 |
| 6340 | cg42719763 | 755 | TCTACAACCCAG CACAACTCTCTGC TTTCJCTACAACC AGCACAACTCTCT GGTCC | T | C | Ser | Pro (8511) | NON- CONSER VATIVE | struct | Human Gene SWISSPROT-ID:P98088 TRACHEOBRONCHIAL MUCIN (TBM) (MAJOR AIRWAY GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 1056 aa (fragment). | 0 | 11 (11p15) |

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|------|------------|------|---|---|---|---------------|---------------|--------------------------|--------|--|----------|----------|
| 6341 | cg42491601 | 1247 | CAGATTCGGAGT A AACATGGAACGC C[A/C]GAACAAC GAATACCATATC CTTCTT | A | C | Gln | Pro (8512) | NON- CONSER VATIVE | struct | Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa. | 1.4E-215 | 17 |
| 6342 | cg42491601 | 1394 | GAAGAGAGAGAT G ATAAAGAAAACC A[G/C]GAAGATTA AGACAGTCGTGC AAGAA | G | C | Arg | Thr (8513) | NON- CONSER VATIVE | struct | Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa. | 1.4E-215 | 17 |
| 6343 | cg42491601 | 1395 | AAGAGAGAGATA G TAAAGAAAACCA G[G/C]AAGATTA GACAGTCGTGCA AGAAG | G | C | Arg | Ser (8514) | NON- CONSER VATIVE | struct | Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa. | 1.4E-215 | 17 |
| 6344 | cg43956325 | 1195 | TGCATTTGACCT C CTCAGTCAGAAT G[C/T]TGATGAGC ATTTCTCATCA GTTCC | C | T | Ser (8515) | Asn (8515) | NON- CONSER VATIVE | struct | Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa. | 3.1E-169 | 4 (4q21) |
| 6345 | cg43985529 | 972 | CCATCCGAGTCC G TGGTTGAATAGG C[G/T]TTTGGCAG CTGAGAAAGTTCC TGGAG | G | T | Arg | Ser (8516) | NON- CONSER VATIVE | struct | Human Gene SPTREMBL-ID:Q95284 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment). | 1E-163 | |
| 6346 | cg43051155 | 1027 | TCAGCACCCATG C ACAGTGCCATTG C[C/T]CTCCTTGT CAAAGACACGCA GGCCC | C | T | Gly | Ser (8517) | NON- CONSER VATIVE | struct | Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 186 aa. | 5.3E-103 | 17 |
| 6347 | cg42475997 | 512 | ACTTTAACAGGT T GGGACTTCAGG CTT[C/T]TTAGGA GGAGCCCACTGG CGCTTTC | T | C | Lys | Glu (8518) | NON- CONSER VATIVE | struct | Human Gene Similar to SPTREMBL- ID:Q10465 TITIN, SKELETAL MUSCLE ISOFORM (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 7962 aa (fragment). | 8.6E-98 | |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------------------|---|----------------------|----|
| 6348 | cg44014373 | 674 | TAACATGTTTTC CAAAGCAGATTT C[G/T]TGCTGTAC TGTGCCTGCAGG TCAAT | G | T | Thr | Lys (8519) | NON- CONSER VATIVE | struct | Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa. | 6.1E-70 | 17 |
| 6349 | cg44014373 | 675 | AACATGTTTTC AAAGCAGATTC GT[G]GCTGTACT GTGCCTGCAGGT CAATC | T | G | Thr | Pro (8520) | NON- CONSER VATIVE | struct | Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa. | 6.1E-70 | 17 |
| 6350 | cg44014373 | 687 | AAAGCAGATTC GTGCTGTACTGT G[C/T]CTGCAGG TCAATCTCCAGG GCCTGG | C | T | Ala | Thr (8521) | NON- CONSER VATIVE | struct | Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa. | 6.1E-70 | 17 |
| 6351 | cg43961860 | 1781 | GTCTTCTCCTAGG CTTCTGTGACC CT[C]GCTTTTA GCCTCCTTCTT AATTT | T | C | Gln | Arg (8522) | NON- CONSER VATIVE | struct | Human Gene Similar to SPTREMBL- ID:Q84703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment). | 3.5E-51 | |
| 6352 | cg43918310 | 232 | TCCAGCAGCAGCAG AAGCAGCCCTGC ATT[C]CCCACCCC CTCAGCTTCAGC AGCAG | T | C | Ile | Thr (8523) | NON- CONSER VATIVE | struct | Human Gene Similar to SWISSPROT- ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa. | 4E-50 1 (1q21) | |
| 6353 | cg43999676 | 535 | ATTGGGTATACA GCACTCAGTGAA A[C/G]GGAGAGT CCACGTTTATTC TCCTCC | C | G | Thr | Arg (8524) | NON- CONSER VATIVE | sulfotran sferase | Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa. | 7.8E-157 2 (2q12) | |
| 6354 | cg40388639 | 2168 | TCATCCGCTACG CTGGCTACAAGC A[G/C]CCTGACG GCTCCACCCCTGG GGGACC | G | C | Gln | His (8525) | NON- CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa. | 0 (12q24.2) | 12 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------|--|---|-----------------|
| 6355 | cg40388639 | 2170 | ATCCGCTACGCT | C | G | Pro | Arg (8526) | NON- CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa. | 0 | 12 (12q24.2) |
| 6356 | cg40388639 | 4911 | TATTTTGGAGT CACCTGCGAAC GT/AJACGAAAGTG ACCAACCGCCTT AGATC | T | A | Tyr | Asn (8527) | NON- CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa. | 0 | 12 (12q24.2) |
| 6357 | cg43987111 | 1807 | ACAGAGGCATAG GAGTCTGAGAAC TT/CJCGTGATT TGCCCAACAAGG GCAATA | T | C | Lys | Glu (8528) | NON- CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa. | 0 | 18 (1p34.1) |
| 6358 | cg43971304 | 1348 | GCAACAGCTTT GGGACACGGCC AA/CJCGCGTG AAGGGAAGTTC GGGAGGA | A | C | Lys | Asn (8529) | NON- CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa. | 0 | 19 (19q13.3) |
| 6359 | cg43971304 | 1349 | CAACAGCTTTG GGACACGGCCA AA/CJGCGTGAA GGGAAAGTTCG GGAGGAA | C | A | Arg | Ser (8530) | NON- CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa. | 0 | 19 (19q13.3) |
| 6360 | cg43971304 | 1359 | TGGACACGGC CAAACGCGTGAA GG/GJAJAAAGTTC GGGAGGAAGCT TTATGAA | G | A | Gly | Glu (8531) | NON- CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa. | 0 | 19 (19q13.3) |
| 6361 | cg43971304 | 2282 | GTCTGCACCTC CTCCACCAAGCG GC/A/CJGCAAGC GCAACTCTGTGG ACACGGC | A | C | Ser | Arg (8532) | NON- CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa. | 0 | 19 (19q13.3) |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------|--|---------|---------------------|
| 6362 | cg43948262 | 1103 | GGCTTCTTCCTT GTGCTGCTGGAT AT/C[CCCTCAGA ATCTGCTCTGTC TGCTC | T | C | Asp | Gly (8533) | NON- CONSER VATIVE | synthase | Human Gene SWISSPROT-ID:P22102 PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE) / PHOSPHORIBOSYLFORMYLGLYCINA MIDINE CYCLO-LIGASE (EC 6.3.3.1) (AIRS) (PHOSPHORIBOSYL- AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2) (GART) (GAR TRANSFORMYLASE) (5'- PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE) - HOMO SAPIENS (HUMAN), 1010 aa | 0 | 21 (21q22.1) |
| 6363 | cg43983214 | 594 | TCCCACTCACTC ATGAGCTCAAAG T[G/TTACAGGAC GGCGACAGAAAT TGACG | G | T | His | Asn (8534) | NON- CONSER VATIVE | synthase | Human Gene SPTREMBL-ID:Q13735 5- AMINOLEVULINATE SYNTHASE PRECURSOR - HOMO SAPIENS (HUMAN), 587 aa. | 0 | X (Xp11.2 1) |
| 6364 | cg42721903 | 318 | CCTAAATGACAT CACGAAAAGGGA A[G/A]AATTCTCT CCGCTGACGGC CAACCT | G | A | Glu | Lys (8535) | NON- CONSER VATIVE | synthase | Human Gene Similar to SWISSPROT- ID:Q06847 ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL (EC 3.6.1.34) (OSCP) - RATTUS NORVEGICUS (RAT), 213 aa. | 7.4E-79 | |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------|--|----------|---------------------|
| 6365 | cg43261057 | 1186 | CATGTCATCAAT CCTGCCAGTGAT C/A/CJAGTAATAG CCATCCTGGTCC CGCTG | A | C | Leu | Trp (8536) | NON- CONSER VATIVE | synthase | Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.jpcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. | 7.1E-76 | 20 |
| 6366 | cg43933068 | 534 | TTTAATGCGCTG AAGGTTCCCGTG C/C/TJAGAGGATA AATATACTGCCG AGGTG | C | T | Pro | Leu (8537) | NON- CONSER VATIVE | synthase | Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa. | 1.9E-75 | 12 |
| 6367 | cg43064068 | 1386 | CTCGGAGGTAGA GAATGCACTGAT G/A/GJAGCACCC TGCTGTGGTTGA GACGGC | A | G | Lys | Glu (8538) | NON- CONSER VATIVE | synthase | Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.jpcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. | 7.4E-65 | |
| 6368 | cg43958927 | 2793 | GTTGATGTTCTT GTTAATTTATAG G/C/AJGTTTTTG GGGATGTGGAG GTAGTT | C | A | Ala | Ser (8539) | NON- CONSER VATIVE | tgf | Human Gene SP TREMBL-ID:Q13118 TGF-BETA INDUCIBLE EARLY PROTEIN - HOMO SAPIENS (HUMAN), 480 aa. | 1.2E-246 | |
| 6369 | cg43980446 | 3858 | ATCTACACATTC ATTCCTGCTAG A/A/GJTAAACCA AAGGGACACTCG CAGCG | A | G | Ile | Thr (8540) | NON- CONSER VATIVE | tgf | Human Gene SP TREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa. | 1.3E-166 | 15 (15q21.1) |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------|--|----------|-----------------|
| 6370 | cg42711317 | 1113 | TGCTGCATCTAT GGTCTTAAAGA TGAJTGGAATTG AAAAAAGAAGAT ATTGC | G | A | Val | Met (8541) | NON- CONSER VATIVE | thiolase | Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa. | 2.9E-221 | 11 (11q22.3) |
| 6371 | cg42711317 | 1233 | CCAAAAAGTGAA TATCAATGGAGG A/G/TCTGTTTCT CTGGGACATCCA ATTGG | G | T | Ala | Ser (8542) | NON- CONSER VATIVE | thiolase | Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa. | 2.9E-221 | 11 (11q22.3) |
| 6372 | cg42711317 | 1329 | GCAAGGAGAATA CGGCTCTGCCAG T/A/TJTTGCAAT GGAGGAGGAGG TGCTTC | A | T | Ile | Phe (8543) | NON- CONSER VATIVE | thiolase | Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa. | 2.9E-221 | 11 (11q22.3) |
| 6373 | cg43278427 | 1119 | CCTTGATGTGTA ATGAGAGCAGTA TIG/CJACAGCTT GCGCCAGAGAA AATCTG | G | C | Met | Ile (8544) | NON- CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa. | 0 | 14 (14q31) |
| 6374 | cg43278427 | 1125 | TGTGTAATGAGA GCAGTATGCAGA G/C/GJTTCGCC AGAGAAAATCTG TGAATG | C | G | Ser | Arg (8545) | NON- CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa. | 0 | 14 (14q31) |
| 6375 | cg43278427 | 2002 | TGCCCTCGTCAT CGTCTGCTGCTG T/T/CJATGTGAAG ATCTACATCACA GTCCG | T | C | Tyr | His (8546) | NON- CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa. | 0 | 14 (14q31) |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|-----|--|----------|-----------------|
| 6376 | cg36988276 | 2239 | TGCTCTTCAGCT CCCAGAGTCACC A/GA/TGGTTCCA CTTACATACTTG TCCCT | G | A | Ser | Asn (8547) | NON- CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa. | 0 | 2 (2p21) |
| 6377 | cg42899808 | 1092 | CTGGCCACGAAC AGCAGGAAGGT GGC/TGGCCGA GCGGCGGCGTC GCAGGCGG | C | T | Ala | Thr (8548) | NON- CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P34995 PROSTAGLANDIN E2 RECEPTOR, EP1 SUBTYPE (PROSTANOID EP1 RECEPTOR) (PGE RECEPTOR, EP1 SUBTYPE) - HOMO SAPIENS (HUMAN), 402 aa. | 2.9E-212 | 19 (19p13.1) |
| 6378 | cg43306266 | 316 | CTACACAGGCAT GTGGCGGCCCG AGC/G/GTTCCG CCGAGGCGCGG GGCAACCT | C | G | Arg | Gly (8549) | NON- CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa. | 4.8E-212 | 1 (1p31.2) |
| 6379 | cg43264978 | 153 | GATGGATCTGCA CCTCTTCGACTA CTT/G/CAGAGCC AGGGAACCTTCTC GGACAT | T | G | Ser | Ala (8550) | NON- CONSER VATIVE | tm7 | Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa. | 1.4E-196 | |
| 6380 | cg3001696 | 1341 | CCCGTCCGATG GTCCCGGCGGT GGC/G/C/GTGCC GCCTGACCAGG CCATCCGGC | G | C | Gly | Arg (8551) | NON- CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P41143 DELTA-TYPE OPIOID RECEPTOR (DOR-1) - HOMO SAPIENS (HUMAN), 372 aa. | 2.1E-195 | 1 (1p36.1) |
| 6381 | cg42704646 | 312 | CTACACAGGCAT GTGGCGGCCCG AGC/G/GTTCCG CCGAGGCGCGG GGCAACCT | C | G | Arg | Gly (8552) | NON- CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa. | 3.1E-194 | 1 (1p31.2) |
| 6382 | cg2514276 | 645 | GTACGTCACCAT CTTCTACGCCCT GGC/G/GCTACCA CCACATCATGAC GGCGAG | G | C | Gly | Arg (8553) | NON- CONSER VATIVE | tm7 | Human Gene SWISSPROT-ID:P33032 MELANOCORTIN-5 RECEPTOR (MC5- R) (MC-2) - HOMO SAPIENS (HUMAN), 325 aa. | 7E-172 | |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------------------|---|---------|---|
| 6383 | cg43040271 | 1300 | GCITTCCTCATCT CTATCCCGCCCA T[G/C]CTGGCT GGCGCACCCCG GAAGACC | G | C | Met | Ile (8554) | NON- CONSER VATIVE | tm7 | Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.[pds:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. | 2.9E-74 | |
| 6384 | cg38841806 | 112 | CAGCTGGCAGCT GGCACTGTGGG CA[C/A]CAGCCTA CCTGGCCCTGGT GCTGGT | C | A | Pro | Thr (8555) | NON- CONSER VATIVE | tm7 | Human Gene Similar to SWISSPROT- ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa. | 2.1E-67 | |
| 6385 | cg1408914 | 623 | ATCACTCATGTT AAGTTATCATCT G[A/C]TTGGTATA TGGGTCAGGGG AAGTTT | A | C | Asp | Ala (8556) | NON- CONSER VATIVE | tm7 | Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa. | 2E-62 | |
| 6386 | cg1408914 | 671 | TTTCTCTCAGTG TTTACACAAAT G[A/T]GGTACCCA TGCTGAACCCCT TCATC | A | T | Glu | Val (8557) | NON- CONSER VATIVE | tm7 | Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa. | 2E-62 | |
| 6387 | cg43958312 | 1989 | GACGATTGGTGA GATGGTGGCCC GA[A/C]GTAGCCT CTCCGTGGCCCT CAAGTT | A | C | Ser | Arg (8558) | NON- CONSER VATIVE | transcript factor | Human Gene SPTREMBL-ID:Q15361 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 886 aa. | 0 | 9 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------------------|--|---|----------|
| 6388 | cg43948839 | 1029 | GCGGAAGCCTG GGGCTGCTGC TGG[C/T]GCCCT GGGCTGCTGGG GCCGGGGCC | C | T | Ala | Thr (8559) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa. pds:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa. | 0 | 17 |
| 6389 | cg43328754 | 934 | AAGGACGTCGG GCATCCCCCGTT TC[C/G]GCTTCTT GTCCACGCCGTA GCTGTC | C | G | Arg | Pro (8560) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:Q01201 TRANSCRIPTION FACTOR RELB (I- REL) - HOMO SAPIENS (HUMAN), 579 aa. | 0 | 19 |
| 6390 | cg43328754 | 935 | AGGACGTCGGG CATCCCCCGTT CC[G/C]CTTCTTG TCCACGCCGTAG CTGTCA | G | C | Arg | Gly (8561) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:Q01201 TRANSCRIPTION FACTOR RELB (I- REL) - HOMO SAPIENS (HUMAN), 579 aa. | 0 | 19 |
| 6391 | cg43962797 | 770 | TCTACAGGATTT GCAGGGTCAAAT TTC/AJAGCTCATT TCTGCAGGTAAT AATCA | C | A | Gln | Lys (8562) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:Q02446 TRANSCRIPTION FACTOR SP4 (SPR- 1) - HOMO SAPIENS (HUMAN), 784 aa. | 0 | 7 (7p15) |
| 6392 | cg44925200 | 651 | GTGCCGGTGGT GCTCAGGGAGG GGG[G/C]ATGGG GAGAGCTGAAA TCCAGGAC | G | C | Ile | Met (8563) | NON- CONSER VATIVE | transcript factor | Human Gene SPTREMBL-ID:Q61191 TRANSCRIPTION FACTOR C1 (HCF) - MUS MUSCULUS (MOUSE), 2045 aa. | 0 | X |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------------------|---|----------|---------------------|
| 6393 | cg43921342 | 2582 | TGCTGCTCCAGC CCCAGGATGACC T[G/A]CACGGCC TGCTGCAGGATG AGCAGC | G | A | Gln | End (8564) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.jpds:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa | 0 | 0 |
| 6394 | cg43921342 | 2592 | GCCCCAGGATG ACCTGCACGGC CTG[C/G]TGCAG GATGAGCAGCTT GGTCTGCG | C | G | Gln | His (8565) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.jpds:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa | 0 | 0 |
| 6395 | cg44130900 | 1153 | TGATCCTATAGC TAAATGGCAA A[A/G]CTGTTAAG TACGATGTACAA GCTGT | A | G | Thr | Ala (8566) | NON- CONSER VATIVE | transcript factor | HOMO SAPIENS (HUMAN), 654 aa Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment). | 7.5e-310 | 2 |
| 6396 | cg43011561 | 987 | CAGACGACGAG GCCTCGAGGAC AG[G/C]GGTGAT GGGACTTCGA GGGCCAAG | G | C | Arg | Ser (8567) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:P35269 TRANSCRIPTION INITIATION FACTOR IIF, ALPHA SUBUNIT (TFIIF-ALPHA) (TRANSCRIPTION INITIATION FACTOR RAP74) - HOMO SAPIENS (HUMAN), 517 aa. | 4.3E-275 | 19 (19p13.3) |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------------------|--|----------|----|
| 6397 | cg44024015 | 1547 | TGCCCTGGCTG GACACATGGCAC CTG/AJTGGGCC ACCTCCCGCCCT TCAGCCA | G | A | Val | Met (8568) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa. | 1.6E-250 | 3 |
| 6398 | cg43129605 | 1073 | GGGATCAGCCCT GGGAAGACCCC ATC/AJCCAGGA GGTCACCTCTGA GGAGGAG | C | A | Ser | Tyr (8569) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa. | 2.8E-232 | 20 |
| 6399 | cg43129605 | 1100 | CAGGAGGTCAC TCTGAGGAGGA GA/AJCAGGGC CACTGACTCTGC CACCATA | A | C | Asn | Thr (8570) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa. | 2.8E-232 | 20 |
| 6400 | cg43129605 | 1121 | GAGAACAGGGC CACTGACTCTGC CA/C/AJCATAGTG TCACCACCACCA TCATCT | C | A | Thr | Asn (8571) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa. | 2.8E-232 | 20 |
| 6401 | cg43129605 | 400 | GCCCGCGCTCG GCCGCCGCCG GTG/AJAGCGG AGCTGGACCT GGAACTGA | A | C | Lys | Gln (8572) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa. | 2.8E-232 | 20 |

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|------|------------|-----|---|---|---|-----|---------------|--------------------------|----------------------|--|----------|----|
| 6402 | cg43129605 | 443 | GAAACTGACCAT CAGTACCTGGCC G/A/C]GAGCAGT GGGCCAGCTCG GGGCAGA | A | C | Glu | Ala (8573) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa. | 2.8E-232 | 20 |
| 6403 | cg43129605 | 445 | AACTGACCATCA GTACCTGGCCGA G/A/C]GCAGTGG GCCAGCTCGG GCAGAGG | A | C | Ser | Arg (8574) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa. | 2.8E-232 | 20 |
| 6404 | cg43257305 | 921 | CATTCAGTTCT TGCCAGAAGGAA A[G/T]CTCGTGAT TTTCATGCCAAG CTAAA | G | T | Ala | Ser (8575) | NON- CONSER VATIVE | transcript factor | Human Gene SWISSPROT-ID:P28347 TRANSCRIPTIONAL ENHANCER FACTOR TEF-1 (PROTEIN GT-1IC) (TRANSCRIPTION FACTOR 13) (NTEF- 1) - HOMO SAPIENS (HUMAN), 426 aa. | 2.9E-228 | 9 |
| 6405 | cg43929348 | 743 | AAGCCAGGGA TAAATTTCAAGA GT[T/A]GCTTTTCG GACACTCCCTT TCTGCT | T | A | Gln | Leu (8576) | NON- CONSER VATIVE | transcript factor | Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa. | 6.5E-169 | 2 |
| 6406 | cg43929348 | 930 | ATAAAGCACTCA TCATCTGTACTC TT[G]CTGCCGAC TGAAGGCACCCC TGCTG | T | G | Lys | Gln (8577) | NON- CONSER VATIVE | transcript factor | Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa. | 6.5E-169 | 2 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|----------------------|---|---------|---------------|
| 6407 | cg43051067 | 1324 | TCAAACCTGCAC ATCCACCAGCGA GTTA/JACACACAG GAGAGAGGCC TACAAG | T | A | Val | Glu (8578) | NON- CONSER VATIVE | transcript factor | Human Gene Similar to SWISSNEW- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. pcls:SWISSPROT- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. | 1.3E-91 | |
| 6408 | cg43051067 | 1648 | TCAGCCAGAGC TCCAACCTTCAC ATTGJCCACCAG CGGGTTCACAAG AAAGAT | T | G | Ile | Ser (8579) | NON- CONSER VATIVE | transcript factor | Human Gene Similar to SWISSNEW- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. pcls:SWISSPROT- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. | 1.3E-91 | |
| 6409 | cg42849540 | 1840 | CTCCAGAAAGAG CTCTGCAGGCG GA[G/C]CAAAGG CAGGGCAGCCG GAAAGCAG | G | C | Ala | Pro (8580) | NON- CONSER VATIVE | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcls:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 2E-88 | 20 (20q13) |
| 6410 | cg42532030 | 317 | TTATAAATGTGAT GAGTGTGGGAAA IG/AJCCCTTCAGTC AGAGCTCAGATC TTAT | G | A | Ala | Thr (8581) | NON- CONSER VATIVE | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcls:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 1.9E-57 | |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|----------------------|--|----------|---------------|
| 6411 | cg43984952 | 1026 | CTCGGTCCCCGT CCCTGTCCCCCA A/C/G]TCACCCCT CCCTTCTGAACA CAGAA | C | G | Asn | Lys (8582) | NON- CONSER VATIVE | transcript factor | Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa. | 9.6E-53 | 12 (12q23) |
| 6412 | cg43984952 | 767 | CCAGACGCCTTC AAGCCCATCAAG A/C/G]GGAGAAG CTGGAGGAGCC GCCCGAA | C | G | Thr | Arg (8583) | NON- CONSER VATIVE | transcript factor | Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa. | 9.6E-53 | 12 (12q23) |
| 6413 | cg43946772 | 1682 | ATCTGGTCCAG TTCTTTTATTTT A/C]TATCAATATT TAATATACTGGC TAC | A | C | Tyr | End (8584) | NON- CONSER VATIVE | transferase | Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa. | 0 | 18 |
| 6414 | cg43946772 | 2216 | TCTAATGCTGGG CACCTGGCTATC C/T/C]CTCTGTG GCTTATCCAGG CACTG | T | C | Glu | Gly (8585) | NON- CONSER VATIVE | transferase | Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa. | 0 | 18 |
| 6415 | cg43916882 | 674 | AAGATGAAGAGC CCCAGCATCATG G/A/G]GAAGCG CTGGCGTAGTAG GGGTAG | A | G | Ser | Pro (8586) | NON- CONSER VATIVE | transferase | Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa. | 5.3E-245 | 1 |
| 6416 | cg44017777 | 364 | AAACTGTGGAAG CAGCAGTTTGCC C/G/A]AGGATGC AGAAGGATGGCT TTTGGG | G | A | Ser | Leu (8587) | NON- CONSER VATIVE | transferase | Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)(+)- ARGININE ADP- RIBOSYLTRANSFERASE) (TESTIS MONO(ADP- RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa. | 9E-195 | |

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|------|------------|-----|--|---|---|-----|---------------|--------------------------|-----------------|---|----------|----|
| 6417 | cg44017777 | 469 | CACACCATGGTC TTCAAGCTTCTG G/A/T/T/T/T/TCTCA CCATGGTCTTCA AGCTT | A | T | Ile | Asn (8588) | NON- CONSER VATIVE | transfere se | Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)+)- ARGININE ADP- RIBOSYLTRANSFERASE (TESTIS MONO(ADP- RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa. | 9E-195 | |
| 6418 | cg44017777 | 526 | TTTCTCACTATG GTCTTCAAGCTT C/A/T/JGGTTTTTC TCACCAGGTTG TAGAC | A | T | Leu | Gln (8589) | NON- CONSER VATIVE | transfere se | Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)+)- ARGININE ADP- RIBOSYLTRANSFERASE (TESTIS MONO(ADP- RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa. | 9E-195 | |
| 6419 | cg44000740 | 721 | TGCCAGTGTCTG GGGAGATACTG GCT/C/C/CACCCA GGAAACAGGG AACATCAC | T | C | Glu | Gly (8590) | NON- CONSER VATIVE | transfere se | Human Gene Homologous to SWISSPROT-ID:P30711 GLUTATHIONE S-TRANSFERASE THETA 1 (EC 2.5.1.18) (CLASS-THETA) - HOMO SAPIENS (HUMAN), 239 aa. | 1.6E-117 | 16 |
| 6420 | cg42344304 | 154 | ATCTCACTGCAC CGCCGCCTGCC CG/A/T/JGCGCTG GAACCCGCTGTG CAAAGAG | A | T | Glu | Val (8591) | NON- CONSER VATIVE | transfere se | Human Gene Homologous to SPTREMBL-ID:O08832 POLYPEPTIDE GALNAC TRANSFERASE-T4 - MUS MUSCULUS (MOUSE), 578 aa. | 1.2E-101 | |
| 6421 | cg43954704 | 888 | TCGGATAATTGCC CTTCTGGATGGA G/A/G/ACTCCTTG GGGATGCTGAGT TCAGG | A | G | Phe | Ser (8592) | NON- CONSER VATIVE | transfere se | Human Gene Similar to SPTREMBL- ID:Q29121 UDP- GALNAC:POLYPEPTIDE ALFA-1, O N- ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa. | 1.1E-68 | 2 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|-----------|---|---------|---------------|
| 6422 | cg43020771 | 438 | ATGGACATCTGG GGGGGAGAGAA TTCTTTGAGCTC TCCTTCAAGGTG TGGATG | C | T | Ser | Phe (8593) | NON- CONSER VATIVE | transport | Human Gene Similar to SPTREMBL- ID:O08912 POLYPEPTIDE GALNAC TRANSFERASE-T1 - MUS MUSCULUS (MOUSE), 559 aa. | 9.2E-51 | |
| 6423 | cg38869466 | 218 | CGGCGGAAGGT GGTGGACTGTAG CCGCGGGAGGA GACGCGGCTGT CTCGCTGC | G | C | Arg | Pro (8594) | NON- CONSER VATIVE | transport | Human Gene SWISSPROT-ID:P30825 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG) HOMO SAPIENS (HUMAN), 629 aa. | 0 | 13 |
| 6424 | cg43998978 | 4040 | GGCGCCCTGGC AAATCCAGGAGA CA[G/C]CTCCGC CCAGCAGCTGG CCCCAGGT | G | C | Ala | Pro (8595) | NON- CONSER VATIVE | transport | Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa. | 0 | 16 |
| 6425 | cg43935986 | 1982 | CTCCGGTTCTGT GAGGAACAACAT TIG/AJCTTATGGG CTGCAGAGCTGC GAAGA | G | A | Ala | Thr (8596) | NON- CONSER VATIVE | transport | Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa. | 0 | 6 (6p21.3) |
| 6426 | cg43935986 | 2282 | GCTGGTGATTGC TCACAGGCTGCA GJAGJCAGTTCA GCGCGCCACCC AGATCCT | A | G | Thr | Ala (8597) | NON- CONSER VATIVE | transport | Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa. | 0 | 6 (6p21.3) |
| 6427 | cg43935986 | 2348 | CAAGCTGCAGAA GCTTGCCAGCT CT/CJAGGAGGG ACAGGACCTCTA TTCCCG | T | C | End | Gln (8598) | NON- CONSER VATIVE | transport | Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa. | 0 | 6 (6p21.3) |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|-----------|--|---|--|
| 6428 | cg43112765 | 4285 | GCTCTGATGCTT TCTATTGTTATCC [C/T]TCCTTTTGG CGAATACCCCGC TTTG | C | T | Pro | Leu (8599) | NON- CONSER VATIVE | transport | Human Gene TREMBLNEW- ID:G2959643 RIM ABC TRANSPORTER HOMO SAPIENS (HUMAN), 2273 aa. | 0 | |
| 6429 | cg44008864 | 3409 | CAAGGACACAGA CACAAAGGCCTT C/T/CJCGGCGTC CAGCACATTGTT TGGGTC | T | C | Glu | Gly (8600) | NON- CONSER VATIVE | transport | Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa.lpcis:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa. | 0 | |
| 6430 | cg44008864 | 3410 | AAGGACACAGAC ACAAAGGCCTTC TTC/TJGGCGTCCA GCACATTGTTG GGTCC | C | T | Glu | Lys (8601) | NON- CONSER VATIVE | transport | Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa.lpcis:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa. | 0 | |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|-----------|---|----------|---|
| 6431 | cg44008864 | 599 | ATGAGGTGGCT GGAGATCAAT TTTCJAGCTACTA CTCCTTTGTCCA GGACC | T | C | Lys | Glu (8602) | NON- CONSER VATIVE | transport | Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa. pcis:SPTRMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa. | 0 | |
| 6432 | cg43300953 | 244 | GGCATGCGGGA CTACGACGAGGT GATTCJGCGCTTC CTGGGCGAGTG GGGGCCC | T | C | Ile | Thr (8603) | NON- CONSER VATIVE | transport | Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa. | 1.6E-261 | 5 |
| 6433 | cg43300953 | 336 | CCCCAATGGCTT CAATGGTATGTC A[G/TTCGTGTTT CTGGCGGGGAC CCCCGGA | G | T | Val | Phe (8604) | NON- CONSER VATIVE | transport | Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa. | 1.6E-261 | 5 |
| 6434 | cg43300953 | 414 | GAACCTGAGCAGA CGCCTGGCGCA AC[A/C]ACAGTGT CCCGCTGCGGC TGCGGGA | A | C | Asn | His (8605) | NON- CONSER VATIVE | transport | Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa. | 1.6E-261 | 5 |
| 6435 | cg43300953 | 465 | CGGCCGCGAGG TGCCCCACAGCT GC[A/C]GCCGCT ACCGGCTCGCC ACCATCGC | A | C | Ser | Arg (8606) | NON- CONSER VATIVE | transport | Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa. | 1.6E-261 | 5 |
| 6436 | cg43964039 | 2693 | TGCAGGGTGCC CAGGGCCCCAC GAA[G/A]GGCTG TGGGTGACACTT CACCCACA | G | A | Leu | Phe (8607) | NON- CONSER VATIVE | transport | Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa. | 1.6E-259 | 1 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|-----------|---|----------|----|
| 6437 | cg43992017 | 1612 | CAGCAGGAGGC CGAGAAAGACAA CG[G]ATGACCA CGCGGCGCTCC GGCGGCTG | G | A | Thr | Ile (8608) | NON- CONSER VATIVE | transport | Human Gene SPTREMBL-ID:Q14728 TETRACYCLINE TRANSPORTER-LIKE PROTEIN MRNA - HOMO SAPIENS (HUMAN), 455 aa. | 4.4E-241 | |
| 6438 | cg43919967 | 3399 | TCGTGTATGTCA CAGGCCGGCCC GA[A]TAAGAAGA AGCACCGCGTG GTGGCAT | A | T | Lys | Ile (8609) | NON- CONSER VATIVE | transport | Human Gene SWISSPROT-ID:P43125 RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1054 aa. | 8.8E-208 | 11 |
| 6439 | cg43919967 | 3401 | GTGTATGTGACAA GGCCGGCCCCGA AA[A]TGAAGAAG CACCGCGTGGT GGCATGG | A | T | Arg | End (8610) | NON- CONSER VATIVE | transport | Human Gene SWISSPROT-ID:P43125 RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1054 aa. | 8.8E-208 | 11 |
| 6440 | cg43919967 | 3456 | CGCAGCACAACT TCCCCACGGC GT[G]GTCCTCTCT TCTGCGACGGC CTCACCC | G | C | Trp | Ser (8611) | NON- CONSER VATIVE | transport | Human Gene SWISSPROT-ID:P43125 RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1054 aa. | 8.8E-208 | 11 |
| 6441 | cg42876412 | 531 | GATGCCCTCTCTCT CCATACATCTA C[A]TJGCAAAGG GATCTACGACGG AGACCT | A | T | Ser | Cys (8612) | NON- CONSER VATIVE | transport | Human Gene SWISSPROT-ID:Q14973 SODIUM/BILE ACID COTRANSPORTER (NA(+)/BILE ACID COTRANSPORTER) (NA(+)/TAUROCHOLATE TRANSPORT PROTEIN) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE) - HOMO SAPIENS (HUMAN), 349 aa. | 1.3E-184 | 14 |
| 6442 | cg43924839 | 1242 | TCACCCAAAGAG AAGTATCTGAAC T[C/A]TTTAAAC TTTTTCAAAATAT ACTC | C | A | Lys | Asn (8613) | NON- CONSER VATIVE | transport | Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa. | 1.6E-172 | 6 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------------|---|----------|----|
| 6443 | cg43945806 | 600 | AATCCTTCCACA GGGACGGAATG ATG/CJCTGCCA GTTCACTGTCAG CATGGGT | G | C | His | Asp (8614) | NON- CONSER VATIVE | transport | Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa. | 2.2E-145 | 6 |
| 6444 | cg43945806 | 601 | ATCCTTCCACAG GGACGGAATGAT G/CJGTGCCAGT TCACTGTCAGCA TGGGTG | C | G | Gln | His (8615) | NON- CONSER VATIVE | transport | Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa. | 2.2E-145 | 6 |
| 6445 | cg42726186 | 821 | ATCCAGCAGTTG GTTCACTCCAACA G/CJAAAATCTG AGGATCTCCTAA AATGG | G | C | Phe | Leu (8616) | NON- CONSER VATIVE | transport | Human Gene Similar to SPTREMBL- ID:Q92473 ABC-C TRANSPORTER - HOMO SAPIENS (HUMAN), 1704 aa. | 2.5E-60 | 17 |
| 6446 | cg43120117 | 1168 | ATCATAATAACC GAACAACGCAGT TGTJACAGACCC AAGGTTACACCA CATCA | G | T | Leu | Phe (8617) | NON- CONSER VATIVE | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa. | 7E-121 | |
| 6447 | cg43262192 | 3285 | CCCACTGGCACCA AAATACTGGGCT CJA/TCCGGTCTG GGACACATATCT GGAGA | A | T | Val | Glu (8618) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75068 KIAA0480 PROTEIN - HOMO SAPIENS (HUMAN), 1252 aa. | 0 | 1 |
| 6448 | cg43917756 | 889 | GTCAATCATAACC ATATACTTGTGG C/G/TGGTAGGC ATGTAACAGCCCC TGGAGC | G | T | Pro | Gln (8619) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14157 HYPOTHETICAL PROTEIN KIAA0144 - Homo sapiens (Human), 983 aa. | 0 | 1 |
| 6449 | cg43929067 | 3507 | ACCTTGCTTCTT AGATTTTTCCTTC T/A/TTTTCTTTG ACTTAATTCCTC AAG | T | A | Lys | Met (8620) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa. | 0 | 1 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|------------------|---|---|---|
| 6450 | cg43948542 | 1110 | TGAAAAAAGGGA GCCAGTTTGGTC A[G/C]TCCTGTTG TTTGCAGCAAA AATTG | G | C | Gln | His (8621) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa. | 0 | 1 |
| 6451 | cg43948542 | 1890 | AAATCATATCTCT TGATGCAAAAGTT G/TJAATTTGGAA AACAAAGACTAC AAGA | G | T | Leu | Phe (8622) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa. | 0 | 1 |
| 6452 | cg43948542 | 517 | AAAAGGAAATGC TGCCTGGCAAGA A[C/T]AGTTGAAA CAGAAGAAAGCT CCAGT | C | T | Gln | End (8623) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa. | 0 | 1 |
| 6453 | cg43950151 | 3235 | CACCTCCTCCGT AATCTGCTTAATT [A/C]GCAGCTTAT AGTCTTGAGCCA AGAG | A | C | Leu | Arg (8624) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa. | 0 | 1 |
| 6454 | cg43950151 | 4084 | CTCATGGCCATC TGTGCCCTCTAC C[G/C]GCAGGAA GCAATTGGTGT GTGGCC | G | C | Pro | Arg (8625) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa. | 0 | 1 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------------|---|---|---|
| 6455 | cg43926985 | 1450 | CATCATCATGGAT CCTCATCCAGTT T[G/T]CATTTAGG AGGACTGACAAA TGGA | G | T | Leu | Phe (8626) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment). | 0 | 2 |
| 6456 | cg43961763 | 1526 | CTCATCGTTGAT TTGTTCAATTTTT T[C]CTATATCT CTTGCTGCTC TCAC | T | C | Glu | Gly (8627) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P13521 SECRETOGNANIN II PRECURSOR (SGII) (CHROMOGRANIN C) - Homo sapiens (Human), 617 aa. | 0 | 2 |
| 6457 | cg43301812 | 3665 | GGCACTGTCTTA TCCTCCTCCCTG C[A/T]GACCTCTG GGTTGCGTCTT TCTCC | A | T | Cys | Ser (8628) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa. | 0 | 3 |
| 6458 | cg43301812 | 3980 | TGACCCCTCAGCT TCAGCTGCAAAAT TT[C]AGAGTTTG TGGAGTTATGAG AACTA | T | C | Lys | Glu (8629) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa. | 0 | 3 |
| 6459 | cg43925942 | 2191 | GGTTGCTTGGGA GACCCCTACAAGA A[A/G]AATTTTCC CGCTTTATGACA GAACC | A | G | Lys | Glu (8630) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment). | 0 | 3 |
| 6460 | cg43931104 | 825 | GTGTGTTTCATG TGGACATTGTTC ATT[C]GGCTGGC ACTTTGGCAACC TTTGTG | T | C | Met | Val (8631) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75329 ATAXIN-7 - HOMO SAPIENS (HUMAN), 892 aa. | 0 | 3 |
| 6461 | cg43939697 | 314 | GGCCGCTCAAA GCCGGGAGATC GAC[G/T]GTTTGA GCCCGGAAGCG CAGAAGCT | G | T | Gly | Cys (8632) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa. | 0 | 3 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------------|---|---|---|
| 6462 | cg43940975 | 315 | TCTGGATCCACG GAGAAATATCCA A[G/A]ACGCTCAA ACTGGAACTTGT CGAAG | G | A | Leu | Phe (8633) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa. | 0 | 3 |
| 6463 | cg43917191 | 3407 | TCCTTTAATACT GAAGTTGTATCC T[C/A]AGGCAGC CGGCTGTTAGCA TTATCT | C | A | Glu | End (8634) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBL-NEW- ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment). | 0 | 4 |
| 6464 | cg43934651 | 1011 | AGGATTTTGATA ATTCTCATAATA [G/C]AATCCAGTA TCCTGATATCAG TGTT | G | C | Arg | Thr (8635) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15399 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 786 aa. | 0 | 4 |
| 6465 | cg43934651 | 2577 | GCTGTGACTGTG ACCTCCCTCTGC A[G/T]CTACTTGG ATCTGCCCTGGT ATCTC | G | T | Ser | Ile (8636) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15399 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 786 aa. | 0 | 4 |
| 6466 | cg44035533 | 1188 | GAGAGCGACAG CCCAGATAGCCA CTT[C/G]GGACCTG GAATCCAACGTG GAGAGT | T | C | Leu | Ser (8637) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:P78316 HYPOTHETICAL 99.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 873 aa (fragment). | 0 | 4 |
| 6467 | cg43933355 | 1258 | GTTC TTGAAACA TTCCTCCATCCG G[A/T]CATGGAAG GGTCGCAAGTTA TCTGA | A | T | Val | Asp (8638) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment). | 0 | 5 |
| 6468 | cg44026925 | 3702 | CCCTGTGTGCTC TAGGGTTGGCAA TT[T/G]CAGGATGC TACACTGTCAAA AGCAG | T | G | Ile | Met (8639) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa. | 0 | 5 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------------|---|---|----|
| 6469 | cg43924112 | 4800 | GGTTTAAAGGAT TGAAGAAATTCAC G[C/A]GTGAAGG GGAAAGTGTTCC AAAGGC | C | A | Arg | Leu (8640) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa. | 0 | 6 |
| 6470 | cg43975893 | 517 | CTTTGGTGAGC TTCAGTATTCTC A[C/A]AAGAATCT TGGGTAGGTTTC TTGGT | C | A | Cys | Phe (8641) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45157 FLASH - HOMO SAPIENS (HUMAN), 1269 aa (fragment). | 0 | 6 |
| 6471 | cg43918128 | 2125 | TCATCAAGGGCT CCGTCCTCTCCC TT[C/C]CTCGCCGC CTTCGTCATCAT CCTCA | T | C | Lys | Glu (8642) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14137 HYPOTHETICAL PROTEIN KIAA0124 - Homo sapiens (Human), 682 aa (fragment). | 0 | 8 |
| 6472 | cg43968274 | 1803 | AATGACTGAAGT GGACCTCTTCAT T[C/T]TTACCCAG AGAATCAAAGTG CTGAA | C | T | Leu | Phe (8643) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14914 NEURONAL MUNC18-1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 837 aa. | 0 | 9 |
| 6473 | cg43968274 | 1804 | ATGACTGAAGTG GACCTCTTCATT C[T/C]TACCCAGA GAATCAAAGTGC TGAAC | T | C | Leu | Pro (8644) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14914 NEURONAL MUNC18-1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 837 aa. | 0 | 9 |
| 6474 | cg43287069 | 2139 | ATACTCTATCTG GATCTTCTCTCA G[A/T]CAGGCAC CATCTCATATGT ATGGCA | A | T | Arg | Ser (8645) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P55197 AF-10 PROTEIN - Homo sapiens (Human), 1027 aa. | 0 | 11 |
| 6475 | cg43925880 | 1137 | TCTTCTCAGTC TTGGTCTGAAAT T[T/C]AGCAGCAT TGGTCCAAACA CGTCC | T | C | Lys | Glu (8646) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q13435 SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150) - Homo sapiens (Human), 872 aa. | 0 | 11 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|------------------|--|---|----|
| 6476 | cg43916884 | 2403 | GATCCCTTTTGG TAGCTTTCCAGG C[A/G]ATGTTTG GCCTCAGGAGA CTTATT | A | G | Leu | Ser (8647) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa. | 0 | 12 |
| 6477 | cg43916884 | 340 | GCAGCTTTCTCA AAAGGCTGCTCT G[G/C]CAACTGC TGCTTCTCAACC CCCTTG | G | C | Pro | Ala (8648) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa. | 0 | 12 |
| 6478 | cg43916884 | 341 | CAGCTTTCTCAA AAGGCTGCTCTG G[C/G]AACTGCT GCTTCTCAACCC CCTTGG | C | G | Leu | Phe (8649) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa. | 0 | 12 |
| 6479 | cg43924701 | 1114 | AGAACTCGGCA CTGTTTCGTAGG A[A/T]CGCGTGAA GTTTCAGGAAC AGTCC | A | T | Phe | Ile (8650) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13099 TG737 - HOMO SAPIENS (HUMAN), 824 aa. | 0 | 13 |
| 6480 | cg43929104 | 2468 | TGGTGGCCATAG AGGACGTGGAG GAT[C/T]CAATAT GCGTGGTGGAA ATTTCAG | T | C | Phe | Leu (8651) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa. | 0 | 14 |
| 6481 | cg44018598 | 4168 | GCAGGATACCAT TCAGTCTCTCC G[C/T]TGCAGACA CCACACTTACAA CTTTT | C | T | Ala | Thr (8652) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa. | 0 | 14 |
| 6482 | cg43936094 | 1825 | ACTCGGGGCAC GACACGCGTGAA GG[G/A]TTTATCA TCTGGTGACAAG TTAGGT | G | A | Pro | Ser (8653) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAC62018 P53 TUMOR SUPPRESSOR-BINDING PROTEIN 1 - HOMO SAPIENS (HUMAN), 1972 aa. | 0 | 15 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------------|--|---|----|
| 6483 | cg43928515 | 508 | GCATTTTCTACA CTTGTTGTGAAC AT/C]GTGGCTCA GGGAAAGGGGT AGGATC | T | C | Met | Val (8654) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment). | 0 | 16 |
| 6484 | cg43945577 | 2253 | GTTGACAAGCCG GCTACAGGGAGT C[G/C]GCGCGCT CGGCCAGGCAG CCTCTGA | G | C | Gly | Arg (8655) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa. | 0 | 16 |
| 6485 | cg43945577 | 408 | GGAGGTGGAAG TGCTGGAGGATG AC[G/A]TGTCTGC AGTTGAGTTCAG GCAGAC | G | A | Val | Met (8656) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa. | 0 | 16 |
| 6486 | cg43964911 | 2441 | AAGCAGAACAGG CACAGGATGTAG G[G/T]GGTAGTC AGGAGTGCGGG CAGCTGG | G | T | Pro | Thr (8657) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q12767 HYPOTHETICAL PROTEIN KIAA0195 - Homo sapiens (Human), 1356 aa. | 0 | 17 |
| 6487 | cg43983241 | 1570 | ACCAACCAGCAG TTTAAAGTTTAC [C/A]AGAATATCT TGAAAATATGGT AATA | C | A | Pro | Gln (8658) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa. | 0 | 18 |
| 6488 | cg43983241 | 402 | TACTTGGAAATC AAATACATTCTAT [T/G]CTGCTGGG AAAAATTACTTAC TACG | T | G | Ser | Ala (8659) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa. | 0 | 18 |
| 6489 | cg43991657 | 2076 | CCACGGCCCTC CAGGCGGCTCC AGG[C/T]GCGGC TGAGGAGGCCCC ATCACTGGG | C | T | Ala | Thr (8660) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa. | 0 | 19 |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------------|--|---|----------------------|
| 6490 | cg43919691 | 1205 | CTTTCCAGCTC TGCCTCCAAATG C/A/G/ACGTGTG CTCCCTCACCTG GTCCGA | A | G | Leu | Ser (8661) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa. | 0 | 20 |
| 6491 | cg43919691 | 830 | GAGCTTCTCCAA TTCTTCTTGTAAAC [C/A]GACATGCC GAGGTCTGAGC CTCCTC | C | A | Arg | Leu (8662) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa. | 0 | 20 |
| 6492 | cg43949984 | 1626 | AGGAACACCCAC AACATCTTCCAA A[A/G]TCTTAGTA GGGCAAGGTCT GGAATG | A | G | Ile | Thr (8663) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76931 FLS353 - HOMO SAPIENS (HUMAN), 747 aa. | 0 | 20 |
| 6493 | cg43981483 | 439 | GGCAGCCAGG TGATGTTGAGGT TG[G/A]AATTCTT GGAGGCATTGAT GAACAT | G | A | Ser | Phe (8664) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75882 ATTRACTIN - HOMO SAPIENS (HUMAN), 1198 aa. | 0 | 20 |
| 6494 | cg43955358 | 2797 | TTTTCTGCAATCT CCAAAGCTTTCC[A/C]TGCTTTTCT GTAGTAAAGAGC TCA | A | C | Trp | Gly (8665) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANTRANSFERASE) AMYLO-1,6- GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa. | 0 | 1 (1p21) |
| 6495 | cg17663981 | 361 | GGCCGCCACCC GGAAGGCCGCC TGC[A/G]CCTGC GACCAAAAACCC TGCAGCTG | A | G | Thr | Ala (8666) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa. | 0 | 10 (10p11.2 3) |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------------|--|---|----------------------|
| 6496 | cg17663981 | 388 | CTGCGACCAAAA ACCCTGCAGCTG C[C/T]CCAAAGG GGATGTCAACTA CGCGTT | C | T | Pro | Ser (8667) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa. | 0 | 10 (10p11.2 3) |
| 6497 | cg43968854 | 9932 | GACAATGTGTGT GTCAAGAAAATA A[G/C]AACCAAGAA GTCATAGGGACA GTGAA | G | C | Arg | Thr (8668) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa. | 0 | 10 (10q25) |
| 6498 | cg43968854 | 5060 | GCCTGCAAAATCT TCACAACCAGAC C[C/T]AGACAAAA ACCCAGCAAGCT CCAAG | C | T | Pro | Leu (8669) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa. | 0 | 10 (10q25) |
| 6499 | cg43968854 | 8018 | ACAAAGAGATGC CCCAAGACACGT C[C/T]CAGGAAA GAAGTAAAGAG GAGCTC | C | T | Pro | Leu (8670) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa. | 0 | 10 (10q25) |
| 6500 | cg43269831 | 1626 | GTGGCGATCATC ATGAAAGAGGGC T[C/A]AAAGTTGG ACTTGTAGTCCA GAAAG | C | A | Glu | End (8671) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P15586 N-ACETYLGLUCOSAMINE-6- SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6- SULFATASE) - Homo sapiens (Human), 552 aa. | 0 | 12 (12q14) |
| 6501 | cg44920831 | 1083 | CTAGAAAGGGGTA ACAGCTCTGTTC G[C/A]TGCAGGA CTAGCAGGCGTA GGAGAT | C | A | Ala | Ser (8672) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q99493 SCA2 PROTEIN - HOMO SAPIENS (HUMAN), 914 aa (fragment). | 0 | 12 (12q24) |

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| 6502 | cg43979900 | 2115 | GGTCTCTATGTA AACATCACACTT TTA/GTAGTCAGA TTGGTCCAGTTG TAGTC | A | G | Ile | Thr (8673) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa. | 0 | 14 (14q24.3) |
| 6503 | cg43979900 | 2601 | AAATTGTTGTGA CACATTGAAATA A[G/A]GAAGAAAT GGCCGTATGCAC TTAGA | G | A | Pro | Leu (8674) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa. | 0 | 14 (14q24.3) |
| 6504 | cg43960198 | 1948 | GAACACGATCTG GTTTCATGTGACC AIG/TGAAGAACC ACGCCAGGCAG GCGGGA | G | T | Arg | Met (8675) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa. | 0 | 20 (20p13) |
| 6505 | cg43960198 | 1978 | AACCACGCCAG GCAGGCGGGAG TTC/GTAGGTCT TGGACATCAAAG CTGAGTC | G | T | Arg | Leu (8676) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa. | 0 | 20 (20p13) |
| 6506 | cg43973129 | 1847 | CAACTATGACTG GTGGGAGAAAAA GIC/GICCTTCTCT GAGGATGTGAAC TGGGG | C | G | Pro | Ala (8677) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P05060 SECRETORIN I PRECURSOR (SGI) (CHROMOGRAININ B) - Homo sapiens (Human), 677 aa. | 0 | 20 (20pter) |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------------|--|---|----------------|
| 6507 | cg43973129 | 657 | GGAGAGAACTAT CAAAAAGGGA GCJA/GJAGGGA AGATAGCAGTGA AGAGAAA | A | G | Gln | Arg (8678) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P05060 SECRETAGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) - Homo sapiens (Human), 677 aa. | 0 | 20 (20pter) |
| 6508 | cg43955813 | 1322 | CTGGATACAAGT TATGCTTTGATA G[GJA]TGAAACA GTAAATAATTATA GATCT | G | A | Gly | Asp (8679) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa. | 0 | 4 (4q12) |
| 6509 | cg43955813 | 691 | ACAAAATGTTATT CCATCTAGTGCC [A/C]AAAAAGAGAG AGACTTACACTT TTGA | A | C | Lys | Gln (8680) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa. | 0 | 4 (4q12) |
| 6510 | cg25268354 | 1654 | CTCTGTTCCCTG GAACTCCTTCAA C[C/T]GCGACGT ACTGAAGGCCCT GTACAG | C | T | Arg | Cys (8681) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P09172 DOPAMINE BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE) (DBH) - Homo sapiens (Human), 603 aa. | 0 | 9 (9q34) |
| 6511 | cg43311566 | 794 | AAGAGCGAGTG GGCCACGCGAG CGA[A/G]CCCTG AGGACCTGGAAT TCATCCGC | A | G | Asn | Ser (8682) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment). | 0 | X |
| 6512 | cg43992229 | 1269 | CCAGCCAGACTG TGAATATGTTGT G[GJA]AATTGCAA GCCATAACGTAC TGGGG | G | A | Glu | Lys (8683) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P23352 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE- LIKE X-LINKED) - Homo sapiens (Human), 680 aa. | 0 | X (Xp22.3) |
| 6513 | cg43992229 | 1770 | CAAGCCTATTGG CTGCCTGGCG AA[C/G]GAGGTC ATGTTCTTCTAA GGTGCT | C | G | Arg | Gly (8684) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P23352 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE- LIKE X-LINKED) - Homo sapiens (Human), 680 aa. | 0 | X (Xp22.3) |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|------------------|---|---|---------------|
| 6514 | cg43992229 | 1771 | AAGCCTATTGGC TGCCTGGGCGA AC[G/C]AGGTCA GTCTTTCTAAG GTGCTA | G | C | Arg | Pro (8685) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P23352 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE- LIKE X-LINKED) - Homo sapiens (Human), 680 aa. | 0 | X (Xp22.3) |
| 6515 | cg42681986 | 1609 | GCCAGTGGTGG CGGGGAAGAGA ATT[C/T]GCGACA CAGACGTGGGG ATTGCGCA | C | T | Glu | Lys (8686) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14827 RAS-GRF2 - HOMO SAPIENS (HUMAN), 1237 aa (fragment). | 0 | |
| 6516 | cg42682094 | 3090 | GACTGCTGTGAG GACAGGGCTGG CG[C/T]AGAGCG AGCAGTCACAGG TGGGTGA | C | T | Cys | Tyr (8687) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14674 KIAA0165 PROTEIN - HOMO SAPIENS (HUMAN), 1795 aa. | 0 | |
| 6517 | cg43054046 | 717 | TTTTAAGTGA GTTCAAGAGTTT TTT/AAGAATGT GGCAGTGATCCC TCCTG | T | A | Phe | Leu (8688) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P48200 IRON-RESPONSIVE ELEMENT BINDING PROTEIN 2 (IRE-BP 2) (IRON REGULATORY PROTEIN 2) (IRP2) - Homo sapiens (Human), 963 aa. | 0 | |
| 6518 | cg43139712 | 1735 | TAAGACCAGGGA AAGGGGGAGC AG[G/C]GGACAA AGAGGGGCCCG GGCAAGCA | G | C | Gly | Arg (8689) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60378 F23858_1 - HOMO SAPIENS (HUMAN), 608 aa (fragment). | 0 | |
| 6519 | cg43139712 | 1745 | GAAAGGGGGGA GCAGGGGACAA AGA[G/T]GGGCC GGGGCAAGCAC TTCATCGGA | G | T | Arg | Met (8690) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60378 F23858_1 - HOMO SAPIENS (HUMAN), 608 aa (fragment). | 0 | |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------------|--|---|--|
| 6520 | cg43920875 | 2051 | CCTATACTGAGA TAAAGCAGCCCC A/G/TTGAGCACA TCTGTTGGCCAG GGCCA | G | T | Thr | Asn (8691) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P46199 TRANSLATION INITIATION FACTOR IF- 2, MITOCHONDRIAL PRECURSOR (IF- 2MT) (IF-2(MT)) - Homo sapiens (Human), 727 aa. | 0 | |
| 6521 | cg43932090 | 251 | GACTTTAAGGCC TTGTCTTTACCTT [C/T]ATCCTTTAT GAAGGAAGCTTT GCCA | C | T | Glu | Lys (8692) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment). | 0 | |
| 6522 | cg43934688 | 1393 | GGTTCAGTTAAA CCTACTCAAACCT A/A/TJTGCTGTTA AAGAATCATTGA CTACA | A | T | Asn | Ile (8693) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment). | 0 | |
| 6523 | cg43992835 | 1306 | TTCATCATTGTC CGAGTCCACAAC C/A/CJCTGCACCTG ATACCGTCCGCT ACAGT | A | C | His | Pro (8694) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q60292 KIAA0545 PROTEIN - HOMO SAPIENS (HUMAN), 1129 aa (fragment). | 0 | |
| 6524 | cg44016445 | 1774 | TCCTCCCCGGG GACATGGCTGTC GA/A/TJGAAGTCA ATCTGCACAGGG TCCCCG | A | T | Phe | Ile (8695) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75427 LEUCIN RICH NEURONAL PROTEIN - HOMO SAPIENS (HUMAN), 832 aa. | 0 | |
| 6525 | cg44024279 | 1391 | TGAATGCCAAGA TAAAGGAGAAGA A/G/TJAATTACAG AAATACATCCAG GAGAG | G | T | Glu | End (8696) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa. | 0 | |
| 6526 | cg44130923 | 2147 | CCAGTTTCTCAA GATATGCCTGGC T/A/GJAAGACGAA GGGCTCCTCACC ACTGA | A | G | Lys | Glu (8697) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREVISIAE) HOMOLOG (SUPT6H) - MUS MUSCULUS (MOUSE), 1726 aa. | 0 | |

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|------|------------|------|--|---|---|-----|---------------|--------------------------|------------------|---|----------|----------|
| 6527 | cg43957199 | 801 | CCCATGAGGTTG GGGGTGAAGTCG ACTTCGATGTCA ATGGTCAAGATG TCCCGG | T | C | Ser | Gly (8698) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa. | 1.0e-313 | 1 |
| 6528 | cg43978095 | 1436 | GTGCCTCTTCAC CAAGAAATGCTGC A[G]TCGGAGCA CGCAGACCCACAA ACGACG | G | T | Gln | His (8699) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15326 BS69 PROTEIN - HOMO SAPIENS (HUMAN), 562 aa. | 2.0e-317 | 10 |
| 6529 | cg43937128 | 2000 | GTTTCTGGCACC CACTTGAGTCCG G[A]GCTGCAGT CTCTGGAAGAAG GAGCGG | A | G | Ser | Pto (8700) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa. | 4.0e-317 | X |
| 6530 | cg43956210 | 1439 | CCCTGTAATCCT TTCTGCTCCTTG G[T/A]ACTTAGAT TTGATTAGCTAT GGACA | T | A | Tyr | Asn (8701) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA- GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa. | 3E-307 | 5 (5q13) |
| 6531 | cg43956210 | 1477 | TTAGCTATGGAC AAGATTGGAGGA A[A/C]TACTATAA AGTGGAACCTCT TGATT | A | C | Lys | Asn (8702) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA- GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa. | 3E-307 | 5 (5q13) |
| 6532 | cg43254411 | 1198 | TGTGGGATTTT CAGAGGACAGT GC[T/C]GACGTG CATACCATCTT GAGAATA | T | C | Gln | Arg (8703) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P35610 STEROL O-ACYLTRANSFERASE (EC 2.3.1.26) (CHOLESTEROL ACYLTRANSFERASE) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) - Homo sapiens (Human), 550 aa. | 5E-305 | 1 (1q25) |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|------------------|--|----------|----------|
| 6533 | cg43917155 | 256 | AGTGACATTTGG AAGCTTTTCAAA C[G/A]TGGTTCCC TG TAGTCATCCA TATAT | G | A | Val | Met (8704) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa. | 2E-301 | |
| 6534 | cg43998124 | 2794 | TCGCACAGGTCT CCATTCCTCTCC T[A/C]TGCATTAC ACGTGCTCTAA GACCT | A | C | His | Gln (8705) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75174 KIAA0689 PROTEIN - HOMO SAPIENS (HUMAN), 547 aa (fragment). | 4.7E-293 | |
| 6535 | cg40918088 | 1870 | ATTAAACCTCTG GATGTCGCCACC ATT[A/C]GCTCTCCA GTGCAAAAGCCA CAGAG | T | A | Ile | Asn (8706) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51854 TRANSKETOLASE 2 (EC 2.2.1.1) (TK 2) (TRANSKETOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa. | 1.8E-287 | X (Xq28) |
| 6536 | cg43931056 | 975 | AAGCACTACAGC AGCTGGAGAAAT A[A/T]AAACCCTA TGAAGAAGCACT GTTGC | A | T | End | Tyr (8707) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15020 ORF - HOMO SAPIENS (HUMAN), 963 aa. | 4.5E-286 | 12 |
| 6537 | cg42709686 | 1613 | CATCTCTGACTG GCTGCCAACACT C[A/G]TGAAGCT GGCCAGGGGAC ACACCAA | A | G | Met | Val (8708) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P15848 ARYLSULFATASE B PRECURSOR (EC 3.1.6.12) (ASB) (N- ACETYL GALACTOSAMINE- 4- SULFATASE) (G4S) - Homo sapiens (Human), 533 aa. | 4.3E-283 | |
| 6538 | cg42709686 | 1667 | CACAAAGCCTCT GGATGGCTTCGA C[G/A]TGTGGAA ACCATCAGTGAA GGAAG | G | A | Val | Met (8709) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P15848 ARYLSULFATASE B PRECURSOR (EC 3.1.6.12) (ASB) (N- ACETYL GALACTOSAMINE- 4- SULFATASE) (G4S) - Homo sapiens (Human), 533 aa. | 4.3E-283 | |
| 6539 | cg43949830 | 1097 | ACTTTTCTGGA TTCACCATTCAG A[C/G]AATGTTTC AGGCTGGCACTC TTACA | C | G | Cys | Ser (8710) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment). | 2.7E-281 | 16 |

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| 6540 | cg43949830 | 1106 | GGATTACACATT CAGACAATGTTT CjA/GjGGCTGGC ACTCTTACACCC AGCACT | A | G | Leu | Pro (8711) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment). | 2.7E-281 | 16 |
| 6541 | cg43949830 | 852 | AACAATCTAATT GCTCGGTACATT CjTjGACAAATTTT CCAGACTCAAAG CTG | C | T | Glu | Lys (8712) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment). | 2.7E-281 | 16 |
| 6542 | cg44910613 | 515 | AGCACCTCCTGT TATTCCAAATGT GjC/GjCTTTCCTC TGCGCCTGGAAT GCCCC | C | G | Pro | Ala (8713) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P38567 HYALURONIDASE PRECURSOR (EC 3.2.1.35) (SPERM SURFACE PROTEIN PH-20) (SPERM ADHESION MOLECULE 1) - Homo sapiens (Human), 509 aa. | 1.2E-280 | 7 |
| 6543 | cg43963979 | 1906 | AGGAGGCGTTTG TCTTGGTAGCGC CjGjA/CAGAGCA GACAGACGCTG CTGGCGA | G | A | Arg | Tyr (8714) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment). | 2E-276 | 14 |
| 6544 | cg43333012 | 1030 | CCATACTTGTC TCTGAGATCCTA A[GjA/CATGATCA TGCCATGCAACT CCATA | G | A | Leu | Phe (8715) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa. | 3.5E-272 (11q23.3) | 11 |
| 6545 | cg43333012 | 1864 | AATAAGCCCTCA ATCCGAGTTCGG GTjGjCATTTCGA CAAAGTGTGCGAG AAACA | T | G | Thr | Pro (8716) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa. | 3.5E-272 (11q23.3) | 11 |
| 6546 | cg43958878 | 1321 | TGGTGGGCGTC TGGCTGTTTTCA GjGjA/CTGGTTCT CCTTGCTCAGGA GGAAG | G | A | Pro | Ser (8717) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa. | 3E-269 | 9 |

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|------|------------|------|---|---|---|-----|---------------|--------------------------|------------------|---|----------|-----------------|
| 6547 | cg43313186 | 417 | CCGCGTGACGG TGCGCAAGGCC GAC/A/GJCCGT GGCTGGGCAT CAGCATCAA | A | G | Thr | Ala (8718) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa. | 8.3E-265 | 20 (20q11.2) |
| 6548 | cg43056973 | 691 | AAGTGCCAGTGA AGCCACCCCTGGT G/GCJCCCTGCT GGCCGCTCGGA CCAAAGT | G | C | Ala | Pro (8719) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P20711 AROMATIC-L-AMINO-ACID DECARBOXYLASE (EC 4.1.1.28) (DOPA DECARBOXYLASE) (DDC) - Homo sapiens (Human), 480 aa. | 5.2E-262 | 7 (7p11) |
| 6549 | cg43980777 | 1015 | CATGGGCTCTGG TACAATCTGGGG T/C/GJGTGAGCA AGTGGCTTCTTG GCCCTC | C | G | Arg | Pro (8720) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa. | 6.2E-259 | 2 |
| 6550 | cg43980777 | 1016 | ATGGGCTCTGGT ACAATCTGGGT C/GCJTGAGCAA GTGGCTTCTTG CCCTCC | G | C | Arg | Gly (8721) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa. | 6.2E-259 | 2 |
| 6551 | cg39711096 | 943 | GTGGAGGTGA CATGTCGGGAGA CTT/CJGGGGTG GCTGTTGAACCT CTCCAC | T | C | Leu | Ser (8722) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa. | 1E-251 | |
| 6552 | cg42101957 | 375 | CATGAGATCCAT GTTGGTGTCTGC C/T/GJTTTGTC ATGACTGAGTAG GTCTT | T | G | Lys | Asn (8723) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P04279 SEMENOGELIN I PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC PROTEIN; ALPHA- INHIBIN-92; ALPHA-INHIBIN-31] - Homo sapiens (Human), 462 aa. | 5.5E-251 | 20 (20q12) |
| 6553 | cg44910581 | 2259 | CTTGAGCCATCT AGCTTCTCACCA C/T/CJGCAATACC GGTTGGGTACTG TGCCA | T | C | Cys | Arg (8724) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa. | 5.8E-251 | |

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| 6554 | cg44910581 | 2780 | GGTAGATAGCT CTTTATTGTCAC G/GATTTGGTG AAAATACTTAG GGATG | A | G | Glu | Gly (8725) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa. | 5.8E-251 | |
| 6555 | cg43995664 | 1356 | CAGAGGCCGCG AGGACGCAGTG CCC[G/C]CCCCA GCTGGAGGGTG CCTGCCATC | G | C | Arg | Gly (8726) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa. | 2.9E-245 | 3 |
| 6556 | cg43965612 | 708 | TTGATAGATCTT GATTCCAAAATG CT/AJCAATCTCC TCCCGGATTTTG CGTTT | T | A | Glu | Val (8727) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:O43236 BRAIN PROTEIN H5 (PEANUT-LIKE PROTEIN 2) - Homo sapiens (Human), 478 aa. | 6.9E-244 | 17 |
| 6557 | cg44021361 | 332 | CCAGCACCAAC AACCTGAGCAGG T[G/T]GTGAGCC AGCGTGCAGGC ATGGCC | G | T | His | Asn (8728) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q92685 NOT56-LIKE PROTEIN - Homo sapiens (Human), 438 aa. | 6.3E-241 | 3 |
| 6558 | cg44021361 | 334 | CAGCACCAACAA CCTGAGCAGGT GT[G/T]TGAGCCA GCGTGCAGGCA TGGCCCA | G | T | Thr | Lys (8729) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q92685 NOT56-LIKE PROTEIN - Homo sapiens (Human), 438 aa. | 6.3E-241 | 3 |
| 6559 | cg43950654 | 111 | TCCCTTTCTTG GGCAAGATGGC GG[C/A]GTACGA CTTGACTACTCG CATCGCG | C | A | Ala | Glu (8730) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa. | 3.2E-239 | 6 |
| 6560 | cg43950654 | 202 | TTCTCTCTGTAA AGGAGATATATA ATT/AJGAAAAGGA ATTATTACAAGG TAAAT | T | A | Asn | Lys (8731) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa. | 3.2E-239 | 6 |

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| 6561 | cg42750618 | 359 | ATGCGCATGAAT GCGGGCCAGCC TG[G]GTCAGT GGGGCTGAAAG GGCAGAGG | G | C | Pro | Ala (8732) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q99764 HYPOTHETICAL 48.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 437 aa (fragment). | 2.9E-238 | 1 |
| 6562 | cg43922856 | 1184 | TTTCCATAGCTT GATAGACCAAAA A[C/A]AAAAAAC TGCCACAACAAC AAACA | C | A | Leu | Phe (8733) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P42167 THYMOPOLYMER BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2E-237 | 12 (12q22) |
| 6563 | cg44013460 | 1021 | ACTGAGTTGAAA AAGCTGGACTTC C[C/G]AGCTCCA ATTGGACCCAGC AGCAGA | C | G | Gly | Arg (8734) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa. | 2.6E-237 | 1 |
| 6564 | cg44013460 | 621 | CACACCAGCGTT TACCAACTCCCT T[C/T]GAATCTT TTGATCTTTACTA TCAT | C | T | Arg | Gln (8735) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa. | 2.6E-237 | 1 |
| 6565 | cg41027023 | 815 | AGCAAGAGACAA CTGCAACTGGG GGT[A]GGTCAC CCTGGACAGCA GCTCTGTT | T | A | His | Leu (8736) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P24278 ZINC FINGER PROTEIN 48 (ZINC FINGER PROTEIN KUP) - Homo sapiens (Human), 433 aa. | 3.5E-233 | |
| 6566 | cg43968343 | 2741 | CTGAATAGGAAG TGTCATGAGGTC TTC/TGGTCCAAG AAGAGTCTCAGA AGGAA | C | T | Arg | Gln (8737) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa. | 9.6E-231 | 18 (18q21.3) |
| 6567 | cg43916785 | 3089 | TCCATGGGTCT TCTCGTTTTCTT T[C/T]TTTTCTTG CTTTCTCTCTCC TCC | T | C | Lys | Glu (8738) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment). | 2.5E-230 | 14 |

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| 6568 | cg43916785 | 3425 | GCCATTCTCTT CTCTTTCTCTT [C/T]CTTTTCAGC TTCTTTCTCATAT TCC | C | T | Glu (8739) | Lys (8739) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment). | 2.5E-230 | 14 |
| 6569 | cg43916785 | 3431 | TCCTCTCTCTTT CTCTCTCTCTTT C/TJAGCTTCTTTC TCATATTCCCGG GTT | C | T | Glu (8740) | Lys (8740) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment). | 2.5E-230 | 14 |
| 6570 | cg43918854 | 1087 | CAGTTCTCTCATG ACTTCCCCCATG C/G/CJTGGGCA GAACTGGGAACA GCATGT | G | C | Arg (8741) | Pro (8741) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa. | 3.3E-228 | 22 (22q11.2) |
| 6571 | cg43918854 | 1438 | TTACACATATGAA ACACAGGCCTCC TT/C]GTCAGGCC CCTACTTAACCT CCGTG | T | C | Leu (8742) | Ser (8742) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa. | 3.3E-228 | 22 (22q11.2) |
| 6572 | cg43929685 | 303 | CACCAGCTCACT GAGGAGCTTTGT C/T/C]TCTCTGGA TCAAGAGTCCCA CCTGA | T | C | Arg (8743) | Gly (8743) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P29080 (2'-5')OLIGOADENYLATE SYNTHETASE 1B (EC 2.7.7.-) (2'-5')OLIGO(A) SYNTHETASE 1B) (2-5A SYNTHETASE 1B) - Mus musculus (Mouse), 414 aa. | 2.4E-225 | 12 |
| 6573 | cg43929685 | 444 | CCTGTGGGGTG GATGCTGCCTGG AGT/C]GTGCTG GGTCTATGAGAG AAATGAG | T | C | Thr (8744) | Ala (8744) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P29080 (2'-5')OLIGOADENYLATE SYNTHETASE 1B (EC 2.7.7.-) (2'-5')OLIGO(A) SYNTHETASE 1B) (2-5A SYNTHETASE 1B) - Mus musculus (Mouse), 414 aa. | 2.4E-225 | 12 |
| 6574 | cg43918561 | 1232 | GAAATTGAGAAG CTGTCCACGCTG T/A/C]CTGGTTCA CGGTGGAGTTC GGGCTG | A | C | Tyr (8745) | Ser (8745) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa. | 2.1E-224 | 11 (11p15.5) |

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| 6575 | cg43918561 | 1233 | AAATTGAGAAGC TGTCACACGCTGT A/C/A/TGGTTAC GGTGGAGTTCC GGCTGT | C | A | Tyr | End (8746) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa. | 2.1E-224 | 11 (11p15.5) |
| 6576 | cg43062448 | 1351 | ACAACCTTAAAG GAATCCATAAAA T/G/T/GTGAAGTC CCAGGAGCTCCA CAAAAT | G | T | His | Asn (8747) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa. | 9.9E-213 | 3 (3q21.3) |
| 6577 | cg44021565 | 1014 | CCTCAAGGCCAG AGGTTCTCCTTC C/G/A/TGAAGACT CTGCTGGAGACC TGCAG | G | A | Thr | Met (8748) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa. | 1E-203 | 1 |
| 6578 | cg44021565 | 345 | ATGTCTGTCTTC TTGAAGGCTGGA A/A/G/TTACCTTC TTCTCATGACCA GAATC | A | G | Ile | Thr (8749) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa. | 1E-203 | 1 |
| 6579 | cg44021565 | 507 | ATGAAACCAGAC AGGAGTTGGTAA C/T/C/JGGAGGCC AAGCACTTGAAG CTCCAA | T | C | Gln | Arg (8750) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa. | 1E-203 | 1 |
| 6580 | cg43959472 | 1586 | TTGAGCCACACG ATGCCGCAGGTA C/G/A/CGTGAAG GGGTTCTCGTTG ATCTGC | G | A | Arg | Cys (8751) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa. | 2.4E-203 | 15 |
| 6581 | cg44128902 | 1009 | CAGGTGGAGTCT GTACAGCTCAAA G/T/A/CAACATAG CCCGAAAACAGC CCATG | T | A | Val | Asp (8752) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa. | 1E-201 | 1 (1p36.2) |

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| 6582 | cg44128902 | 1068 | CGCTACTGGCAA GTCTGTCTGGGG CT[G]CCCTCGCT GTCCAGAACAGC CCTAA | T | G | Ser | Ala (8753) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa. | 1E-201 | 1 (1p36.2) |
| 6583 | cg44128902 | 81 | CGAGGAAGAGG AGGCTCTGCAGA AG[G/A]AATTCAA CAAGCTCAAGAA AAAGAA | G | A | Glu | Lys (8754) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa. | 1E-201 | 1 (1p36.2) |
| 6584 | cg43973314 | 598 | ACTGTTTTAACA GGAAATGGTGAC T[A/G]TTACAGTA GTGGGAATGATC TGACT | A | G | Tyr | Cys (8755) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:O75521 DBI-RELATED PROTEIN 1 (DRS-1) - Homo sapiens (Human), 364 aa. | 3.6E-192 | 6 |
| 6585 | cg43988090 | 964 | ATTCCTACACCT GCGTATCAGTCC TTC/TACCAGCAG GAGGACATGCAC CAACT | C | T | Ser | Leu (8756) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O88695 ALIX - MUS MUSCULUS (MOUSE), 869 aa. | 5.8E-192 | 3 |
| 6586 | cg43968431 | 442 | GCCTTGATACATC TTCTTCATGGCC TT[G]GGGAGCC AGGAACTGAGAA GATTTA | T | G | Lys | Gln (8757) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa. | 1E-191 | 11 |
| 6587 | cg43968431 | 547 | ATGACGCAGCTC TTGGGCCCTGTG CT[C]CTGGATGA GGTAGCCCGTCT GGATG | T | C | Ser | Gly (8758) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa. | 1E-191 | 11 |
| 6588 | cg43939832 | 1182 | GTCTTCACTCCT GATGGAACCTGC A[G/A]CAGAGAG GCTTCGACGTG TACCTT | G | A | Ser | Asn (8759) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAA06754 JM5 PROTEIN - HOMO SAPIENS (HUMAN), 360 aa. | 1E-191 | |

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| 6589 | cg43933608 | 378 | CCGAGACCAAT CCTTGAGTTCA G[G/C]AGGGCT GTAAGGTGAAGA AGCATG | G | C | Arg | Ser (8760) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa. | 4.5E-189 | 8 |
| 6590 | cg43933608 | 380 | GAGACCAATCC TTGAGTTTCAGG A[G/C]GGGCTGT AAGGTGAAGAAG CATGAA | G | C | Arg | Thr (8761) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa. | 4.5E-189 | 8 |
| 6591 | cg43933608 | 386 | AAATCCTTGAGT TTCAGGAGGG CT[G/C]TAAGGTG AAGAAGCATGAA ACTCAG | G | C | Cys | Ser (8762) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa. | 4.5E-189 | 8 |
| 6592 | cg43957632 | 1221 | GGCCACCGCG CGGGCGGCGCA ACC[G/C]GCGGG GGCCCGCAGGC GGCCAGGCG | G | C | Pro | Arg (8763) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa. | 2.2E-185 2 (2q33) | |
| 6593 | cg43957632 | 433 | GCGGTCTACTGC ATCCGCTGGGTG T[G/C]CACCCCG CGAGCCTCCTGC TGCTCA | G | C | His | Asp (8764) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa. | 2.2E-185 2 (2q33) | |
| 6594 | cg43957632 | 442 | TGCATCCGCTGG GTGTGCACCCC GC[G/A]AGCCTC CTGCTGCTCATT GTAGAA | G | A | Arg | Cys (8765) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa. | 2.2E-185 2 (2q33) | |
| 6595 | cg44128927 | 838 | GGGGCTGCCCG AGTGCACGCGCT GC[G/T]GCCACG GCATCGTGCGC ACCATCGT | G | T | Gly | Cys (8766) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD38070 REVERSION-INDUCED LIM PROTEIN - HOMO SAPIENS (HUMAN), 330 aa. | 2.8E-183 | 5 |

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| 6596 | cg43249165 | 770 | GGAAGTCCTTGT TCCTGAAGCCTC A/A/G/AATTTGAT GAGTGGGAGCC TGAAGG | A | G | Lys | Glu (8767) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa. | 7.5E-183 | |
| 6597 | cg42733081 | 806 | CTGAGGTGTGG GCCTCCCTGGG ACC/A/TCCGGTC CAGGCTGTTGCC CCGGTGA | A | T | Trp | Arg (8768) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75791 GADS PROTEIN - HOMO SAPIENS (HUMAN), 330 aa. | 1.8E-181 | 22 |
| 6598 | cg43918452 | 391 | TAGCCAGTCTC TCCGACCTTCCC TT/C/CACGCGTG CCCAGTGACTGG CCTCA | T | C | Phe | Ser (8769) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA83027 KIAA1075 PROTEIN - HOMO SAPIENS (HUMAN), 1400 aa (fragment). | 3E-179 | 12 |
| 6599 | cg44035161 | 712 | CAATGCTGGAGC AGAAAGGATCAC A/G/C/ATGTGGCT TTGGATTTCTGG AGGAG | G | C | Asp | His (8770) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14656 TORSINA - HOMO SAPIENS (HUMAN), 332 aa. | 2.1E-178 | 9 |
| 6600 | cg43933591 | 3997 | CTGAGATAAAAT TGTGACACCAAT G/C/A/TGCAGTAT TCAACACTATCC TGTA | C | A | Ser | Ile (8771) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa. | 1.7E-176 | 8 |
| 6601 | cg43285900 | 288 | AAATATGATCCA AGGAAACTACGG A/C/TTCCTTCCT GAACCTGCCCTGCT GTTGG | C | T | Leu | Phe (8772) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34058 CGI-63 PROTEIN - HOMO SAPIENS (HUMAN), 373 aa. | 4.1E-175 | 1 |
| 6602 | cg43941890 | 1343 | AGGCTGGGCTT GGGACCTTGTC T/C/TCCCAAGTTG GCCTACTGTTAC ACATT | C | T | Pro | Ser (8773) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD43024 MNUDC PROTEIN - HOMO SAPIENS (HUMAN), 331 aa. | 5.2E-175 | |

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| 6603 | cg43918085 | 1492 | AAGGCTTTTGCT TCACTTGAGTGT TTC/AJACATGTT CACGTCTCTCTG GAGCT | C | A | Glu | End (8774) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB45699 HYPOTHETICAL 37.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 361 aa. | 1.9E-173 | |
| 6604 | cg43926685 | 355 | ATGCGCATGACA GTGGCTGACGG CA/CJTGTATAC ATAGCCCAGCAG ATGCAC | C | T | Thr | Ile (8775) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa. | 2.5E-168 (1p36.33) | |
| 6605 | cg43926685 | 491 | TTCACTACAATT CTAAATACAAGA G/C/GJTATGATAT AGCCCAAGATGC GCCGG | C | G | Ser | Arg (8776) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa. | 2.5E-168 (1p36.33) | |
| 6606 | cg43926685 | 857 | ATTACCGCAGGA CCCAGCCCTGA A/C/AJACAGAGT GGTGAATCCAA CTTCC | C | A | Asn | Lys (8777) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa. | 2.5E-168 (1p36.33) | |
| 6607 | cg43959938 | 1723 | TGTTGCACCTCA CGCAATGCTTGG C/A/CJAACCTTGGT CTCATGGCAAGT CACGC | A | C | Phe | Leu (8778) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q13642 SKELETAL MUSCLE LIM-PROTEIN 1 (SLIM 1) (SLIM) (FOUR AND A HALF LIM DOMAINS PROTEIN 1) (FHL-1) - Homo sapiens (Human), 280 aa. | 5.2E-168 | X |
| 6608 | cg42477985 | 863 | ATGACACTGAGT CCAGATCTTCAC ATT/CJAGGCAT GGGTCGATTCTC GCCTGC | T | C | Met | Thr (8779) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa. | 3.6E-167 | 17 |
| 6609 | cg43996522 | 383 | GTCATAGTATGT AGGAAGATTCTGA A/G/TJAGAAAAAC TGCACCTTCACA TCATC | G | T | Ser | Tyr (8780) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P56180 PUTATIVE PROTEIN-TYROSINE PHOSPHATASE TPTE (EC 3.1.3.48) - Homo sapiens (Human), 551 aa. | 3.3E-166 | |

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| 6610 | cg44003630 | 966 | GGAAAGTCCAG GCGGGGCTTGT GGT/CJGGCCGT GTACCACAGGAA GATGCTG | T | C | Thr | Ala (8781) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa. | 5.1E-164 | |
| 6611 | cg44003630 | 1613 | GAGTGCCGAC AGCCAAGACGTA CTG/TJGGAGGA GAAAGCGCCGC CGTGAGCC | G | T | Gln | Lys (8782) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa. | 5.1E-164 | |
| 6612 | cg42712022 | 386 | CGCTTTGACCA GAGAGGAAAGC GAJ/GJAATTTGA AAGATATGGTGG GAATGA | A | G | Lys | Glu (8783) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75804 KI-1/57 INTRACELLULAR ANTIGEN - HOMO SAPIENS (HUMAN), 299 aa (fragment). | 2.4E-161 | 9 |
| 6613 | cg43986534 | 768 | TTCTGCTACGAA TTCCCCCTCCCG C[G/C]GGTGGCC ACCACCCACCCG CCCCCC | G | C | Arg | Pro (8784) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75900 METALLOPROTEASE MMP2/122A - HOMO SAPIENS (HUMAN), 390 aa. | 4.7E-160 | |
| 6614 | cg43055617 | 1416 | CCTGAGGCTGTGA TACCAGCTCCCA G[A/C]GTGACTG GCTTCTCAGCAG ACCACT | A | C | Ser | Ala (8785) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD27736 CGI-27 PROTEIN - HOMO SAPIENS (HUMAN), 297 aa. | 3.7E-158 | 21 |
| 6615 | cg43287561 | 745 | CATAGGCCCCAC TTTCAGTTGAGG A[T/G]AATCTGCC AGCATCACGTGC CTCTC | T | G | Leu | Phe (8786) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa. | 1.4E-156 | 9 (9q34) |
| 6616 | cg43287561 | 799 | CAGGGTCCACCA TGGTCCGAGGC ATT/CJATGTACA GCTCCTTGAAT GGTCAA | T | C | Ile | Met (8787) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa. | 1.4E-156 | 9 (9q34) |

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| 6617 | cg41629243 | 582 | CTCCCATGCTT GAAGTGCTCTGC C[G/T]CCTTCACG CGCCACAGCATC TCCAG | C | T | Gly | Glu (8788) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75229 R31449_3 - HOMO SAPIENS (HUMAN), 813 aa (fragment). | 7.8E-155 | 19 (19p13.3) |
| 6618 | cg43992304 | 588 | CAGCTGTCCAGCA AAATCGCCATCT G[A/G]AGATCATA GAGATGGAGTG GGACTG | A | G | Phe | Ser (8789) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q92503 SEC14-LIKE PROTEIN - Homo sapiens (Human), 715 aa. | 1.1E-151 | 17 (17q25.1) |
| 6619 | cg42712956 | 357 | TGTCATCCGACA GCTGGCAGCC TG[A/G]GTAATA TGCAGAGGACAT TTTTGG | A | G | Ser | Gly (8790) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA81795 WASP-FAMILY PROTEIN - HOMO SAPIENS (HUMAN), 498 aa. | 3.1E-151 | |
| 6620 | cg42197063 | 739 | GGCGCCATTGC CCTCAGCCTCGT GG[A/C]CATGGG GAGTCTGATGG GGAACG | A | C | Asp | Ala (8791) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75631 UROPLAKIN III - HOMO SAPIENS (HUMAN), 287 aa. | 3.3E-150 | |
| 6621 | cg43919239 | 396 | ACCAGCATTAC ATGCATGGCTGC A[G/T]CATAGAAC CTCGCCACTTCC TCGTT | G | T | Ala | Asp (8792) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa. | 4.2E-150 | |
| 6622 | cg43919239 | 645 | GTTGCTCTTGCA CGTGTGGGAGG TG[T/A]GACAATC CTCCCACGAGCG CTGACA | T | A | His | Leu (8793) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa. | 4.2E-150 | |

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| 6623 | cg44921374 | 2813 | GTGAAATCTGG ATATAAACTGG T[AG]GTCCTGAG GATAACGGAATG AGGCA | A | G | Tyr | His (8794) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |
| 6624 | cg44921374 | 3118 | TGTAAGATCTTG TGCCACTGCTAA C[G/A]AGCCTCT GGGGCCGCCTC GGAACAA | G | A | Ser | Leu (8795) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa. | 3.4E-148 | 12 (12q23) |
| 6625 | cg43927534 | 701 | CCAGTCAGGGTCA ATGGCCCAGGA GA[A/C]GGGGT TCCCCACGATGA TGAGCAG | A | C | Leu | Arg (8796) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P23249 PROTEIN MOV-10 - Mus musculus (Mouse), 1004 aa. | 9E-148 | 1 |
| 6626 | cg42929454 | 321 | CTCTAAATTTTCCA CCAGAAATCTTCA[A/G]TTCTGTCTT GAAGCCATGGTA CACT | A | G | Ile | Thr (8797) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P78345 RNASEP PROTEIN P38 - HOMO SAPIENS (HUMAN), 283 aa. | 1.1E-144 | 10 |
| 6627 | cg43946394 | 239 | ACACACTGAATC TGAGCTTCCGG AT[A]ACCGTAGC CCACGGGCACC AGCTTG | T | A | Ile | Phe (8798) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa. | 2.8E-144 | 19 |
| 6628 | cg43946394 | 617 | TGGCCAGGCCGA GCTCTTCTCCAG CA[C/T]GTTACGC CGGGCCTCCAG CTTGAG | C | T | Val | Met (8799) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa. | 2.8E-144 | 19 |

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| 6629 | cg43324690 | 775 | TGTACGAGAAAA ACAAAAAGGAAA TGCJAATATTCA ACAGCTCACCAA CTACA | G | C | Met | Ile (8800) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P22676 CALRETININ (CR) (29 KD CALBINDIN) - Homo sapiens (Human), 271 aa. | 1.6E-143 | 16 (16q22.1) |
| 6630 | cg43024858 | 1114 | TGTGTGTGTCT GACGGCTTCGAA GJA/GJACGGAA GATGCCCTGTGTG CCGCCG | A | G | Glu | Gly (8801) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q60438 HT PROTEIN - CRICETULUS GRISEUS (CHINESE HAMSTER), 348 aa. | 2.3E-142 | 22 |
| 6631 | cg43935709 | 1680 | AGATAAATGCCT TGGAAGTGGCAC AT/CJAGAAACAT TCTGATATTACC ACCAA | T | C | Tyr | Cys (8802) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment). | 8E-140 | 20 |
| 6632 | cg43973762 | 594 | CCAGGGGCTCA GTGAAGCTATGA ATT/GJAATTAGA TGCTGTTTCAGCG GGAATA | T | G | End | Glu (8803) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa. | 2.2E-137 | |
| 6633 | cg43973762 | 741 | AGAGAAACATCT TGAGGAGCAGAT TGC/CJCTAAAGTT GATAGAGAATAT GAAGA | G | C | Ala | Pro (8804) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa. | 2.2E-137 | |
| 6634 | cg43948495 | 677 | GCTCCCTGCTT GATGCGTCGTGT GJAT/CCTCGTCA AGCTTGGGCTG GTCCAG | A | T | Val | Asp (8805) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa. | 9.7E-135 | 3 |
| 6635 | cg42923692 | 395 | ACAGGAAGACCC AAGGTAACACAA TTC/GJACTTTCAT ATACCGAGAAAA GGACA | C | G | Ile | Met (8806) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to REMTREMBL-ACC:G298105 GAMMA- DELTA T-CELL RECEPTOR - HOMO SAPIENS (HUMAN), 260 aa. | 3E-133 | 14 (14q11.2) |

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| 6636 | cg43918679 | 613 | CCCCGTGCTGCG GCACACAGCCCC CAC[C/G]GCTAC CGCATGACCGTG CTGCGCAC | C | G | Arg | Gly (8807) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa. | 3E-131 | 21 |
| 6637 | cg43918679 | 614 | CCGTGCTGCGG CACACAGCCCCCA CC[G/C]CTACCG CATGACCGTGCT GCGCAC | G | C | Arg | Pro (8808) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa. | 3E-131 | 21 |
| 6638 | cg42382358 | 835 | CATGCAGCGG GGACGACGAC GGC[A/G]CGCTC CACGCCGCGCTG CCAGGTGCA | A | G | Thr | Ala (8809) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P08294 EXTRACELLULAR SUPEROXIDE DISMUTASE [CU-ZN] PRECURSOR (EC 1.15.1.1) (EC-SOD) - Homo sapiens (Human), 240 aa. | 5.7E-130 | 4 (4pter) |
| 6639 | cg44128041 | 215 | CAGAAGGAGCT GCTGGAAAAGG GCA[A/G]CATCAC GCGCAGGGCA AGAGCCAG | A | G | Asn | Ser (8810) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa. | 2.8E-128 | |
| 6640 | cg43300586 | 705 | CAGGGCACATTC GCCTCCCAGGT GAT[C/G]GCTGGA GGGGGACAAAGT TGAAAGTG | T | C | Met | Thr (8811) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P38117 ELECTRON TRANSFER FLAVOPROTEIN BETA- SUBUNIT (BETA-ETF) - Homo sapiens (Human), 255 aa. | 3.6E-128 (19q13.3) | 19 |
| 6641 | cg43949061 | 408 | GCAGGCCACG ACCACAACCCGG GC[C/G]TGCGGC TGTCGCTCATTC ACCAGTT | C | G | Gln | His (8812) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa. | 2.1E-125 | 19 |

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| 6642 | cg43986720 | 2320 | GGGCACACACTC CAGGCCCTCGTC A/C/TTCAGCAG CCCCCGCATCG CATCAG | C | T | Ser | Asn (8813) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa. | 1.1E-121 | 6 (6p12) |
| 6643 | cg43943363 | 167 | AGTGTGCGGCA CCAGCAGGCAG CTG/G/C/CTCCG GCTTTGGGGTAT CTGGGCTC | G | C | Ala | Pro (8814) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P04179 SUPEROXIDE DISMUTASE [MN] PRECURSOR (EC 1.15.1.1) - Homo sapiens (Human), 222 aa. | 1.7E-120 | 6 (8q25.3) |
| 6644 | cg43933691 | 286 | ACTCTTCAGCAG CTCTCCTAGGGT C/A/G/TTCCCTCA CAACGTATATTC CGTTT | A | G | Met | Thr (8815) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14976 PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 248 aa. | 4.1E-120 | 2 |
| 6645 | cg43933691 | 881 | CATCTTTTCTTT TCTTCTCTTTCTT T/C/G/TCTGAAGG TGTGCTGGACAC CTCC | T | C | Lys | Glu (8816) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14976 PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 248 aa. | 4.1E-120 | 2 |
| 6646 | cg42551270 | 472 | GAAGTCTGTGCG GCAACCTACATG A/T/C/JGGGGAAT GAGTTGACCTTC CTAGAT | T | C | Met | Thr (8817) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P16410 CYTOTOXIC T-LYMPHOCYTE PROTEIN 4-1 PRECURSOR (CTLA-4) (CD152 ANTIGEN) - Homo sapiens (Human), 223 aa. | 5.4E-118 | |
| 6647 | cg43067745 | 155 | ATACACACAGAA AGAGATCACAGA C/T/G/CCCTACCT TAGAAGAAGGGA GGTGG | T | G | Ser | Arg (8818) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |
| 6648 | cg43067745 | 164 | GAAGAGATCAC AGACTCCCTACC T/T/G/JAGAAAG GGAGGTGGTAG ATGAAA | T | G | Lys | Gln (8819) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |

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| 6649 | cg43067745 | 205 | G TAGATGAAATG AACTGTATGAAG A/GTCCACTAGC CTGGCCACACA CAGAA | G | T | Ala | Asp (8820) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |
| 6650 | cg43067745 | 227 | AGAGCCACTAGC CTGGCCACACA C/A/G[GAAGAAG GACTGGCCCGT CTTCTTG | A | G | Cys | Arg (8821) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |
| 6651 | cg43067745 | 260 | GACTGGCCCGT CTTCTTG CTTCTTGAAGCC CA/T/A/GCTCTGG TAGAGGCCATA GCAGAG | T | A | Met | Leu (8822) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |
| 6652 | cg43067745 | 403 | CTGACGACGGT GCTCACTGTCCA CA/G/A/JAGAGAT GAAACAGCTGCA ACCGCTT | G | A | Ser | Phe (8823) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa. | 6.9E-118 | |
| 6653 | cg43919033 | 1675 | CCCCAGGCCAT GGTGACTAGGG GCA/G/TJAAGTAC CCAGAGAAAGACT GAGGTCC | G | T | Leu | Met (8824) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB46893 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa. | 6.2E-117 | 1 (1q12) |
| 6654 | cg43926002 | 391 | GGGCACAGAAA CACAGCAGCGG GAGC/GJAGCAA CACCAGCACTGC CAACAGAT | C | G | Ser | Arg (8825) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa. | 1.6E-116 | 10 |
| 6655 | cg43268843 | 781 | GACTGCTTCCAG GAAAACCTCTGA C/A/GTGGTACTG AAAAGAAAGCAA ACTAA | A | G | Met | Val (8826) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43260 HYPOTHETICAL 25.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 218 aa (fragment). | 9E-116 | 1 |

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| 6656 | cg43298119 | 420 | TGTAGAATGGAT CAAAGCTAGAGT G/A/GCTGAGTT GAACCCAGACAA GAACTG | A | G | Thr | Ala (8827) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34039 CGI-44 PROTEIN - HOMO SAPIENS (HUMAN), 450 aa. | 1.3E-114 | |
| 6657 | cg43971133 | 312 | GCTGAGGCGCG TCTTCGAGAAGT AC/A/GJGGCGCG TCGGCGACGTGT ACATCCC | A | G | Arg | Gly (8828) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa. | 6.6E-113 | 4 |
| 6658 | cg43942219 | 293 | TTTCGGCGCTGG GTCGCCCAAAGC A/G/AJAATGGAGA CGGATAGAGTG GTGGCT | G | A | Ser | Phe (8829) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |
| 6659 | cg43942219 | 317 | AGAATGGAGACG GATAGAGTGGTG G/C/AJTCGCCAGAA TCCCGAAGAACA TAAGC | C | A | Ser | Ile (8830) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa. | 2.2E-111 | 2 |
| 6660 | cg43036790 | 114 | TCAACAATCAA GAGAAAGTCAIT CT/AJTGTAAGTGT AACATCTTCCTC TTCCC | T | A | Gln | His (8831) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa. | 1.5E-110 | |
| 6661 | cg43036790 | 152 | TCITCCTCTCC CCATCGGGGTTG A/A/CJCTCTATTGA AATGTATACTGA AATCA | A | C | Phe | Val (8832) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa. | 1.5E-110 | |
| 6662 | cg43116651 | 752 | TCTGTGTGGCAG AAGGATCAGCTG GT/AJGACACAG CTGCACCTGGCAA GAAAT | T | A | Val | Glu (8833) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD28300 DNA- BINDING PROTEIN PREB - RATTUS NORVEGICUS (RAT), 417 aa. | 1.6E-109 | 2 |

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| 6663 | cg43325271 | 810 | ATCCAGCCCCCAGT CCCCTGTCTTCC CTTAJGGCCCCCT CTCGCGAAGCAC CTGCAG | A | Leu | Gln (8834) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43675 HYPOTHETICAL 97.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 892 aa (fragment). | 1.5E-108 | |
| 6664 | cg42657906 | 257 | GAGGGTGTGCG GGGGGCTCTGA AAGTAAJGGGCA GAGGGGTGGCT GGCCITGGGG | A | His | Leu (8835) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14919 NC2 ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 205 aa. | 6.2E-108 | 11 |
| 6665 | cg43976960 | 634 | TGGCTGGAGACA ACACTTTATCAG TTTCTTGACACT GACAGGAGTGG AACAGT | C | Phe | Leu (8836) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa. | 1E-107 | 7 (7q21.1) |
| 6666 | cg43967668 | 470 | TTCCTCCGAGCCA GTCTGAGGGGT GCCTTCAGGGT GCCCCCGCGCG AGATGCGAG | T | Gly | Ser (8837) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa. | 5.6E-107 | 3 (3p22) |
| 6667 | cg43959985 | 1027 | GTCGTTGGAGTCA CACTTTGTCTAT GAAJGGTAAAG GTACGTCCTCTG GCTCAT | A | Leu | His (8838) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O43329 HYPOTHETICAL 23.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa. | 2.4E-106 | 16 |
| 6668 | cg43932706 | 197 | AGAGATTGATAT TCGTTTGAGAGA GAAJGAATTTTCT AAATGTGTTTT GAAAC | G | Lys | Glu (8839) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA82992 KIAA1040 PROTEIN - HOMO SAPIENS (HUMAN), 544 aa (fragment). | 5.2E-104 | |
| 6669 | cg43941552 | 757 | CCGGCCTTCCTGA GGCATGGCCGT GAAGJGACCCCT GTGTGGCGAGG TGCCCGCTC | G | Asn | Ser (8840) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 1.6E-100 | |

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| 6670 | cg43252708 | 486 | CGACCTCAGGA GCGTCCGAAGT GGG[C/T]TCATCA CACAGAAATCGGC AAGACCT | C | T | Leu | Phe (8841) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75879 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa. | 2.1E-100 | |
| 6671 | cg43049606 | 457 | CAGAAAGGAAAGT CAAGTTTACTTG TT[G]GGAACT GGACTCCGAGG GAAAGAG | T | G | Leu | Trp (8842) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13094 SLP-76 TYROSINE PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 533 aa. | 4.3E-100 | 5 |
| 6672 | cg43941550 | 525 | GAGCGGCACCT CGCCACACACAGG GTG[C/T]TCACG GCCATGCCCCAG GAAGGCCCGG | C | T | Ser | Asn (8843) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 6673 | cg43941550 | 669 | CATCTGGAAGTT GTGGACTTTTCT A[G/T]TGAGAGC CTCAAGACTGGG GATGCT | G | T | Thr | Asn (8844) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 6674 | cg42903839 | 211 | GGACCGGCGGC CCAAGCTGTGGA GA[C/G]GCCGGG CTGGAAGGCC GGAGGACG | C | G | Thr | Arg (8845) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32099 SOUL PROTEIN - HOMO SAPIENS (HUMAN), 205 aa. | 8.6E-100 | 6 |
| 6675 | cg42903839 | 717 | GTCAAATTGCTT AATAGAAATAAT G[A/C]AGTGTGG TTGATTCAAAA AATGAA | A | C | Glu | Ala (8846) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32099 SOUL PROTEIN - HOMO SAPIENS (HUMAN), 205 aa. | 8.6E-100 | 6 |

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| 6676 | cg43971745 | 1964 | CTCTTATCTGGG AACAGTGCCAGC T[G/T]GTTGATGG GTGGTGGGGCA GCCAGT | G | T | Gln | Lys (8847) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa. | 2E-95 | 1 |
| 6677 | cg43992729 | 709 | CCTGGGGCCATAT GTTGCTGGGAAT T[C/T]CCTCCACC CTTCGTCATGCA GTGGA | C | T | Pro | Ser (8848) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O70303 CELL DEATH-INDUCING DNA FRAGMENTATION FACTOR, ALPHA SUBUNIT-LIKE EFFECTOR B (CELL DEATH ACTIVATOR CIDE-B) - MUS MUSCULUS (MOUSE), 219 aa. | 2.6E-95 | 14 |
| 6678 | cg43927693 | 667 | CCCCTACCTGGC CTGGCTGGCCTT C[G/A]CGACCAC ACTCAACTACTG CGTATG | G | A | Ala | Thr (8849) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa. | 5.3E-95 | 22 |
| 6679 | cg36896591 | 81 | TCCGGAGCCATG CAGGCCGAAGG CC[G/A]GGGCAC AGGGGGTTTCA CGGGCGAT | G | A | Arg | Gln (8850) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75637 LAGE-1A PROTEIN - HOMO SAPIENS (HUMAN), 180 aa. | 6.8E-95 | |
| 6680 | cg42914758 | 224 | ATTCACCAGTTC TGGATGAAAGAC T[G/C]ATGTTGAT TTATGCAGCCAT TTTAG | G | C | Ser | End (8851) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88422 UDP- GALNAC:POLYPEPTIDE N- ACETYL GALACTOSAMINYL TRANSFER ASE T5 (EC 2.4.1.41) - RATTUS NORVEGICUS (RAT), 930 aa. | 7.8E-94 | |
| 6681 | cg42907594 | 354 | GCCAATAATGCA ATCAGGGTTTCT T[C/A]ATCAGGAG CTTTGACCACCA CCTTG | C | A | Glu | End (8852) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34142 CGI-147 PROTEIN - HOMO SAPIENS (HUMAN), 179 aa. | 3.8E-92 | 17 |

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| 6682 | cg43964799 | 743 | TACAACAAGACT ACAATGCTTCTC T[C/A]CAAGCAAT TCGTGCAGTGG GATGAG | C | A | Ser | Tyr (8853) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75935 DYNACTIN SUBUNIT - HOMO SAPIENS (HUMAN), 186 aa. | 4.9E-92 | 9 |
| 6683 | cg43921592 | 158 | AGGCTGGCTCA GGACTATCTGCA GT[G/A]CGTCCTA CAGATACCACAA CCTGGA | G | A | Cys | Tyr (8854) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16548 BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC- SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) - Homo sapiens (Human), 175 aa. | 4.9E-92 | 15 |
| 6684 | cg43921592 | 219 | GCAAAACGTCCA GAGTGCTACAAA A[T/G]GTTGCGTT CTCAGTCCAAAA AGAAG | T | G | Asn | Lys (8855) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16548 BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC- SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) - Homo sapiens (Human), 175 aa. | 4.9E-92 | 15 |
| 6685 | cg43987971 | 403 | AGCTGCAAGCGA ATGAGGTAGAAT G[G/A]ACACAGA CATGAGATAGAC ATCAGC | G | A | Pro | Ser (8856) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92535 PHOSPHATIDYLINOSITOL-GLYCAN- CLASS C (PIG-C) - HOMO SAPIENS (HUMAN), 297 aa. | 7.2E-91 | 1 |
| 6686 | cg25236776 | 881 | CAGTGCCTCCCC TGCGGCCCCGG GG[G/A]CAAAGG CCGCTGCTTCGG GCCCAGC | G | A | Gly | Asp (8857) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa. | 7.2E-91 | |
| 6687 | cg43978148 | 707 | TGTAGCCCATGC TGTTTATCAAGC A[A/G]TGCTCAGC TTGAAGAATATT CCTGT | A | G | Met | Val (8858) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment). | 4E-90 | 16 |

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| 6688 | cg43978148 | 815 | CCTGCACAGTCT GCAACTTCTCTGA G[G]CTCTGTTCT GAAATAAACAT GAGGC | G | T | Ala | Ser (8859) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment). | 4E-90 | 16 |
| 6689 | cg43963913 | 707 | CAAGTCCGATC CCACCAGGACTG G[A/G]AGACTCG CGTCCAGCTGGA GCTTTG | A | G | Phe | Ser (8860) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment). | 5.1E-90 | 11 |
| 6690 | cg43922714 | 416 | CCTCGCTGGATC AATCGACTTGCC T[A/G]CTTCAGCT CCTGTATACGCT TTCTA | A | G | Tyr | Cys (8861) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34141 CGI-146 PROTEIN - HOMO SAPIENS (HUMAN), 193 aa. | 9.8E-87 | 19 |
| 6691 | cg43068353 | 208 | CCTGGTCTGCT GCTCCGGGGT CT[C/T]GGCTGC CAAAC TGAATC CTTCTCC | C | T | Arg | Gln (8862) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa. | 1E-86 | 2 |
| 6692 | cg43068353 | 391 | TTTCTTTTCTTGA TTTCTCTGGTTCC[G/A]AAATGCCAA ATTAAATCCATC AGC | G | A | Ser | Leu (8863) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa. | 1E-86 | 2 |
| 6693 | cg44018226 | 1252 | CCCTGCAGGCAA TTACTCTCACCG G[T/A]GGTAAAA TCAATCGCAGCA GAGAA | T | A | His | Leu (8864) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa. | 1.6E-86 | |
| 6694 | cg36842490 | 547 | GGAAACGTTGTT AGCAGTAACATC TTC/TAGAAAGACC CTGTACCAGTCA AACGT | C | T | Ser | Leu (8865) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P01282 VASOACTIVE INTESTINAL PEPTIDE PRECURSOR (VIP) - Homo sapiens (Human), 170 aa. | 2.3E-85 | |

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|------|------------|-----|---|---|---|-----|---------------|--------------------------|------------------|--|---------|---|
| 6695 | cg36842490 | 606 | TGCAGTCTTCAC TGACAACTATAC C[C/G]GCCCTTAG AAACAAATGGC TGTAAG | C | G | Arg | Gly (8866) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P01282 VASOACTIVE INTESTINAL PEPTIDE PRECURSOR (VIP) - Homo sapiens (Human), 170 aa. | 2.3E-85 | |
| 6696 | cg43142459 | 281 | GGGTGGTCACC CTCCAATACAAT AA[G/C]ATGCCA GGAAGAGTAAGT TGCCCTT | G | C | Ser | Cys (8867) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15205 DIUBIQUITIN - HOMO SAPIENS (HUMAN), 165 aa. | 1.9E-83 | 6 |
| 6697 | cg43969140 | 348 | GCCATCTGGTTC CACATTGAGGC CT[AT]CACTATG CCATCCTGTACC ACCAT | T | A | Lys | Met (8868) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa. | 1.7E-80 | |
| 6698 | cg43969140 | 441 | CGAATCATCTAG TAATAAGTCTGT CT[G/C]CTTCCCA AAGGCCCCAGT GGGATC | T | G | Glu | Ala (8869) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa. | 1.7E-80 | |
| 6699 | cg43969140 | 730 | GGCTCCGCTTCA AACACCTCCACT G[C/A]TGGGATG GCATCTCCACCC TTGATT | C | A | Ala | Ser (8870) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa. | 1.7E-80 | |
| 6700 | cg43989505 | 634 | ATCAGCGGCTCT TTGTATGATGAC G[AT]AAGGATGA GGCGGCAGGGA AGAAGA | A | T | Glu | Val (8871) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75274 F16601_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 158 aa (fragment). | 2.2E-80 | |
| 6701 | cg43969316 | 745 | CAGCAGCTGAG CTTGAATCAGCA CA[G/A]CCGAGC CTTTAACATCGA AAGAGCG | G | A | Ser | Asn (8872) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa. | 7.5E-79 | 5 |

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| 6702 | cg42331787 | 384 | TCATCCCCCGTG CTCCGGACACAA TTCATCTTTTGC GCAGTGGATGC CTGCAA | C | A | Arg | Ser (8873) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75951 LYSOZYME HOMOLOG - HOMO SAPIENS (HUMAN), 148 aa. | 7.5E-78 | 17 |
| 6703 | cg44936941 | 897 | TTAAGATAATATA TACATGTCACAC A/GTCTTCCATC TCCATTTGGATT ATCA | A | G | Cys | Arg (8874) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa. | 7E-77 | 1 |
| 6704 | cg42462901 | 430 | ACTTTATTGGG AACTGTGGAAT TTTCJTTTCAGCA ACTCAATAAAAT GGGTG | T | C | Lys | Glu (8875) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA83043 KIAA1091 PROTEIN - HOMO SAPIENS (HUMAN), 1359 aa (fragment). | 1.4E-75 | |
| 6705 | cg43969639 | 955 | ATGCCCCAGACCC ACTCTGCAGTAA GIG/CJTGTTTCAA AACAGAAATGCG ACAAA | G | C | Pro | Ala (8876) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME 1 - Schizosaccharomyces pombe (Fission yeast), 322 aa. | 2.3E-74 | 3 |
| 6706 | cg38276737 | 336 | AGACCTCAATGA CAAGAGTGTGCA GTC/CJGTGCCCT GGACTTTGCCAT CAGCGA | T | C | Cys | Arg (8877) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P28325 CYSTATIN D PRECURSOR - Homo sapiens (Human), 142 aa. | 3.1E-74 | |
| 6707 | cg44004729 | 520 | AGTTTCTCCGGC CACGAGGCCCT GGG/AJTAACCT AGACTGATACCT CCTCAT | G | A | Thr | Ile (8878) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P22749 NKG5 PROTEIN PRECURSOR (LYMPHOKINE LAG-2) (T- CELL ACTIVATION PROTEIN 519) - Homo sapiens (Human), 145 aa. | 1.7E-73 | |
| 6708 | cg43933021 | 621 | ACAGCTATCAA CTTCTACCACT CTT/CJCTGCTGGT CGACGTCGGCG TCTGGC | T | C | Arg | Gly (8879) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD38506 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa. | 2.8E-73 | 13 |

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| 6709 | cg43932428 | 597 | GCTCGATTITTC CAAGCACCTGGT TJA/CJTGGGTAT GGCCCGTCCGC TCTCAT | A | C | Asn (8880) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa. | 2.5E-72 | |
| 6710 | cg42691635 | 483 | TAGAGAGAGTTG ACGGTGTCTCG TT/CJGGGTGG TCGTTGCTGATT TTGAAA | T | C | Gln (8881) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q16378 PHL E1F1 - HOMO SAPIENS (HUMAN), 134 aa. | 1.8E-71 | 12 |
| 6711 | cg43271682 | 339 | GGGGCGGACA GGCCCGCTGC TGG[G/C]GGCTC CCGGAGCTCTC GGGGGGCGG | G | C | Pro (8882) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa. | 1.3E-70 | 1 |
| 6712 | cg43917616 | 146 | TTGGCACTTTT GATGCATTTTC GJA/GJTTTGGTT CCCAGAGGGCA TTTTT | A | G | Ser (8883) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13901 C1D DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 141 aa. | 6.9E-70 | |
| 6713 | cg43942922 | 229 | TGAGCCCACTC TCAGGCCACTAG G[G/A]GCAGAAC AAATAGTCTCTC TGTCAA | G | A | Ser (8884) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.3E-68 | |
| 6714 | cg43942922 | 265 | TAGGTCCTCTGT CAAGACCCCTGA AJA/CJAGTTGTC CCCACAGCCCCT GAGCT | A | C | Thr (8885) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.3E-68 | |
| 6715 | cg43942922 | 362 | TCTCAGGCCACT AGGGGAAGAAAA AJA/GJTAGGTCCT CTGTCAAGACCC CTGAA | A | G | Ser (8886) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.3E-68 | |

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| 6716 | cg43942922 | 407 | CCTGAAACAGTT GTGCCACAGC CC[C/T]TGAGCTC CAGCCTTCCACC TCCACA | C | T | Pro | Leu (8887) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.3E-68 | |
| 6717 | cg43942922 | 437 | CTCCAGCCTTCC ACCTCCACAGAC C[A/G]ACCTGTCA CCTCTGAACCCA CATCT | A | G | Gln | Arg (8888) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.3E-68 | |
| 6718 | cg41400057 | 447 | CACCTGGCCTGA ATGCAGCATGGG G[G/C]TTTTGGCT GGCAGCAGTGAT TGTTG | G | C | Pro | Ala (8889) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P49901 SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS) - Homo sapiens (Human), 116 aa. | 2.7E-68 | 9 |
| 6719 | cg43955219 | 980 | GGATCCTCAAAA CTCAGAACGTGG C[C/T]GGGCGTG GTGGCTCACGC CTGTAAT | C | T | Arg | Trp (8890) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa. | 6.4E-68 | |
| 6720 | cg42831353 | 787 | TGCACCGCGC GGTGGTGAGGA CAC[A/G]GGCTG CGGTGTAAGCCC GCGTCACC | A | G | Cys | Arg (8891) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa. | 1.3E-67 | 22 |
| 6721 | cg43927424 | 353 | TCCCTGTCTGCA AGTCGGGCAGG AA[C/T]AGAAACA CACCTACCTGCC ACTAGA | C | T | Gln | End (8892) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa. | 1.9E-65 | |
| 6722 | cg42381630 | 244 | GAGTTGGCGAG GAAGATCGACCT ATT[G/A]TTGGCC TAGACCAAGGCG CTATGT | T | C | Tyr | His (8893) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa. | 5.9E-64 | |

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| 6723 | cg42381630 | 439 | AGGTCAAGGC CGAAGCCTGAAG CTC/GJATAGCCA GGAACAGGGTC ACCCACA | C | G | His | Asp (8894) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa. | 5.9E-64 | |
| 6724 | cg43950549 | 273 | CTTATTGTCACA TTCTTCTTGGGA A/A/TACAGTGT TGCTGTTGCTGA TGCAA | A | T | Lys | Asn (8895) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa. | 1.4E-62 | |
| 6725 | cg43950549 | 485 | CAAGAACTTCAG AATGGGTCAGAA T/A/CJGGAAGTG GTGATGGAACCA GCCCTG | A | C | End | Ser (8896) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa. | 1.4E-62 | |
| 6726 | cg43308257 | 773 | GACCCGTGACCC CTGTTCAAGATC T/A/GJGTGGCG GAGCTGATCCAG CAGCTG | A | G | Tyr | Cys (8897) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa. | 2.9E-62 | |
| 6727 | cg42686636 | 719 | GGTTATACCACA AGCTGTGCTTGC A/A/TJTGAGACT GAGCAAAAGGAA ATGTG | A | T | Gln | His (8898) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O08904 BRAIN X-LINKED GENE (BRX PROTEIN) - MUS MUSCULUS (MOUSE), 216 aa (fragment). | 4.4E-59 | |
| 6728 | cg42566513 | 351 | TTCTACCCCTGAG TGCGAGATAAGA A/C/TJGATGGT GGAAGAGAGCA ACGCCAG | C | T | Thr | Met (8899) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O70576 NUCLEAR PROTEIN SA3 - MUS MUSCULUS (MOUSE), 1240 aa. | 9.6E-59 | |
| 6729 | cg43930685 | 1007 | CAGCGATTCTTT TTTTGTTTCGGTT T/A/JTCAAGAGA CTTGCTTTGCTC TTCA | T | A | Lys | End (8900) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa. | 4E-58 | |

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| 6730 | cg43930685 | 821 | GGAGTCAAATC TTTTGGATCTTT IC/TACCAACAAC TACTGGATTTC TTTT | C | T | Glu | Lys (8901) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa. | 4E-58 | |
| 6731 | cg40968986 | 251 | TGTGCAGATGAA GGCCAGTGAGC TG/GA/JAGCAGG AGCAAGAGAGA GAGGGCTC | G | A | Glu | Lys (8902) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa. | 5.1E-58 | 11 (11p15.2) |
| 6732 | cg40968986 | 267 | AGTGAGCTGGA GCAGGAGCAAG AGA/GC/JAGAGG GCTCCAGAATCA TTGCCAG | G | C | Arg | Thr (8903) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa. | 5.1E-58 | 11 (11p15.2) |
| 6733 | cg40968986 | 372 | AGCAGATCAGG GGGTGTGGTGA AGA/GJCAACTT TGTGCCCCACCA TGTGGGT | A | G | Asn | Ser (8904) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa. | 5.1E-58 | 11 (11p15.2) |
| 6734 | cg43934461 | 766 | TCGGGGACCCC AAGAGAAATTCAT ATG/TCTGGTGG ATTGGTGTGAGG CACCCG | G | T | Ala | Glu (8905) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD33392 BREAST CANCER ASSOCIATED GENE 1 PROTEIN - HOMO SAPIENS (HUMAN), 606 aa. | 8.8E-57 | 3 |
| 6735 | cg43968980 | 1126 | TGCTTCCTTGGA CTGAAGAATAAA CIA/CJTTCCTCCT ACACCTTCATAC ATGTT | A | C | Met | Arg (8906) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.5E-56 | 5 |
| 6736 | cg44011808 | 554 | AACCACATGAGT CCGCTGAAGAAC T/C/TJGCTCTGGA ACACCTGGGATC TGGTC | C | T | Glu | Lys (8907) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O95178 NADH-UBIQUINONE OXIDOREDUCTASE AGGG SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-AGGG) (CI-AGGG) - Homo sapiens (Human), 105 aa. | 2.5E-56 | |

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| 6737 | cg43916991 | 120 | GACATCTGGCCA GGTCCATCTCTG A/C/TJCGGCTCCT GGTCAACCCCA GGGAG | C | T | Thr | Ile (8908) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD33400 CARBOXY TERMINUS OF HSP70-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa. | 3E-55 | 16 |
| 6738 | cg43916991 | 74 | AATGTGGGGAAG TGTGGATGTTAG CT/GJCTGAGATT GGGGTGTGGTC AGACAT | T | G | Ser | Ala (8909) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD33400 CARBOXY TERMINUS OF HSP70-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa. | 3E-55 | 16 |
| 6739 | cg39695368 | 203 | CGGGATGGCTTA CATTGATATCAT C/A/GJTACGTAG GTCCTTCTCATA GATGTC | A | G | Met | Thr (8910) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD33910 HYPOTHETICAL 21.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 190 aa. | 1.7E-50 | X |
| 6740 | cg40357240 | 240 | ACCGGATGTCTT CGGCCAGTGCT GA/A/GJGGGGAC TGACTGGGGATA CAGCTTT | A | G | Leu | Pro (8911) | NON- CONSER VATIVE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45741 HYPOTHETICAL 112.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 1008 aa (fragment). | 5.4E-50 | |
| 6741 | cg44917490 | 1621 | GGGACCGTTTCC TCTTCTCTTCA G/C/gap/CTGCGG AGGCTCCACGAA GTAATCA | C | gap | Ala | Leu (8912) | FRAMES HIFT | amyloid | Human Gene SWISSPROT-ID:P51693 AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP) - HOMO SAPIENS (HUMAN), 650 aa. | 0 | 19 |
| 6742 | cg44917490 | 873 | GGGGTGTTCAT CCTTGGAAATCTG GA/G/gap/GCTGC AGCCACCCCTTG TCCTCGCT | G | gap | Pro | Leu (8913) | FRAMES HIFT | amyloid | Human Gene SWISSPROT-ID:P51693 AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP) - HOMO SAPIENS (HUMAN), 650 aa. | 0 | 19 |
| 6743 | cg42663825 | 2303 | GACAAAACACTG TTTGTTGGGTTTA C/C/gap/GCCCCC TGCAGATCGCCT TGCCATC | C | gap | Pro | Arg (8914) | FRAMES HIFT | ATPase_ associate d | Human Gene TREMBLNEW- ID:G2406580 NUCLEAR VCP-LIKE PROTEIN NVLP.1 - HOMO SAPIENS (HUMAN), 750 aa. | 0 | 1 |

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|------|------------|------|---|---|-----|-----|---------------|----------------|---------------------------|--|---|---|
| 6744 | cg43987714 | 2730 | TGGTTACGTTTG ATGAGGAGCTGC G[G/gap]CCATTG CCAGTGTCTGTC CGTGTGG | G | gap | Pro | His (8915) | FRAMES HIFT | ATPase_ associate d | Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.lpcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa. | 0 | 3 |
| 6745 | cg43987714 | 2785 | GGCAGTGGATGT GGTGGGCCAGG CT[G/gap]GCAAG CCGAAGACTATC ACAGGGTT | G | gap | Gly | Ala (8916) | FRAMES HIFT | ATPase_ associate d | Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.lpcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa. | 0 | 3 |
| 6746 | cg43987714 | 2786 | GCAGTGGATGTG GTGGGCCAGGC TG[G/gap]CAAGC CGAAGACTATCA CAGGGTTC | G | gap | Gly | Ala (8917) | FRAMES HIFT | ATPase_ associate d | Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.lpcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa. | 0 | 3 |

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|------|------------|------|---|-----|-----|---------------|----------------|---------------------------|---|----------|---------------------|
| 6747 | cg43987714 | 2914 | CCCCATTCCTGGA C AGGTTTGTAT C[C/gap]TTCGGA AGAACCCCAATT ATGATCT | gap | Leu | Phe (8918) | FRAMES HIFT | ATPase_ associate d | Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 908 aa.[pds:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 908 aa. | 0 | 3 |
| 6748 | cg43277632 | 1676 | GCAAATATCGGT G GTCTTTGGCCGA A[G/gap]GGACTG CAACAGTCTTT ATAATCC | gap | Gly | Gly (8919) | FRAMES HIFT | ATPase_ associate d | Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa. | 0 | 13 (13q14.3) |
| 6749 | cg43933946 | 1781 | AGCCAAATCCCA G GAGTGCTGGTG GG[G/gap]CCAGG CCAGTGTCAGAT TCITTAAT | gap | Ala | Ala (8920) | FRAMES HIFT | ATPase_ associate d | Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa. | 5.2E-231 | 7 |
| 6750 | cg43958825 | 343 | GGATCTGCATGA C TTCTGGCCCGG GC[C/gap]TCCTC ATTGGGCATCGG GAACCTCA | gap | Glu | Glu (8921) | FRAMES HIFT | ATPase_ associate d | Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa. | 7.8E-228 | 11 |
| 6751 | cg43933600 | 1192 | TGCCCCCGACG G AAGATCCACTTC AG[G/gap]CTGCG CTGCTCGATGAT GTTGCTAA | gap | Ser | Ser (8922) | FRAMES HIFT | ATPase_ associate d | Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa. | 4E-185 | 19 |
| 6752 | cg43933600 | 348 | CGCACCTCATGG G GGTAACAGCGG CA[G/gap]CTTCA CGATGTGGAAGT CTTCATAC | gap | Leu | Cys (8923) | FRAMES HIFT | ATPase_ associate d | Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa. | 4E-185 | 19 |

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|------|------------|------|--|---|-----|-----|---------------|----------------|---------------------------|---|----------|----|
| 6753 | cg43933600 | 556 | CATACAGGGACA GGAACCTCAGCAA T[G/gap]CATACG CAGATGAAAGTT GTCTGCT | G | gap | Cys | End (8924) | FRAMES HIFT | ATPase_ associate d | Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa. | 4E-185 | 19 |
| 6754 | cg43916747 | 1057 | GAATCCGGGGC ACCAGCTACCAG AG[C/gap]CCTCA CGGCATCCCCAT AGACCTGC | C | gap | Pro | Leu (8925) | FRAMES HIFT | ATPase_ associate d | Human Gene SPTREMBL-ID:Q12464 CHROMOSOME XVI READING FRAME ORF YPL235W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 471 aa. | 4E-163 | 19 |
| 6755 | cg43947105 | 1581 | AGAGCAAGATCA AACCCAGCTCT T[G/gap]GCGGTG CGCCCCAGGAAT TCTCCGG | G | gap | Ala | Ala (8926) | FRAMES HIFT | ATPase_ associate d | Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa. | 4.6E-152 | |
| 6756 | cg43947105 | 1582 | GAGCAAGATCAA ACCCAGCTCTT G[G/gap]CGGTGC GCCCCAGGAAT CTCCGGT | G | gap | Ala | Ala (8927) | FRAMES HIFT | ATPase_ associate d | Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa. | 4.6E-152 | |
| 6757 | cg43927442 | 1437 | CACAGCAAATTT GTTCTCTAGGGG G[G/gap]ACCACT TCACAAAAGTAG CTGCGCG | G | gap | Ser | Ser (8928) | FRAMES HIFT | ATPase_ associate d | Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa. Jcds:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa. | 6.4E-146 | 17 |

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| 6758 | cg43927442 | 653 | TCACTCAGCTTC ACATTATCCGA G[G/gap]CCCCTGG ATGGAAGACTCG AGGGTCT | G | gap | Gly | Gly (8929) | FRAMES HIFT | ATPase_ associate d | Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa. pcds:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa. | 6.4E-146 | 17 |
| 6759 | cg43967912 | 1267 | AGCTGCAACAC CCGGCCACGCA CT[gap]TGCACA TACTGCGAACTA TCACTTGA | gap | T | Gln | Gln (8930) | FRAMES HIFT | ATPase_ associate d | Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREVISIAE VACUOLAR H(+)-ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa. | 5.6E-108 | 8 |
| 6760 | cg43304881 | 1413 | CAGGGCCAGCT GCCGGAGGCGC TCC[C/gap]TGGG GTCACGGTTGCT CTCGGAGGA | C | gap | Arg | Arg (8931) | FRAMES HIFT | ATPase_ associate d | Human Gene Similar to SPTREMBL- ID:Q19335 F11A10.2 - CAENORHABDITIS ELEGANS, 610 aa. | 8.7E-94 | |
| 6761 | cg43132502 | 208 | GGCAGGAGGCA GGAGTTGGCGAT GC[C/gap]ACCTG GGGGTCACATTG AGTCTGGA | C | gap | Pro | His (8932) | FRAMES HIFT | ATPase_ associate d | Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa. | 9.4E-58 | 11 |
| 6762 | cg43132502 | 309 | CAGGGAAGAAG GGGAGGCGCCA GAG[G/gap]CAGG GCCATGCTTGGC TTCCACAGCT | G | gap | Ala | Gln (8933) | FRAMES HIFT | ATPase_ associate d | Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa. | 9.4E-58 | 11 |
| 6763 | cg43132502 | 346 | TGGCTTCCCAGC TGGCCCCCAGTG CA[gap]A/GTGGG TGGCACCCGCCG AGGCTGCTG | gap | A | Gln | Gln (8934) | FRAMES HIFT | ATPase_ associate d | Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa. | 9.4E-58 | 11 |

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|------|------------|------|--|-----|-----|---------------|----------------|---------------------------|---|--------------------|----|
| 6764 | cg44015998 | 469 | TGGCTGTTGAAG TCGGGCGAGGA GC[C/gap]GAGGA GCAGGCCAATGA TGGCCAGG | gap | Gly | Ala (8935) | FRAMES HIFT | ATPase_ associate d | Human Gene Similar to SWISSPROT- ID:P39986 PROBABLE CALCIUM- TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa. | 1.5E-53 | |
| 6765 | cg43918042 | 1862 | GCTGACCCTGC GAGTGCGCGAC GGC[gap]GJCGA CCCGCTCGCTCC TCGCAGGCC | gap | Ala | Ala (8936) | FRAMES HIFT | cadherin | Human Gene TREMBLNEW- ID:G2852363 NF-PROTODADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa. | 0 | 4 |
| 6766 | cg43918042 | 2009 | ACCCCCATCCTG CAACTGCGCGCA G[C/gap]CGACTT GGACGTGGGG TCAACGGG | gap | Ala | Ala (8937) | FRAMES HIFT | cadherin | Human Gene TREMBLNEW- ID:G2852363 NF-PROTODADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa. | 0 | 4 |
| 6767 | cg43957225 | 2825 | TTGCTACATAGC AGGTGCCAACTG G[G/gap]TCCTTT TCTGGTGTCGGT TTAAGAG | gap | Asp | Asp (8938) | FRAMES HIFT | cadherin | Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa. | 0 | 10 |
| 6768 | cg43957225 | 2832 | TAGCAGGTGCCA ACTGGGTCCTTT T[gap]TCTGGTG TCGGTTTAAGAG TTCTCCA | gap | Glu | Glu (8939) | FRAMES HIFT | cadherin | Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa. | 0 | 10 |
| 6769 | cg43977440 | 3175 | GCATCACACTGC CACCAGAGCCCTC T[G/gap]CCCCCT GGGCAAGGGGC ACACGGAC | gap | Gln | Arg (8940) | FRAMES HIFT | cadherin | Human Gene SWISSPROT-ID:P11215 CELL SURFACE GLYCOPROTEIN MAC- 1 ALPHA SUBUNIT PRECURSOR (CR-3 ALPHA CHAIN) (CD11B) (LEUKOCYTE ADHESION RECEPTOR MO1) (INTEGRIN ALPHA-M) (NEUTROPHIL ADHERENCE RECEPTOR) - HOMO SAPIENS (HUMAN), 1152 aa. | 0 (16p11.2) | 16 |

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|------|------------|------|--|---|-----|-----|---------------|----------------|----------|---|---|----------------------|
| 6770 | cg44026834 | 1087 | CGGCCGCTCGC ACCGCGGCTCCT GC[C/gap]AGCTC ACTCTGAGAGAT GTGGGCCC | C | gap | Trp | Cys (8941) | FRAMES HIFT | cadherin | Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa. | 0 | 17 (17q11) |
| 6771 | cg44026834 | 1320 | GGGGCACGTGT GGGCTCAGGTG GGT[G/gap]CCAT AGGCAGCAGCA CTGGTCGTGG | G | gap | Gly | Gly (8942) | FRAMES HIFT | cadherin | Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa. | 0 | 17 (17q11) |
| 6772 | cg44026834 | 1433 | TGCTCAGTGTC TCGGAGACGCT GG[G/gap]CCTCT GGCTGCCCGAT GGAGAGCGT | G | gap | Pro | Pro (8943) | FRAMES HIFT | cadherin | Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa. | 0 | 17 (17q11) |
| 6773 | cg40310734 | 1060 | CTCAACACTACA GAATATGTCGTC G[G/gap]TGCCCC CACTTGGAGCTG GACCCCTG | G | gap | Gly | Val (8944) | FRAMES HIFT | cadherin | Human Gene SWISSPROT-ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa. | 0 | 17 (17q21.3 2) |
| 6774 | cg40310734 | 3291 | CTTCTTCAAGCG GAACCGGCCAC CC[C/gap]ITGGAA GAAGATGATGAA GAGGGGGA | C | gap | Leu | Trp (8945) | FRAMES HIFT | cadherin | Human Gene SWISSPROT-ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa. | 0 | 17 (17q21.3 2) |
| 6775 | cg42558238 | 2563 | TCCTCAGAGATG CAGAGACCTCC C[C/gap]GGACTG CGATGACACGGT CACTTAT | C | gap | Pro | Arg (8946) | FRAMES HIFT | cadherin | Human Gene SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.pcls:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. | 0 | 19 (19q13.1) |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|-----------------|--|----------|-----------------|
| 6776 | cg42558238 | 2567 | AGAGATGCAGAG ACCTCCCCCGGA C[<i>gap</i> /C]TGCGAT GACACGGTCACT TATTCAG | gap | C | Cys | Leu (8947) | FRAMES HIFT | cadherin | Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. pcds:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. | 0 | 19 (19q13.1) |
| 6777 | cg43303099 | 1216 | TCTTGCACAGGA ACAGTAGCGTCC A[G/ <i>gap</i>]CTGCCA GTCTGTATGGT CCCCAAA | G | gap | Leu | Cys (8948) | FRAMES HIFT | cadherin | Human Gene SWISSPROT-ID:P32942 INTERCELLULAR ADHESION MOLECULE-3 PRECURSOR (ICAM-3) (CDW50) (CD50 ANTIGEN) (ICAM-R) - HOMO SAPIENS (HUMAN), 547 aa. | 8.7E-158 | 19 (19p13.3) |
| 6778 | cg42528468 | 283 | TGCTCCTGCCTG GGAACAACCGG AA[G/ <i>gap</i>]GTGTA TGAACCTGAGCAA TGTGCAAG | G | gap | Val | Cys (8949) | FRAMES HIFT | cadherin | Human Gene Similar to SWISSPROT- ID:P05362 INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR (ICAM-1) (MAJOR GROUP RHINOVIRUS RECEPTOR) (CD54) - HOMO SAPIENS (HUMAN), 532 aa. | 8.4E-78 | 19 (19p13.3) |
| 6779 | cg43976467 | 882 | TGGTGGTCAACA TAAGTGACCTGG G[G/ <i>gap</i>]TACCCT AAGTCTTTGCAC ACGCTTG | G | gap | Tyr | Thr (8950) | FRAMES HIFT | cadherin | Human Gene Similar to TREMBLNEW- ID:G2852363 NF-PROTODCADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa. | 1.2E-64 | 13 |
| 6780 | cg43307361 | 1212 | CACAGGCACTAG GGAAGGCGGCT GC[C/ <i>gap</i>]ACATA GCGCCTTCTCC CTGCAGGG | C | gap | Val | Val (8951) | FRAMES HIFT | carboxyla se | Human Gene SWISSPROT-ID:Q16822 PHOSPHOENOLPYRUVATE CARBOXYKINASE, MITOCHONDRIAL PRECURSOR (GTP) (EC 4.1.1.32) (PHOSPHOENOLPYRUVATE CARBOXYLASE) (PEPCK-M) - HOMO SAPIENS (HUMAN), 640 aa. | 0 | 14 |

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| 6781 | cg43264626 | 637 | CATCTTGGGAA GCTGGCCAGGTT G[G/gap]CAATGC CACAGCGGTTGT TCTTATT | G | gap | Ala | Ala (8952) | FRAMES HIFT | cathepsin | Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa. | 4.1E-183 | 1 |
| 6782 | cg43264626 | 642 | TGGGGAAGCTG GCCAGGTTGGC AAT[G/gap]CCAC AGGCGTTGTTCT TATTCGAG | G | gap | Gly | Gly (8953) | FRAMES HIFT | cathepsin | Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa. | 4.1E-183 | 1 |
| 6783 | cg42094324 | 596 | AGATGTTGTGAA GGTCCTGGGCC TG[C/gap]CCACC CAGGAGCCAGC ACTGGGGAC | C | gap | Pro | Pro (8954) | FRAMES HIFT | cathepsin | Human Gene Homologous to SWISSPROT-ID:P20151 GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (PROSTATE) (HGK-1) - HOMO SAPIENS (HUMAN), 261 aa. | 2.1E-147 (19q13.2) | 19 |
| 6784 | cg43970982 | 2435 | GGGATAGTTGGA CAGAAGGGAGA CC[C/gap]TGGCT ACCCAGGACCA GCTGGTCCC | C | gap | Pro | Leu (8955) | FRAMES HIFT | collagen | Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa. | 0 | 2 |
| 6785 | cg43011543 | 1879 | TTGATGGCGTGA AACCCCCCATG C[C/gap]TACGGG GGCTAAGAAAGG CAAGAAAT | C | gap | Tyr | Thr (8956) | FRAMES HIFT | collagen | Human Gene SWISSPROT-ID:P27658 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) - HOMO SAPIENS (HUMAN), 744 aa. | 0 | |
| 6786 | cg43998782 | 110 | ACCTGATTGTGG TGACCGACGGG CA[C/gap]CCCCT GGAGGGCTACA AGGAACCCCT | C | gap | Thr | Thr (8957) | FRAMES HIFT | collagen | Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa. | 1.5E-103 | |

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| 6787 | cg43998782 | 138 | CCTGGAGGGCT ACAAGGAACCCCT GT[G/gap]GGGGG GCTGGAGGATG CTGTGAACG | G | gap | Gly | Gly (8958) | FRAMES HIFT | collagen | Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa. | 1.5E-103 | |
| 6788 | cg43998782 | 144 | GGGCTACAAGG AACCCCTGTGGG GGG[G/gap]CTGG AGGATGCTGTGA ACGAGGCCA | G | gap | Leu | Trp (8959) | FRAMES HIFT | collagen | Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa. | 1.5E-103 | |
| 6789 | cg43998782 | 446 | GACCCCGGCTTT GAGGGAGAAGC AG[G/gap]CAAGC CGGGCTCCCA GGAGAGAAG | G | gap | Gly | Ala (8960) | FRAMES HIFT | collagen | Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa. | 1.5E-103 | |
| 6790 | cg43998782 | 66 | GGAGCAGCTCCT CGTGGGGGGCT CC[C/gap]ACCTG AAGGAGATAAG TACCTGAT | C | gap | His | Thr (8961) | FRAMES HIFT | collagen | Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa. | 1.5E-103 | |
| 6791 | cg43991318 | 3976 | CCCAATGACACA GATCTCTCCTGG C[C/gap]GGCCGT CCCGGCCTGGC TTTCCCGG | C | gap | Arg | Gly (8962) | FRAMES HIFT | collagen | Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa. | 1.3E-73 1 (1p34) | |
| 6792 | cg43938820 | 1581 | TCCTCTTGGCAG CGCGAGACGAG GC[C/gap]TCGCG GTAGAGCGGG TCACATAGC | C | gap | Glu | Glu (8963) | FRAMES HIFT | collagen | Human Gene Similar to SPTREMBL- ID:Q14040 ALPHA-1 COLLAGEN VI (AA 574-1009) - HOMO SAPIENS (HUMAN), 436 aa (fragment). | 5E-59 21 (21q22.3) | |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|----------------|--|----------|----------|
| 6793 | cg43063256 | 258 | TGGCATCTCTG TCACATTGGAA A[A/gap]TGAAGA ATCCAGGACAT GGGCTTG | A | gap | Met | End (8964) | FRAMES HIFT | complem ent | Human Gene SWISSNEW-ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa. pcis:SWISSPROT- ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa. | 0 | 1 (1p32) |
| 6794 | cg43933757 | 2462 | CAGACGATGTCT GAGTGTGAGGC GG[G/gap]CGCTC TGAGATGCAGAG GGCAGAGC | G | gap | Gly | Ala (8965) | FRAMES HIFT | complem ent | Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa. | 0 | 5 (5p13) |
| 6795 | cg43029289 | 1158 | CCTATTACTGTG ATGAACATTTTG A[gap]A/GACTCC GTCAGGAAAGTTA CTGGGAT | gap | A | Glu | Glu (8966) | FRAMES HIFT | complem ent | Human Gene SPTREMBL-ID:Q14570 COMPLEMENT FACTOR H PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa. | 6.4E-265 | |
| 6796 | cg21644442 | 1562 | TAACCTCCGTTCC TTTGACTGACAC A[G/gap]GCCATG AGAGGCAGTCC GAGGGATC | G | gap | Gly | Ala (8967) | FRAMES HIFT | csf | Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa. | 5E-304 | 1 (1p21) |
| 6797 | cg21644442 | 1563 | AACTCCGTTCTC TTGACTGACACA G[G/gap]CCATGA GAGGCAGTCCG AGGGATCC | G | gap | Gly | Ala (8968) | FRAMES HIFT | csf | Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa. | 5E-304 | 1 (1p21) |
| 6798 | cg43920512 | 779 | CCTAGGGAAT GGAGGTTAAATG TT[A/gap]AACCTAA AGTGGGTACAT GAAGAA | A | gap | Lys | Asn (8969) | FRAMES HIFT | cyclin | Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa. | 4.1E-231 | 4 (4q27) |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|------------|--|----------|---------------|
| 6799 | cg43996855 | 4913 | CAGGGCCTGGT GGATGGCGCGC TCG[C/gap]CATT CAGCACCACTAT GGGCGAGCT | C | gap | Gly | Ala (8970) | FRAMES HIFT | cyto450 | Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa. | 3.2E-293 | 2 (2p22) |
| 6800 | cg43996855 | 4941 | TCAGCACCACTA TGGGGCAGCTG CC[gap]CJAGGCG GATCTGGAAAC GTCGCCGT | gap | C | Gly | Gly (8971) | FRAMES HIFT | cyto450 | Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa. | 3.2E-293 | 2 (2p22) |
| 6801 | cg43996855 | 5050 | TCCGATCAGTGG CCACGCAAAACG GG[C/gap]CCGGG GGCGCGGACCG GAGCTGCCG | C | gap | Gly | Ala (8972) | FRAMES HIFT | cyto450 | Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa. | 3.2E-293 | 2 (2p22) |
| 6802 | cg43996855 | 5205 | GGTCGTTCCGG CTGAGGCTGGT GCC[C/gap]ATGC TGCGGGGAGGT GCGGTTTCCA | C | gap | Met | Met (8973) | FRAMES HIFT | cyto450 | Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa. | 3.2E-293 | 2 (2p22) |
| 6803 | cg43315849 | 1727 | CAAGGAAGGGC AGGCGCCAGGG CCC[C/gap]GGCG GGTAGTTCTTTG GGCGCCGTC | C | gap | Pro | Pro (8974) | FRAMES HIFT | cyto450 | Human Gene SWISSNEW-ID:P51589 CYTOCHROME P450 2J2 (EC 1.14.14.1) (CYP11J2) (ARACHIDONIC ACID EPOXYGENASE) - HOMO SAPIENS (HUMAN), 502 aa. pcis:SWISSPROT- ID:P51589 CYTOCHROME P450 1IJ2 (EC 1.14.14.1) (ARACHIDONIC ACID EPOXYGENASE) - HOMO SAPIENS (HUMAN), 502 aa. | 7.2E-257 | 1 (1p31.3) |
| 6804 | cg43966704 | 905 | CGCTGTCTCCTC TCCACAGATGTA GG[gap]CCCCAG CCCCGCGCACC ACAAACAC | G | gap | Ala | Ala (8975) | FRAMES HIFT | cytochrome | Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa. | 5.8E-184 | 11 |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|----------------|---|----------|-----------|
| 6805 | cg43966704 | 134 | GGTGGTGGCT AAGAGGCAGCCT GC[C/gap]GGGCC TGATGCTGCTGG GCAAACCG | C | gap | Arg | Arg (8976) | FRAMES HIFT | cytochro me | Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I) DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa. | 5.8E-184 | 11 |
| 6806 | cg42717303 | 320 | GGGGATTGAGC GTAGAATGGCGT AT[G/gap]CAAAT AGGAAATATCAT TCGGGTTT | G | gap | Ala | Asp (8977) | FRAMES HIFT | cytochro me | Human Gene SWISSPROT-ID:P00158 CYTOCHROME B (EC 1.10.2.2) - MUS MUSCULUS (MOUSE), 381 aa. | 1.4E-175 | |
| 6807 | cg43935752 | 1098 | GCCCCAGTGAC CATGAAGAGTGA GG[gap/G]CTGCA GCCAGGGAATA GTCCATCGC | gap | G | Ser | Ser (8978) | FRAMES HIFT | cytochro me | Human Gene Similar to SWISSNEW- ID:O14521 SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE- UBIQUINONE REDUCTASE MEMBRANE ANCHOR SUBUNIT) - HOMO SAPIENS (HUMAN), 159 aa. | 4E-82 | 11 |
| 6808 | cg43935752 | 1238 | TGGAGCCAGAAT GGTGGCTCGGT GA[C/gap]AAGTG TATGTGCTGCAC TCCACACC | C | gap | Leu | Phe (8979) | FRAMES HIFT | cytochro me | Human Gene Similar to SWISSNEW- ID:O14521 SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE- UBIQUINONE REDUCTASE MEMBRANE ANCHOR SUBUNIT) - HOMO SAPIENS (HUMAN), 159 aa. | 4E-82 | 11 |
| 6809 | cg43962888 | 502 | CCATACAATGTA CTGGCCCCAAAG G[G/gap]AGCTTC AGGCACCAGGG AAGACCCCT | G | gap | Gly | Glu (8980) | FRAMES HIFT | cytochro me | Human Gene Similar to SWISSPROT- ID:P10806 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa. | 5.1E-66 | 2 (2cent) |
| 6810 | cg43962888 | 627 | GTTTGGCTGCA CAAAGCGGAGG CC[C/gap]AGCGA TGCCCCCGCTGT GGAGCCCA | C | gap | Gln | Ser (8981) | FRAMES HIFT | cytochro me | Human Gene Similar to SWISSPROT- ID:P10806 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa. | 5.1E-66 | 2 (2cent) |

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| 6811 | cg43941766 | 557 | GCCATGGGCGC CACTCGACATAG GC[C/gap]GCCCC AGCTGTGGCG GGACCGACC | C | gap | Arg | Arg (8982) | FRAMES HIFT | cytochrome | Human Gene Similar to TREMBLNEW- ID:E1248288 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 109 aa. | 1.5E-57 | 6 |
| 6812 | cg43958586 | 144 | TCTTCTGGTCA AAATGGCTGGTA A[G/gap]CAGGCC GTTTCAGCATCA GGCAAAGT | G | gap | Gln | Arg (8983) | FRAMES HIFT | cytochrome | Human Gene Similar to SWISSPROT- ID:P14927 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN (EC 1.10.2.2) (COMPLEX III SUBUNIT VI) - HOMO SAPIENS (HUMAN), 110 aa. | 5.2E-57 | 8 |
| 6813 | cg43923430 | 2583 | GCCACTGTTCCA CTGCAGACCAG GA[G/gap]CCATC GGCCACCCACC CGCTCAGCA | G | gap | Leu | Ser (8984) | FRAMES HIFT | cytochrome | Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa. | 3.7E-54 | 10 |
| 6814 | cg42719440 | 383 | TTGAGCATGCTC ACTCCCACCCCG G[G/gap]CAGCGC CACGAAGTAGGT GAGGGCC | G | gap | Pro | Pro (8985) | FRAMES HIFT | cytochrome | Human Gene Similar to SWISSNEW- ID:P43024 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) - MUS MUSCULUS (MOUSE), 111 aa. [pcis:SWISSPROT-ID:P43024 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) - MUS MUSCULUS (MOUSE), 111 aa. | 1.3E-51 | |
| 6815 | cg43967318 | 1787 | GACCAAGGCC CCCAGCTCCTTG AG[G/gap]CCCTG CCAAGTGGTCTC CTCCACCA | G | gap | Gly | Gly (8986) | FRAMES HIFT | dehydrogenase | Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa. | 0 (17p11.2) | 17 |
| 6816 | cg43967318 | 336 | CTGCCAGGGGT CAGACTGCAGG GCG[G/gap]CCAT GCCCTCTCGGAT CCGAGCTGC | G | gap | Ala | Ala (8987) | FRAMES HIFT | dehydrogenase | Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa. | 0 (17p11.2) | 17 |

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|------|------------|------|--|---|-----|-----|---------------|----------------|-------------------|--|----------|-----------------|
| 6817 | cg43967318 | 417 | TTTCTCATGCTG GGCCGTGGGT GG[C/gap]CCTCA CTCAGGGATCTT GAGGCCCT | C | gap | Gly | Ala (8988) | FRAMES HIFT | dehydrog enase | Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa. | 0 | 17 (17p11.2) |
| 6818 | cg43967318 | 419 | TCTCATGCTGGG CCGTGGGTGG CC[C/gap]TCACT CAGGGATCTTGA GGCCCTCG | C | gap | Glu | Glu (8989) | FRAMES HIFT | dehydrog enase | Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa. | 0 | 17 (17p11.2) |
| 6819 | cg44028421 | 390 | TCGAAGGTCACT GTCTTGACCCGC A[G/gap]GTACTC GTTCAAGAGCCGC CTCTCCT | G | gap | Leu | Cys (8990) | FRAMES HIFT | dehydrog enase | Human Gene SWISSPROT-ID:P28037 10-FORMYL-TETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.6) (FBP- C) - RATTUS NORVEGICUS (RAT), 902 aa. | 0 | |
| 6820 | cg44028421 | 391 | CGAAGGTCACTG TCTTGACCCGCA G[G/gap]TACTCG TTCAGAGCCGCC TCTCCTA | G | gap | Tyr | Tyr (8991) | FRAMES HIFT | dehydrog enase | Human Gene SWISSPROT-ID:P28037 10-FORMYL-TETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.6) (FBP- C) - RATTUS NORVEGICUS (RAT), 902 aa. | 0 | |
| 6821 | cg43962405 | 1134 | ATGGGAAGACGA TTGAGGCTGAGG C[C/gap]GCTCAT GGACCCGTCAC CCGCCACT | C | gap | Ala | Leu (8992) | FRAMES HIFT | dehydrog enase | Human Gene SWISSPROT-ID:P48735 ISOCITRATE DEHYDROGENASE (NADP), MITOCHONDRIAL PRECURSOR (EC 1.1.1.42) (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+- SPECIFIC ICDH) (IDP) (ICD-M) - HOMO SAPIENS (HUMAN), 452 aa. | 8.2E-249 | 15 (15q26.1) |
| 6822 | cg43255016 | 1088 | ATTAGGATTTTA GCCAGTAGTTTTI G[gap]GGTCAAG CCCTAACCTGAT TCCAAG | G | gap | Pro | Gln (8993) | FRAMES HIFT | dehydrog enase | Human Gene SWISSPROT-ID:P29266 3- HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment). | 3.4E-156 | |

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| 6823 | cg43969759 | 949 | GCAGCAACACCT ATGATGGCTGTG G[gap]CTTCAC CAGCCTCACCAC CTCCTCC | G | gap | Pro | Pro (8994) | FRAMES HIFT | dehydrog enase | Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa. | 1.8E-109 | 11 |
| 6824 | cg44000219 | 741 | GCACTGCCTGCC CTACTTCGCAA G[gap]GJCGCAGG GCCACGAGCTG GGCGCCAC | gap | G | Ala | Gly (8995) | FRAMES HIFT | dehydrog enase | Human Gene Similar to SPTREMBL- ID:Q64644 CHOLINE DEHYDROGENASE (EC 1.1.99.1) - RATTUS NORVEGICUS (RAT), 441 aa (fragment). | 3.3E-93 | |
| 6825 | cg42717162 | 370 | GCCCTATCCATA AACTAGGCCTC G[C/gap]CCCAT CCACTTCTGATT ACCAGAA | C | gap | Ala | Ala (8996) | FRAMES HIFT | dehydrog enase | Human Gene Similar to SPTREMBL- ID:Q34799 NADH DEHYDROGENASE SUBUNIT 2 (ND2) - SYMPHALANGUS SYNDACTYLUS (SIAMANG), 347 aa. | 1.3E-90 | |
| 6826 | cg42717162 | 373 | CTATCCATAAAA CTAGGCCCTCGCC C[C/gap]ATTCCA CTTCTGATTACC AGAAAGTA | C | gap | Pro | His (8997) | FRAMES HIFT | dehydrog enase | Human Gene Similar to SPTREMBL- ID:Q34799 NADH DEHYDROGENASE SUBUNIT 2 (ND2) - SYMPHALANGUS SYNDACTYLUS (SIAMANG), 347 aa. | 1.3E-90 | |
| 6827 | cg43248620 | 2674 | CTTTTTTTTGGG AGGAGAAAGGG G[gap]TJTITTTTG GGACAGCTGAA GGCGGCG | gap | T | Pro | Thr (8998) | FRAMES HIFT | dna_ma_ bind | Human Gene SPTREMBL-ID:Q14550 ZINC-FINGER DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 1482 aa. | 0 | 1 |
| 6828 | cg42175288 | 1619 | GAGGTACGGA GGAGATCGAGG AGG[G/gap]TTAT GGAGGAGATCG AGGAGGCTAT | G | gap | Leu | Tyr (8999) | FRAMES HIFT | dna_ma_ bind | Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa. | 0 | 17 |

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| 6829 | cg42175288 | 1813 | AGGTGGGGACG GAGAGACCGAG GTG[G/gap]CTAT GGAGGCAAAATG GGAGGAAGA | G | gap | Gly | Ala (9000) | FRAMES HIFT | dna_ma_ bind | Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa. | 0 | 17 |
| 6830 | cg43962927 | 1470 | GGCACTGGCTG GAGAGGGGCTG GGC[C/gap]ACCG GTCCCTGCTGG GGGTCCCAGG | C | gap | Gly | Ala (9001) | FRAMES HIFT | dna_ma_ bind | Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa. | 0 | 11 (11q13.2) |
| 6831 | cg44005808 | 816 | CAACCACAGATG GCACTGCCAACA G[C/gap]AGATGG CCCATACCTTCA AATATTA | C | gap | Ala | Glu (9002) | FRAMES HIFT | dna_ma_ bind | Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa. lpcds:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa. | 0 | |
| 6832 | cg43931615 | 2554 | CAGGTCCTGTTC GGTTGTTTTCCA TT[G/gap]GGAGAC CCAACACTATTA AATCGGA | G | gap | Pro | His (9003) | FRAMES HIFT | dna_ma_ bind | Human Gene SPTREMBL-ID:Q13148 TAR DNA-BINDING PROTEIN-43 - HOMO SAPIENS (HUMAN), 414 aa. | 4.3E-227 | 20 |
| 6833 | cg43956159 | 1718 | CACCCCTCCTCCT GCCGTCGGGG AG[G/gap]CATCG CCATTTCCCTTG TCACCTGG | G | gap | Ala | Ala (9004) | FRAMES HIFT | dna_ma_ bind | Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 1.4E-159 | 10 |

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| 6834 | cg43956159 | 1725 | CTCCTGCCGTGG GGGGAGGCATC GC[C/gap]ATTC CCTTGTCACCTG GCTTCCCC | C | gap | Gly | Ala (9005) | FRAMES HIFT | dna_rna_ bind | Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 1.4E-159 | 10 |
| 6835 | cg43917883 | 1246 | ATCACACAGGGG CCCCCGCCCG GCG[G/gap]GCCC GGCGCCCGCAG CGAGGAGAAG | G | gap | Gly | Gly (9006) | FRAMES HIFT | dna_rna_ bind | Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa. | 2.7E-138 | 1 |
| 6836 | cg43917883 | 1247 | TCACCAGGGG CCCCCGCCCG CGG[G/gap]CCCG GCGGCCGCAGC GAGGAGAAGA | G | gap | Pro | Pro (9007) | FRAMES HIFT | dna_rna_ bind | Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa. | 2.7E-138 | 1 |
| 6837 | cg43917883 | 1984 | GAAAAACAGCAA AGGGAACAAGTT G[A/gap]AAAAAA CATGAAAGATGC AAAAGAC | A | gap | Glu | Glu (9008) | FRAMES HIFT | dna_rna_ bind | Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa. | 2.7E-138 | 1 |
| 6838 | cg43917883 | 1990 | AGCAAAGGGAAC AAGTTGAAAAAA A[gap/A]CATGAA AGATGCAAAAGA CAAAATTG | gap | A | Asn | Lys (9009) | FRAMES HIFT | dna_rna_ bind | Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa. | 2.7E-138 | 1 |
| 6839 | cg43947431 | 2147 | CCACCAAGGACC GAAGTACCCTGT TIG[gap]GCGATG TCGCCCCCATC TTATACT | G | gap | Ala | Ala (9010) | FRAMES HIFT | dna_rna_ bind | Human Gene Similar to SPTREMBL- ID:Q96327 PUTATIVE NUCLEAR DNA- BINDING PROTEIN G2P (ATG2) - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 392 aa. | 1.2E-91 | |
| 6840 | cg43947431 | 2148 | CACCAAGGACC GAAGTACCCTGT TG[G/gap]CGATG TCGCCCCCATC TTATACTT | G | gap | Ala | Ala (9011) | FRAMES HIFT | dna_rna_ bind | Human Gene Similar to SPTREMBL- ID:Q96327 PUTATIVE NUCLEAR DNA- BINDING PROTEIN G2P (ATG2) - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 392 aa. | 1.2E-91 | |

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| 6841 | cg43940815 | 436 | GAGAAATCTCTCC AGTGTGAGGTTT TTT/gap]ATTGTTG TAAAAAAGAAGA GTTTTG | T | gap | End | End (9012) | FRAMES HIFT | dna_ma_ bind | Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa. | 1E-89 | 6 |
| 6842 | cg43269833 | 295 | TGTGCTGGGCA GGACGAGGCTG CGG[C/gap]CCCC GGGGGCAGCGT TGGGGCGGGC | C | gap | Pro | (9013) | FRAMES HIFT | dna_ma_ bind | Human Gene Similar to SWISSPROT- ID:O00287 REGULATORY FACTOR X- ASSOCIATED PROTEIN (RFX DNA- BINDING COMPLEX 36 KD SUBUNIT) (RFX-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 272 aa. | 6.6E-89 | 13 |
| 6843 | cg43269833 | 412 | ACCTGTTAGACA CTTCGGACCCTC C[G/gap]GGGGGA GGCGAGACGCG GCTAGTTT | G | gap | Gly | (9014) | FRAMES HIFT | dna_ma_ bind | Human Gene Similar to SWISSPROT- ID:O00287 REGULATORY FACTOR X- ASSOCIATED PROTEIN (RFX DNA- BINDING COMPLEX 36 KD SUBUNIT) (RFX-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 272 aa. | 6.6E-89 | 13 |
| 6844 | cg43299462 | 971 | TGAGGGTGGTCA GCGGCGTCCTG GA[gap/G]CGCCT GGTCTGCCCG GGTCTCTGG | gap | G | Ser | (9015) | FRAMES HIFT | dna_ma_ bind_inhi b | Human Gene Similar to SWISSNEW- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa. pds:SWISSPROT- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa. | 9.2E-67 | 3 (2p25) |
| 6845 | cg43947402 | 594 | CTTTCATGTTTG GATCAATTTTTT T/gap]GACCCAG CAGGAATGGGT GACACGC | T | gap | Ser | (9016) | FRAMES HIFT | dynein | Human Gene SWISSPROT-ID:Q90828 DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A) - GALLUS GALLUS (CHICKEN), 515 aa. | 3.7E-214 | 3 |
| 6846 | cg43932150 | 190 | CGGACGTGTCG GTGCTGCAGAAG CA[C/gap]CTGCG CAACTGGTGCG GCTGCTGCT | C | gap | Leu | (9017) | FRAMES HIFT | dynein | Human Gene Similar to SWISSPROT- ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa. | 1.1E-89 | |

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|------|------------|-------|---|-----|-----|---------------|----------------|-----|---|---|----|
| 6847 | cg43958656 | 2145 | TACAAAGCGGAG GACGAGGTGCA GC[G/gap]CGAGA GGGTGTCAGCC AAGAACGCC | gap | Arg | Pro (9018) | FRAMES HIFT | eph | Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa. | 0 | 6 |
| 6848 | cg44017749 | 14201 | CCAGCCAGCCCT TCCCTGGCCCC GC[C/gap]GGATG TATAAATGTAAA ATGAAGG | gap | Arg | Gly (9019) | FRAMES HIFT | eph | Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa. | 0 | 12 |
| 6849 | cg44017749 | 5045 | CAACACCCAGCC CTTGACCTGCA G[G/gap]TGTAAC ACCCCTCCCGCC AGCCCAT | gap | Val | Cys (9020) | FRAMES HIFT | eph | Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa. | 0 | 12 |
| 6850 | cg43950268 | 1346 | AGCTGAGCCAG GCCAGGCTCGC TTG[C/gap]GCCG AGCTGATTGAGC TTCTTGATG | gap | Ala | Gln (9021) | FRAMES HIFT | eph | Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa. | 0 | 16 |
| 6851 | cg43950268 | 1476 | TGCGCAGGAAGT GGCGGGCAGCC CC[C/gap]ATCTC CAGCACGGTGA CCATGGCAG | gap | Met | Met (9022) | FRAMES HIFT | eph | Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa. | 0 | 16 |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|-----|---|----------|----|
| 6852 | cg43950268 | 1895 | GAGAGGCTGGTT AGCTGCCCCGA GG[G/gap]CAGCG CCGAGGACTCGT AGCGCAGC | G | gap | Pro | Pro (9023) | FRAMES HIFT | eph | Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa. | 0 | 16 |
| 6853 | cg43950268 | 2239 | TTTGGCGGTGTA CAGTGCAACGCT G[G/gap]AGCCCA GCTCCCGGCTCA CATCAA | G | gap | Ser | Ser (9024) | FRAMES HIFT | eph | Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa. | 0 | 16 |
| 6854 | cg43945212 | 1867 | AGAACATTTGCG AACTGGCCCGG AG[G/gap]ATGCT CTTCAGCGCCGT CGAGTGGG | G | gap | Met | Cys (9025) | FRAMES HIFT | eph | Human Gene SWISSPROT-ID:P43135 APOLIPOPROTEIN AI REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa. | 5.8E-232 | 7 |
| 6855 | cg43985169 | 659 | GCCTCAAAACAAG ATCCTCCAGTTA TT[gap]CATGAA CTTAGAGTATCA CTTGAAG | T | gap | His | Met (9026) | FRAMES HIFT | eph | Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa. | 2.4E-123 | |
| 6856 | cg43985169 | 738 | AAGATTTCTCGA AAAAGGCTAAAC G[gap]TCTGATG GAAGGAGTTACA GATCTGA | gap | T | Ala | Val (9027) | FRAMES HIFT | eph | Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa. | 2.4E-123 | |
| 6857 | cg43985169 | 843 | ACTTTTCCAAGA GAAGGAGATGAA A[gap]A]CACCAA ATAGTATTCAG CAGACAT | gap | A | Thr | Asn (9028) | FRAMES HIFT | eph | Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa. | 2.4E-123 | |
| 6858 | cg43985169 | 933 | AAGGGATGGATC AAATATAATTTAT [A/gap]CTGCTAA AATTAGTTTACG AGAGGC | A | gap | Thr | Leu (9029) | FRAMES HIFT | eph | Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa. | 2.4E-123 | |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|----------|--|----------|-----------------|
| 6859 | cg43985169 | 968 | TAGTTTACGAGA GGCATTGTGTGG C[gap/G]TGCTCA ATTAATGTACCA ACACTGG | gap | G | Cys | Val (9030) | FRAMES HIFT | eph | Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa. | 2.4E-123 | |
| 6860 | cg43918531 | 443 | TTCACCCCAATCA GAATAGCCGATG G[C/gap]TATGAG CAGGCTGCTCG CGTTGCTA | C | gap | Tyr | Met (9031) | FRAMES HIFT | eph | Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa.lpcis:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa. | 1E-104 | 5 |
| 6861 | cg43949555 | 1550 | CCCTGCTGTAAA GGACATGCTGGA A[G/gap]CTGGTA TTCTAGATACCTA CCTGGG | G | gap | Ala | Leu (9032) | FRAMES HIFT | eph | Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCLUS SP. (STRAIN SY), 545 aa.lpcis:SPTREMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa. | 6.7E-80 | 21 |
| 6862 | cg42889246 | 496 | CTCCAGTGGACT CAGCGGCAGAG AC[G/gap]CCACC CCGAGAAGGCA AATCCACT | G | gap | Pro | His (9033) | FRAMES HIFT | eph | Human Gene Similar to SPTREMBL- ID:Q12988 HEAT SHOCK PROTEIN 27 - HOMO SAPIENS (HUMAN), 241 aa. | 7.5E-73 | |
| 6863 | cg43972010 | 2213 | ATGCCAGATGGG AGCCTCCCAGAG G[C/gap]CCAGAG CCTGTGGCCCAAG GCCACTG | C | gap | Ala | Ala (9034) | FRAMES HIFT | esterase | Human Gene SWISSPROT-ID:P17405 SPHINGOMYELIN PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.12) (ACID SPHINGOMYELINASE) - HOMO SAPIENS (HUMAN), 629 aa. | 0 | 11 (11p15.4) |

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| 6864 | cg43942273 | 858 | TCGGAGAGTGG ATAGCTCATCA CT[G/gap]CATTG GAATCAACCAGC CAAACCTCC | G | gap | Gln | Ser (9035) | FRAMES HIFT | esterase | Human Gene SWISSPROT-ID:P23141 LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE) - HOMO SAPIENS (HUMAN), 567 aa. | 2.2e-310 | 16 |
| 6865 | cg43328419 | 234 | TTACCAAGCTAT ACAGCCGACAAG G[C/gap]TACCAC TTGCAGCTGCAG GCGGATG | C | gap | Tyr | Thr (9036) | FRAMES HIFT | tgf | Human Gene Homologous to SWISSPROT-ID:Q92913 FIBROBLAST GROWTH FACTOR-13 (FGF-13) (FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 2) (FHF-2) - HOMO SAPIENS (HUMAN), 245 aa. pcds:SPTREMBL-ID:Q92913 FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 2 - HOMO SAPIENS (HUMAN), 245 aa. | 2.2E-119 | |
| 6866 | cg43249494 | 602 | ACAAGGGACAG GAGCGACCAGC ACA[C/gap]AGAC ACCAAATGAGGA ATGTTTGTT | C | gap | Gln | Arg (9037) | FRAMES HIFT | tgf | Human Gene Similar to SWISSPROT- ID:P34004 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 155 aa. | 2.3E-61 | 5 (5q31) |
| 6867 | cg43320667 | 1502 | GGTATGCCAGGA ACGCCAGCCCG GG[gap/G]CTGAG GCCGCCACATCA GCAATGGA | gap | G | Pro | Pro (9038) | FRAMES HIFT | gaba | Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa. | 0 | 3 (3p25) |
| 6868 | cg43969076 | 1807 | CACCCACACGAT GGCATAGGAATG G[G/gap]CACTGC CAATCCTCAGCA CCACTCT | G | gap | Ala | Ala (9039) | FRAMES HIFT | glucuronidase | Human Gene SWISSPROT-ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa. | 0 | 7 (7q21.11) |

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| 6869 | cg43286488 | 553 | CAGGCTGGGCT GGGTAGCACAG GCT[G/gap]GCAC AGCCGCTGGGC AGGGGGCTGG | G | gap | Gln | Ser (9040) | FRAMES HIFT | glycoprot ein | Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa. pcds:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa. | 0 | 12 |
| 6870 | cg43065549 | 1570 | GCTGGATGACG CGGCCTGCCTTG CC[C/gap]CAGGG TTATGATGGATG GCAGATTG | C | gap | Gln | Arg (9041) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa. | 0 | 15 (15q15) |
| 6871 | cg43065549 | 1571 | CTGGATGACGC GGCCTGCCTTGC CC[C/gap]AGGGT TATGATGGATGG CAGATTCT | C | gap | Gln | Arg (9042) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa. | 0 | 15 (15q15) |
| 6872 | cg43065549 | 2126 | CTACAACGGTGT CCTTGCTGCCAA G[C/gap]TCTGGA GGAAAGAGCTG CACCTCAC | C | gap | Leu | Ser (9043) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa. | 0 | 15 (15q15) |

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| 6873 | cg44034764 | 586 | CAGGCGAGGCA GCCCCCAGGCA GTA[<i>gap</i> /C]AGAG CTGGTAGAAGAT GTGCAACAG | gap | C | Leu | Cys (9044) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa. | 0 | 7 (Xp21.2) |
| 6874 | cg44034764 | 586 | CAGGCGAGGCA GCCCCCAGGCA GTA[<i>gap</i> /C]AGAG CTGGTAGAAGAT GTGCAACAG | gap | C | Leu | Cys (9045) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa. | 0 | 7 (Xp21.2) |
| 6875 | cg43010733 | 1185 | TTCTCTGGACCAC TTCCCGCCCGG CG[G/ <i>gap</i>]CCGGC AGGACGGCTGG ATCGCCGAC | G | gap | Gly | Ala (9046) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:Q09327 BETA-1,4-MANNOSYL-GLYCOPROTEIN BETA-1,4-N-ACETYLGLUCOSAMINYL- TRANSFERASE (EC 2.4.1.144) (N- GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E II) (N- ACETYLGLUCOSAMINYLTRANSFERAS E II) (GNT-II) (GLCNAC-T II) - HOMO SAPIENS (HUMAN), 531 aa. | 5E-304 | |
| 6876 | cg43094362 | 168 | CACTGAGGTGTC AGAAGGCAAAGC C[C/ <i>gap</i>]ACTGCT CTACTTCATGGT CACCACCT | C | gap | Trp | Trp (9047) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa. | 9.7E-230 | 7 |
| 6877 | cg43094362 | 215 | CACTCCTGTCCA GGAAGATCAGTG G[C/ <i>gap</i>]CCCCAC GGTGACATCTGC TTCTTCT | C | gap | Gly | Gly (9048) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa. | 9.7E-230 | 7 |

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| 6878 | cg43094362 | 219 | CCTGTCCAGGAA GATCAGTGGCCC C[C/gap]ACGGTG ACATCTGCTTCT TCTGTCA | C | gap | Val | Val (9049) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa. | 9.7E-230 | 7 |
| 6879 | cg43094362 | 259 | TCTTCTGTCACA TGCCTGCGGTTA C[gap]A]GGGAAG CAGACGTGGAC CACTGGCT | gap | A | Arg | Leu (9050) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa. | 9.7E-230 | 7 |
| 6880 | cg43924995 | 1264 | TGCAAAATAACAA TCTCAGCTACTG G[G/gap]ATGCCC CCCTGGGAAGTT CTTATAT | G | gap | Asp | Met (9051) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa. | 1.2E-222 X (Xq24) | |
| 6881 | cg43924995 | 330 | TGTGCTTCCGCC TCTTCCCGGTTG C[G/gap]GGCTCA GGGCTCGTTCTG GTCTGCC | G | gap | Gly | Ala (9052) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa. | 1.2E-222 X (Xq24) | |
| 6882 | cg43987514 | 339 | ACTGGCACATGA GGGGCCCCAGC TG[C/gap]CCCCGA GGCCAAGGCTG CGCTGAACA | C | gap | Gly | Gly (9053) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa. | 3.2E-215 | |
| 6883 | cg43987514 | 544 | ACTGGCCAGGTC CACTTGCTGGCC G[C/gap]CTGCTG GCCCGGCTGGT ACGTTTCA | C | gap | Gly | Ala (9054) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa. | 3.2E-215 | |

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| 6884 | cg43987514 | 833 | AAGCTGGCCAG GCCAGGTCCAGT CA[G/gap]GGCCC CCAGCCCACCCA GTCCTCCG | G | gap | Leu | End (9055) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa. | 3.2E-215 | |
| 6885 | cg43958670 | 2191 | AGGCTTGTAAGT AGGCCTAGGAC CT[G/gap]AGGCA CTGGACGCTGG AGATTTTGT | G | gap | Ser | End (9056) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPBLOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa. | 9.6E-207 | 1 (1q32) |
| 6886 | cg44034752 | 1095 | TGAGAACTTGG TGCGGCAGAGG TT[G/gap]CAGTG ACCTGCACGGTG TTCCAAAC | G | gap | Ala | Gln (9057) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa. | 4.9E-203 | 3 (3q27) |
| 6887 | cg44034752 | 1299 | TCCTCCAGGACA CCAGTTGCACCG G[G/gap]CGCACT ACGACCTGCGC CACACCTT | G | gap | Ala | Arg (9058) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa. | 4.9E-203 | 3 (3q27) |
| 6888 | cg44034752 | 1350 | CATGGGTGTGGT CTCATTGGGGTC A[G/gap]CCTCAG GAGAAAGTGTGCG ACCCCCG | C | gap | Pro | Pro (9059) | FRAMES HIFT | glycoprot ein | Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa. | 4.9E-203 | 3 (3q27) |
| 6889 | cg43051796 | 1283 | GCCAAAAAAGC AAGGGGAATGA GG[G/gap]TCCCC CCCAGGCATCTG GCACAGCC | G | gap | Thr | Thr (9060) | FRAMES HIFT | glycoprot ein | Human Gene Homologous to SWISSNEWID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa. [pcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa. | 4E-114 | 3 |

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| 6890 | cg43051796 | 1301 | AATGAGGGGTCCC CCCCAGGCATCT G[G/gap]CACAGC CCCCAGTGCACA TTCTGGG | G | gap | Ala (9061) | Ala | FRAMES HIFT | glycoprot ein | Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.lpcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa. | 4E-114 | 3 |
| 6891 | cg43924574 | 1299 | TCTCAGGGGTGA ATTTTCCTGGTT C[C/gap]TGCCGG TCCTGGGACCAG TTGGTAA | C | gap | Gln (9062) | Gln | FRAMES HIFT | glycoprot ein | Human Gene Homologous to SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP- 39) (39 KD SYNOVIAL PROTEIN) (YKL- 40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa. | 1E-106 | 1 |
| 6892 | cg43255952 | 678 | AGAGGGGGGTG CACGGGTACTGT TC[C/gap]TCACG GCAGTCAAGAG GCCCCAGGCT | C | gap | Glu (9063) | Glu | FRAMES HIFT | glycoprot ein | Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.lpcis:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa. | 2.6E-101 (1p36.1) | 1 (1p36.1) |
| 6893 | cg43255952 | 935 | TCATACTGGCCC TGAGCCAGCAAG C[C/gap]TGCAGG CAGGAATAGCAG GAAGAGG | C | gap | Ala (9064) | Gly | FRAMES HIFT | glycoprot ein | Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.lpcis:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa. | 2.6E-101 (1p36.1) | 1 (1p36.1) |

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| 6894 | cg43967180 | 92 | GGGGACCTGCC CTCCTGGACGC GGA[G/gap]CCTA AACCTGAGTTAC AACAAACTC | G | gap | Ser | Thr (9065) | FRAMES HIFT | glycoprot ein | Human Gene Similar to SPTREMBL- ID:P70193 MEMBRANE GLYCOPROTEIN - MUS MUSCULUS (MOUSE), 1091 aa. | 1.7E-99 | |
| 6895 | cg43917300 | 269 | TGAGGGCCACC ACCCCACTGTGG GG[G/gap]CTCAC CTTCGGGTGGT GAAAAAGC | G | gap | Ser | Ser (9066) | FRAMES HIFT | glycoprot ein | Human Gene Similar to SWISSPROT- ID:Q0878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT- MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa. | 4.4E-99 | 22 (22q13.3) |
| 6896 | cg43917300 | 527 | TCTCAGGGCACT CGAAGGCCAGG CA[G/gap]CGGAA GCCGCCCTGGA TGTTGAAGC | G | gap | Arg | Arg (9067) | FRAMES HIFT | glycoprot ein | Human Gene Similar to SWISSPROT- ID:Q0878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT- MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa. | 4.4E-99 | 22 (22q13.3) |
| 6897 | cg43252493 | 320 | AATGTAATGCCA CCAACGCCATTG G[C/gap]TCCGCC TCTGTTGTCACT GTCCTCA | C | gap | Ser | Pro (9068) | FRAMES HIFT | glycoprot ein | Human Gene Similar to SPTREMBL- ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa. | 1.8E-84 | |
| 6898 | cg43252493 | 326 | ATGCCACCAACG CCATTGGCTCCG C[C/gap]TCTGTT GTCACGTGTCCTC AGGGTGC | C | gap | Ser | Leu (9069) | FRAMES HIFT | glycoprot ein | Human Gene Similar to SPTREMBL- ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa. | 1.8E-84 | |

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|------|------------|------|---|---|-----|-----|---------------|----------------|--------------|--|---------|---------------|
| 6899 | cg43512398 | 91 | TTGCTATTGCAG GACGGACCTGTC C[C/gap]AAGCCA GATGATTACCA TTTTCCA | C | gap | Lys | Ser (9070) | FRAMES HIFT | glycoprotein | Human Gene Similar to SWISSNEW- ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa | 2.7E-83 | 17 (17q23) |
| 6900 | cg44341920 | 91 | TTGCTATTGCAG GACGGACCTGTC C[C/gap]AAGCCA GATGATTACCA TTTTCCA | C | gap | Lys | Ser (9071) | FRAMES HIFT | glycoprotein | Human Gene Similar to SWISSNEW- ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa | 2.7E-83 | 17 (17q23) |
| 6901 | cg43983795 | 1467 | TGCTTCCTTATC CAGGCAAAATGT G[G/gap]CAAGGC CCCTGGATGCAT CTCTTCC | G | gap | Ala | Ala (9072) | FRAMES HIFT | glycoprotein | Human Gene Similar to SPTREMBL- ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa. | 1.2E-74 | X |

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|------|------------|------|--|---|------------|-----|---------------|----------------|------------------|---|---------|----|
| 6902 | cg43056971 | 238 | CAATCCGTCAGC TAAACCCAGTGT GTT[<i>gap</i>]GGCTGA GATCCAAAATTG GGACAGT | T | <i>gap</i> | Trp | Gly (9073) | FRAMES HIFT | glycoprot ein | Human Gene Similar to SPTREMBL- ID:O04711 P-GLYCOPROTEIN-2 - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 1233 aa. | 2.2E-72 | 1 |
| 6903 | cg43995037 | 2835 | GGCTCAGGAAC GCGTGCGGGCG TA[G/ <i>gap</i>]CGGGT GAGCATGCTGAT GATGACCA | G | <i>gap</i> | Arg | Arg (9074) | FRAMES HIFT | glycoprot ein | Human Gene Similar to SWISSNEW- ID:P21851 BETA-ADAPTIN (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (GLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND BOS TAURUS, 937 aa. ID:P21851 BETA-ADAPTIN (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (GLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND BOS TAURUS, 937 aa. | 3E-68 | 15 |
| 6904 | cg42887075 | 230 | CGGGTGAAGAA GTCAGGGCCTC GGC[C/ <i>gap</i>]ACAG GGCCCCAGGGA AAAGGAGGCC | C | <i>gap</i> | Pro | His (9075) | FRAMES HIFT | glycoprot ein | Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa. | 1.3E-58 | |
| 6905 | cg43926142 | 652 | TTTAATTAAGAA TGAGTGCTGGG G[C/ <i>gap</i>]CCITTTT ATTGGGTACTGC ATCTAC | C | <i>gap</i> | Ala | Ala (9076) | FRAMES HIFT | glycoprot ein | Human Gene Similar to SWISSPROT- ID:Q15388 MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20 HOMOLOG (MITOCHONDRIAL 20 KD OUTER MEMBRANE PROTEIN) (OUTER MITOCHONDRIAL MEMBRANE RECEPTOR TOM20) (KIAA0016) - HOMO SAPIENS (HUMAN), 145 aa. | 2.9E-57 | 1 |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|----------|---|---|---|
| 6906 | cg43250682 | 1070 | GCCAAAGAAGCA GGAAAAAGGGG CAG[G/gap]CTTG AGGACGCCTCCA TTCTATGCC | G | gap | Leu | Leu (9077) | FRAMES HIFT | Guanylyl | Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa. | 0 | 4 |
| 6907 | cg43250682 | 1483 | TTTCAAGGAAAG CCTAATTTTGAA G[A/gap]ATACTTT GAAATTCTGACT CCAAAA | A | gap | Glu | Asp (9078) | FRAMES HIFT | Guanylyl | Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa. | 0 | 4 |
| 6908 | cg43250682 | 1484 | TTC AAGGAAAGC CTAATTTTGAA A[A/gap]TACTTTG AAATTCGACTC CAAAAA | A | gap | Tyr | Thr (9079) | FRAMES HIFT | Guanylyl | Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa. | 0 | 4 |
| 6909 | cg43250682 | 2104 | GATGTCTACAAG GTGGAGACCAT G[G/gap]CGATGC CTATTGTGTGGC TGGGGGA | G | gap | Gly | Ala (9080) | FRAMES HIFT | Guanylyl | Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa. | 0 | 4 |
| 6910 | cg43250682 | 2123 | CATTGGCGATGC CTATTGTGTGGC T[Gap/T]GGGGGA TTACACAAAAGAG AGTGATA | gap | T | Gly | Trp (9081) | FRAMES HIFT | Guanylyl | Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa. | 0 | 4 |
| 6911 | cg43250682 | 2551 | TTCCAAAAGAAA GATGTGGAAGAT G[G/gap]CAATGC CAATTTTATAGG CAAAGCA | G | gap | Gly | Ala (9082) | FRAMES HIFT | Guanylyl | Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa. | 0 | 4 |
| 6912 | cg43250682 | 2555 | AAAAGAAAGATG TGGAAGATGGCA A[T/gap]GCCAAT TTTTAGGCAAA GCATCAG | T | gap | Ala | Pro (9083) | FRAMES HIFT | Guanylyl | Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa. | 0 | 4 |

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|------|------------|------|---|---|-----|-----|---------------|----------------|----------|--|----------|----|
| 6913 | cg43250682 | 2574 | TGGCAATGCCAA TTTTTAGGCAA A[G/gap]CATCAG GAATAGATTAGC AACCTAT | G | gap | Ala | His (9084) | FRAMES HIFT | Guanylyl | Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa. | 0 | 4 |
| 6914 | cg43866596 | 2876 | AACCAGCGGTCA GGCGGAGCCGG CA[G/gap]GACGG GCCAGGTCAGT GTTTCAGG | G | gap | Arg | Arg (9085) | FRAMES HIFT | helicase | Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa. pcis:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa. | 0 | 16 |
| 6915 | cg43919913 | 1197 | GGTCGATCAGTG TCCGGTAACCCT C[C/gap]TGCGGG TCTTCTTGGA GCATTAC | C | gap | Gln | Gln (9086) | FRAMES HIFT | helicase | Human Gene SWISSNEW-ID:Q14562 PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN 8) - HOMO SAPIENS (HUMAN), 1220 aa. pcis:SWISSPROT-ID:Q14562 PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN 8) - HOMO SAPIENS (HUMAN), 1220 aa. pcis:SPTREMBL-ID:Q14562 PUTATIVE RNA HELICASE HRH1 - HOMO SAPIENS (HUMAN), 1220 aa (fragment). | 0 | 17 |
| 6916 | cg44026400 | 245 | TTCGCCATTTC TTC TTGGCGGCC G[C/gap]CTTCTT AGGCTTGACAAC CTTGGGC | C | gap | Ala | Arg (9087) | FRAMES HIFT | histone | Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa. | 1.7E-104 | 6 |
| 6917 | cg44026400 | 246 | TCGCCTATTCT TCTTGGCGGCC GC[C/gap]TTCCTT AGGCTTGACAAC CTTGGGCT | C | gap | Lys | Lys (9088) | FRAMES HIFT | histone | Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa. | 1.7E-104 | 6 |

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|------|------------|-----|--|---|------------|---------------|----------------|---------|--|----------|---|
| 6918 | cg44026400 | 282 | TGACAACCTTGG GCTTAGCGCCT TG[<i>gap</i>]GGCTTC ACAGCCTTAGCA GCACTTT | G | <i>gap</i> | Pro (9089) | FRAMES HIFT | histone | Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa. | 1.7E-104 | 6 |
| 6919 | cg44026400 | 356 | ACCTTGGCCTTC TTTGGGCTCTTA G[C/ <i>gap</i>]CACTTT CTTGGTTACAGT GGCCGGG | C | <i>gap</i> | Ala (9090) | FRAMES HIFT | histone | Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa. | 1.7E-104 | 6 |
| 6920 | cg44026400 | 357 | CCTTGGCCTTCT TTGGGCTCTTAG C[C/ <i>gap</i>]ACTTCT TGGTTACAGTGG CCGCCGG | C | <i>gap</i> | Val (9091) | FRAMES HIFT | histone | Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa. | 1.7E-104 | 6 |
| 6921 | cg44026400 | 383 | ACTTCTTGGTT ACAGTGGCCGC GG[C/ <i>gap</i>]CGGCT TCTTCGCTTCTT CGGTGTT | C | <i>gap</i> | Pro (9092) | FRAMES HIFT | histone | Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa. | 1.7E-104 | 6 |
| 6922 | cg44026400 | 384 | CTTCTTGGTTA CAGTGGCCGCG GC[C/ <i>gap</i>]GGCTT CTTCGCTTCTT CGGTGTT | C | <i>gap</i> | Pro (9093) | FRAMES HIFT | histone | Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa. | 1.7E-104 | 6 |
| 6923 | cg44026400 | 532 | AACCTTGGGCTT GGCTTCCCCGG AG[G/ <i>gap</i>]CTGCC TTCITGTTGAGT TTAAAGGA | G | <i>gap</i> | Ala (9094) | FRAMES HIFT | histone | Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa. | 1.7E-104 | 6 |
| 6924 | cg44026400 | 720 | AAACTCCGCTAC GCTCTTTAGAGG C[G/ <i>gap</i>]GCCACA GCCTTGGTGATG AGCTCTG | G | <i>gap</i> | Ala (9095) | FRAMES HIFT | histone | Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa. | 1.7E-104 | 6 |

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| 6925 | cg42689683 | 363 | CCAGCTCCAGGA CCTTGGCCGTCA G[G/gap]TACTCA ATAACCGCAGCG AGGTAGA | G | gap | Tyr (9096) | Tyr (9096) | FRAMES HIFT | histone | Human Gene Similar to SWISSPROT- ID:P98176 HYPOTHETICAL 12.7 KD HISTONE H2A RELATED PROTEIN - HOMO SAPIENS (HUMAN), 115 aa. | 3.7E-53 | |
| 6926 | cg42689683 | 519 | CCGCCCCCGGC CGCCAGCACCG GAG[gap]GACCC TCGGCGTCTCCT CCTCCTCGG | gap | G | Ser (9097) | Ser (9097) | FRAMES HIFT | histone | Human Gene Similar to SWISSPROT- ID:P98176 HYPOTHETICAL 12.7 KD HISTONE H2A RELATED PROTEIN - HOMO SAPIENS (HUMAN), 115 aa. | 3.7E-53 | |
| 6927 | cg43985818 | 429 | AGACGCCGTCAC CTATACGGAGCA C[G/gap]CCAAGC GCAAAACTGTCA CAGCCAT | G | gap | Ala (9098) | Pro (9098) | FRAMES HIFT | histone | Human Gene Similar to TREMBLNEW- ID:G2564108 HISTONE H4 - CHAEPTERUS VARIOPEATUS, 103 aa.pcls:TREMBLNEW-ID:E314007 HISTONE H4 - MUS MUSCULUS (MOUSE), 103 aa.pcls:TREMBLNEW- ID:G62736 H4 HISTONE - CAIRINA MOSCHATA (MUSCOVY DUCK), 103 aa.pcls:TREMBLNEW-ID:G1493809 HISTONE H4-VI - GALLUS GALLUS (CHICKEN), 103 aa | 4E-50 | |
| 6928 | cg43988803 | 464 | CTGCCCCCGGC GCGCTCGTGCA CCT[G/gap]GCCG CTGCCACAGGC GGAGTTTAGC | G | gap | Trp (9099) | Cys (9099) | FRAMES HIFT | homeobo x | Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment). | 1.2E-242 (13q14.1) | 13 |
| 6929 | cg43332152 | 1175 | CAGCTGAGCGC CCTGGCGGCC GGC[G/gap]CCAC GCCCTCTCCGC AGTCCGCGC | G | gap | Arg (9100) | Pro (9100) | FRAMES HIFT | homeobo x | Human Gene SWISSPROT-ID:P36199 HOMEBOX PROTEIN LIM-1 (HOMEBOX PROTEIN LMX-2) - MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND MESOCRICETUS, 406 aa. | 3.4E-227 | 17 |

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|------|------------|------|---|-----------------|-----|---------------|---------------|----------------|--------------|--|----------|----------|
| 6930 | cg41637704 | 1220 | GCGCCGCGGAGA CAAGGGCAGCG GAC[<i>gap</i>]/CJCGCC TGCGGACTTGAG GGACAGTGA | <i>gap</i> | C | Pro | Pro (9101) | FRAMES HIFT | homeobo x | Human Gene SWISSPROT-ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa. | 1.2E-224 | 7 |
| 6931 | cg43983917 | 1204 | CCCGGTGCGGA TCTGGCGGCCTA CA[C[<i>gap</i>]/ACGCT GCGCTAAGCTGC AACGAAAA | C <i>gap</i> | Thr | Asn (9102) | | FRAMES HIFT | homeobo x | Human Gene SWISSPROT-ID:P50458 HOMEBOX PROTEIN LH-2 - HOMO SAPIENS (HUMAN), 423 aa. | 4.3E-216 | |
| 6932 | cg43143467 | 406 | GCAGAACAGCTGA GAGGAACCTGGA GC[A[<i>gap</i>]/CGTTG CTTTTGAGAGAA CTCATTAC | A <i>gap</i> | His | Pro (9103) | | FRAMES HIFT | homeobo x | Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment). | 2.1E-179 | 2 (2q35) |
| 6933 | cg42908326 | 783 | TGTGGCGCACG CGCACCCACCACC TG[C[<i>gap</i>]/ATCCG CACCTGGCCGC GCACGCGCC | C <i>gap</i> | His | Ile (9104) | | FRAMES HIFT | homeobo x | Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa. | 5.8E-136 | 3 |
| 6934 | cg42908326 | 833 | CCTACATGATGT TCCCAGCACCCGC C[C[<i>gap</i>]/TTCGGA CTGCCGCTCGC CACGCTGG | C <i>gap</i> | Phe | Ser (9105) | | FRAMES HIFT | homeobo x | Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa. | 5.8E-136 | 3 |
| 6935 | cg42489148 | 1154 | CACCACAGCCG CCTCCGCCGCC ACC[C[<i>gap</i>]/ACAG CCTCCCCAGCCT CAGCCAGGT | C <i>gap</i> | Pro | His (9106) | | FRAMES HIFT | homeobo x | Human Gene Homologous to SPTREMBL-ID:O00503 CAUDAL-TYPE HOMEBOX PROTEIN 2 - HOMO SAPIENS (HUMAN), 313 aa. | 6E-118 | 13 |

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|------|------------|------|---|-----|---|-----|---------------|----------------|---------------|---|----------|----|
| 6936 | cg42489148 | 872 | GGAACCTGTGC GAGTGGATGCG GAA[gap/G]CCGG CGCAGCAGTCC CTCGGCAGCC | gap | G | Asn | Lys (9107) | FRAMES HIFT | homeobo x | Human Gene Homologous to SPTREMBL-ID:O00503 CAUDAL-TYPE HOMEBOX PROTEIN 2 - HOMO SAPIENS (HUMAN), 313 aa. | 6E-118 | 13 |
| 6937 | cg43983244 | 2275 | TGGTGAGTCCCG GCGACTCCAGCA G[G/gap]CTCCGG CCAGCCTCGCC CACGTTCT | gap | G | Ser | Ser (9108) | FRAMES HIFT | homeobo x | Human Gene Homologous to SWISSPROT-ID:P43271 PAIRED MESODERM HOMEBOX PROTEIN 1 (HOMEBOX PROTEIN MHOM) (HOMEBOX PROTEIN K-2) (RHOX) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 217 aa. | 2.2E-113 | |
| 6938 | cg43932912 | 729 | TGACAGCAAGTC CATTAGCTCAA G[G/gap]CAGAAC TGCCTTAATGT TCATACT | gap | G | Cys | Cys (9109) | FRAMES HIFT | homeobo x | Human Gene Similar to SWISSPROT- ID:P34349 HYPOTHETICAL 30.5 KD PROTEIN C30A5.3 IN CHROMOSOME III - CAENORHABDITIS ELEGANS, 261 aa. | 1.3E-81 | |
| 6939 | cg43988195 | 3178 | TGTCAAATACCA GGAGGGCATCA GC[C/gap]GCAAA CTCCTCTGAGCT GGTGTACC | gap | C | Ala | Ala (9110) | FRAMES HIFT | homeobo x | Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa. | 2.6E-53 | 12 |
| 6940 | cg42503642 | 2466 | ATGCCAATGCAA ACATTATTCTGA [G/gap]GCCAAGC CCGAAGGACCTA GAGTCA | gap | G | Ala | Pro (9111) | FRAMES HIFT | hydrolas e | Human Gene SWISSPROT-ID:Q92995 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T-3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE T-3) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T-3) (DEUBIQUITINATING ENZYME T-3) (ISOPEPTIDASE T-3) (ISOT-3) - HOMO SAPIENS (HUMAN), 863 aa. | 0 | |

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|------|------------|------|--|---|-----|-----|---------------|----------------|------------|---|---------------|----------|
| 6941 | cg42503642 | 2467 | TGCCAATGCAAA CATTATTTCTGA G[G/gap]CCAAGC CCGAAGGACCTA GAGTCAA | G | gap | Ala | Pro (9112) | FRAMES HIFT | hydrolase | Human Gene SWISSPROT-ID:Q92995 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T-3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE T-3) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T-3) (DEUBIQUITINATING ENZYME T-3) (ISOPEPTIDASE T-3) (ISOT-3) - HOMO SAPIENS (HUMAN), 863 aa. | 0 | |
| 6942 | cg43296921 | 405 | TGGAGCCGAAGT TTTCTGGCTCCG G[C/gap]CCGCTG ATGGTCCAGAA GCCAGGA | C | gap | Gly | Gly (9113) | FRAMES HIFT | hydrolase | Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa. | 15 (15q23) | 3.3E-238 |
| 6943 | cg43933380 | 1392 | ACATGTAAGACT CCTTCTGCTGAA A[C/gap]ACAGTA CTGAGAAATTCAG TGAGGAT | C | gap | Val | Phe (9114) | FRAMES HIFT | interferon | Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa. | 6 | 1.4E-261 |
| 6944 | cg43933380 | 300 | ACCTAGGAACCA GGAGTACTGGAT A[C/gap]TGTTCC GTTACTGGTAAC CTATCTG | C | gap | Gln | His (9115) | FRAMES HIFT | interferon | Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa. | 6 | 1.4E-261 |
| 6945 | cg43933380 | 349 | TGGATGTAAAGG TTCATAAGTTAC A[A/gap]TGCTTTT TTTGTTTAAAAA AAAAA | A | gap | Ile | Met (9116) | FRAMES HIFT | interferon | Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa. | 6 | 1.4E-261 |
| 6946 | cg43933380 | 374 | ATGCTTTTTTGT TTAAAAA A/gap]AAAGTCTG TACTTTACAAGC CAAAA | A | gap | Phe | Phe (9117) | FRAMES HIFT | interferon | Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa. | 6 | 1.4E-261 |

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|------|------------|------|--|---|-----|---------------|----------------|------------|---|----------|---------------|
| 6947 | cg43933380 | 377 | CTTTTTTTGTTTA AAAAAAAAAAAAAA[A/gap]GTCGTAC TTTACAAGCCAA AAGTG | A | gap | Phe (9118) | FRAMES HIFT | interferon | Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa. | 1.4E-261 | 6 |
| 6948 | cg43931810 | 819 | GAACACAGAGGG CATAGCGTGGTG AG[C/gap]GTCCG CTTCCTCCGTG AAGGTAAT | C | gap | Arg (9119) | FRAMES HIFT | interferon | Human Gene SWISSPROT-ID:Q14653 INTERFERON REGULATORY FACTOR 3 (IRF-3) - HOMO SAPIENS (HUMAN), 427 aa. | 1.2E-240 | 19 |
| 6949 | cg43956260 | 570 | AGTGTTACCTGG AACTTCGGTGGG G[G/gap]GCCCAG GCCCTGAAAGTA CCTGACC | G | gap | Pro (9120) | FRAMES HIFT | interferon | Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa. | 2.5E-215 | 14 |
| 6950 | cg43956260 | 571 | GTGTTACCTGGA ACTTCGGTGGG GG[G/gap]CCCAG GCCCTGAAAGTA CCTGACCA | G | gap | Gly (9121) | FRAMES HIFT | interferon | Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa. | 2.5E-215 | 14 |
| 6951 | cg43926568 | 1529 | CTCTTCAGGGCT TCCTCATTCTGG C[C/gap]TTTCAG GTGTTTCACATA GGCTAGT | C | gap | Ala (9122) | FRAMES HIFT | interferon | Human Gene Homologous to SPTREMBL-ID:Q13325 RETINOIC ACID- AND INTERFERON-INDUCIBLE 58K PROTEIN RI58 - HOMO SAPIENS (HUMAN), 482 aa. | 4.8E-141 | 10 (10q23) |

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|------|------------|------|---|---|-----|-----|---------------|----------------|-------------|---|--------|---------------|
| 6952 | cg43922672 | 1616 | GGGACCACGCA CCATGATGCCTT GG[C/gap]CATCC TCCGCCAAGCTC GAGAGCCC | C | gap | Ala | Ala (9123) | FRAMES HIFT | interleukin | Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa. | 0 | 15 |
| 6953 | cg43922672 | 1687 | AAGGAAGCTGAC TCCAGAGGCCAT G[C/gap]CCGACC TCAACTCCTCCA CTGACTC | C | gap | Pro | Pro (9124) | FRAMES HIFT | interleukin | Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa. | 0 | 15 |
| 6954 | cg43922672 | 1760 | AGTGATGTTTCT GTAGAATCTACA G[C/gap]AGAGGC CACAGTCTGCAC GGTGACA | C | gap | Ala | Glu (9125) | FRAMES HIFT | interleukin | Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa. | 0 | 15 |
| 6955 | cg43930054 | 1773 | CGATCTGGGCCA GTGGATCACTGC T[G/gap]GCCAAC AGCCGCGCCAC TTCGCTGT | G | gap | Ala | Ala (9126) | FRAMES HIFT | isomerase | Human Gene SWISSPROT-ID:P34949 MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNANOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa. | 2E-222 | 15 (15q22) |
| 6956 | cg43930054 | 1818 | CGCTGTTGGAAC CCATCTTCCCCC A[G/gap]GCATAC TGCTGCACCGCA CAGGAAA | G | gap | Ala | Ala (9127) | FRAMES HIFT | isomerase | Human Gene SWISSPROT-ID:P34949 MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNANOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa. | 2E-222 | 15 (15q22) |
| 6957 | cg43930054 | 633 | AGCAGGCACGG AATATCAGCAGG TC[C/gap]TTCGG CTCAGTAAGCTT CAGTGAGA | C | gap | Lys | Lys (9128) | FRAMES HIFT | isomerase | Human Gene SWISSPROT-ID:P34949 MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNANOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa. | 2E-222 | 15 (15q22) |

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|------|------------|------|---|---|-----|-----|---------------|----------------|--------|---|---|----|
| 6958 | cg43297395 | 1744 | GCGCCCCAGCT GCCTCTGGCTGT GG[C/gap]CACAG ACAACTTCATCA GCACCTGT | C | gap | Ala | Ala (9129) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:Q15589 TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 626 aa. | 0 | 9 |
| 6959 | cg43259301 | 1495 | GCCCCATCCCCA TCCACACAAGTA C[A/gap]GCGCAG CGTGTCGGCCAA TCCCAAG | A | gap | Gln | Arg (9130) | FRAMES HIFT | kinase | Human Gene SPTREMBL-ID:Q15524 SERINE/THREONINE PROTEIN KINASE - HOMO SAPIENS (HUMAN), 745 aa. | 0 | 13 |
| 6960 | cg43299934 | 1634 | TGACCACAATGA CCTCCACGGTGA T[G/gap]CCATCA GGCAGCATGAG CCAGGATG | G | gap | Gly | Gly (9131) | FRAMES HIFT | kinase | Human Gene SPTREMBL-ID:Q92667 KINASE A ANCHOR PROTEIN - HOMO SAPIENS (HUMAN), 903 aa. | 0 | 17 |
| 6961 | cg43336163 | 2426 | CTTCCCCTCTAG ATGGCCCCCG GC[C/gap]GTGGC TGTGGGCCAGT GCCCGCTGG | C | gap | Val | Trp (9132) | FRAMES HIFT | kinase | Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA I}} - HOMO SAPIENS, 616 aa. | 0 | 19 |
| 6962 | cg43336163 | 2464 | CAGTGCCCGCT GGTGGGGCCAG GCC[C/gap]CATG CACCGCCGCCA CCTGCTGCTC | C | gap | Pro | Pro (9133) | FRAMES HIFT | kinase | Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA I}} - HOMO SAPIENS, 616 aa. | 0 | 19 |
| 6963 | cg43336163 | 2465 | AGTGCCCGCTG GTGGGGCCAGG CCC[C/gap]ATGC ACCGCCGCCAC CTGCTGCTCC | C | gap | Met | Cys (9134) | FRAMES HIFT | kinase | Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA I}} - HOMO SAPIENS, 616 aa. | 0 | 19 |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|--------|---|---|---------------|
| 6964 | cg43336163 | 944 | CCGACTTCTTGC AGTGGCGGAG CC[C/gap]ATCGT GGTGAGGCTTAA GGAGGTCC | C | gap | Ile | Ser (9135) | FRAMES HIFT | kinase | Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa. | 0 | 19 |
| 6965 | cg44929725 | 2841 | AAGAGCAGAATC CAGATATTGTTT C[gap/C]AGAAAA AAACCAGCAAC TGAAGTG | gap | C | Ser | Ser (9136) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa. | 0 | 1 (1p31.3) |
| 6966 | cg44929725 | 2851 | TCCAGATATTGT TTCAGAAAAA A[gap/A]CCAGCA ACTGAAGTGGAC CCCACAC | gap | A | Pro | Thr (9137) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa. | 0 | 1 (1p31.3) |
| 6967 | cg44929725 | 2856 | ATATTGTTTCAG AAAAAAACCAG C[gap/C]AACTGA AGTGGACCCAC ACATTTT | gap | C | Ala | Ala (9138) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa. | 0 | 1 (1p31.3) |
| 6968 | cg44929725 | 2864 | GAGCTCTGCAG GTATGACCCCGA AG[G/gap]GGACA ATACAGGGGAG CAGGTGGCT | G | gap | Gly | Gly (9139) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa. | 0 | 1 (1p31.3) |
| 6969 | cg44929725 | 2865 | AGCTCTGCAGGT ATGACCCCGAAG G[G/gap]GACAAT ACAGGGGAGCA GGTGGCTG | G | gap | Asp | Thr (9140) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa. | 0 | 1 (1p31.3) |
| 6970 | cg44929725 | 2866 | GCTCTGCAGGTA TGACCCCGAAG GG[G/gap]ACAAT ACAGGGGAGCA GGTGGCTGT | G | gap | Asp | Thr (9141) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa. | 0 | 1 (1p31.3) |

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|------|------------|------|--|---|-----|-----|---------------|----------------|--------|--|---|---------------|
| 6971 | cg43988890 | 150 | GACATGGAGCC CGAGCGCGCG CCG[G/gap]CGCC GGCCCGCGGCC TCTTCGGCTG | G | gap | Arg | Ala (9142) | FRAMES HIFT | kinase | Human Gene SWISSNEW-ID:P15056 B- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (P94) - HOMO SAPIENS (HUMAN), 765 aa. pcis:SWISSPROT-ID:P15056 B-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (P94) - HOMO SAPIENS (HUMAN), 765 aa. | 0 | 7 (7q34) |
| 6972 | cg43257904 | 505 | GGCGGGGCGCT AAGGCACAAGG CGG[G/gap]CTGC GCTGAGTAGGCA GGCAGGGCAA | G | gap | Ala | Ala (9143) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa. | 0 | X (Xp11.4) |
| 6973 | cg43257904 | 807 | TGTAAGGCAGTG AGCCAGTCATAA G[C/gap]TCGTAG AGCACAAACCCCG TAGGCAT | C | gap | Glu | Asp (9144) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa. | 0 | X (Xp11.4) |
| 6974 | cg43016269 | 1920 | GCAAAGGAGCTA GAAGAGGAGATT A[C/gap]CTTACG GAAAAGTGTGGA ATCAGCA | C | gap | Thr | Thr (9145) | FRAMES HIFT | kinase | Human Gene SPTREMBL-ID:Q28021 RHO-ASSOCIATED KINASE - BOS TAURUS (BOVINE), 1388 aa. | 0 | |
| 6975 | cg43263359 | 1179 | AGATGGGGCCC CGCAGCGCGCG AGA[G/gap]CTCG GCAAGTCGTCCA CCTCGTCCT | G | gap | Ser | Ser (9146) | FRAMES HIFT | kinase | Human Gene SPTREMBL-ID:Q13476 KINASE SUPPRESSOR OF RAS-1 (KSR1) - HOMO SAPIENS (HUMAN), 635 aa (fragment). | 0 | |
| 6976 | cg43263359 | 1239 | CTGCCCTCTGACT TGCCAGCCTCTG G[C/gap]TCCTCA GCCTCCGCTTCG TGAGCTT | C | gap | Glu | Asp (9147) | FRAMES HIFT | kinase | Human Gene SPTREMBL-ID:Q13476 KINASE SUPPRESSOR OF RAS-1 (KSR1) - HOMO SAPIENS (HUMAN), 635 aa (fragment). | 0 | |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|--------|--|----------|----|
| 6977 | cg43947749 | 1457 | CTCATCCCTCCT CACTTGAGGTCC C[C/gap]AGCGGG CACTACCACCCT CACCCCG | C | gap | Pro | Gln (9148) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa. | 5.6E-267 | 19 |
| 6978 | cg43947749 | 1457 | TCATCCCTCCTC ACTTGAGGTCCC C[gap/C]AGCGGG CACTACCACCCT CACCCCG | gap | C | Pro | Pro (9149) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa. | 5.6E-267 | 19 |
| 6979 | cg43947749 | 1461 | TCCCTCCTCACT TGAGGTCCCCAG C[G/gap]GGCACT ACCACCCCTCACC CCGTCCT | G | gap | Gly | Ala (9150) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa. | 5.6E-267 | 19 |
| 6980 | cg43947749 | 1463 | CCTCCTCACTTG AGGTCCCCAGC GG[G/gap]CACTA CCACCCCTCACC CGTCCTCA | G | gap | Gly | Ala (9151) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa. | 5.6E-267 | 19 |
| 6981 | cg43947829 | 910 | TGTTCAAGTACT TCTCTGAGCATT G[G/gap]CCTCTG GCTGGGATTATG CTTCAAC | G | gap | Pro | Gln (9152) | FRAMES HIFT | kinase | Human Gene TREMBLNEW- ID:G2979628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa. | 1.5E-217 | |
| 6982 | cg38438124 | 1248 | GAGAGCGATGG CACCCACCCGGT GG[G/gap]AACCC CCCCAGATAGCC CCGGGAAT | G | gap | Gly | Glu (9153) | FRAMES HIFT | kinase | Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KI-ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P-5- KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa. | 2.8E-216 | 10 |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|--------|---|----------|---------------|
| 6983 | cg43917871 | 1455 | ATTGGGGCTGCT GACGGGCGTAC TG[C/gap]CCCCCT GGCATGCTAGAT GAACCCAT | C | gap | Gly | Ala (9154) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa. | 2E-215 | 11 (20p13) |
| 6984 | cg44131752 | 1284 | TGCCCCCTGCCCA CCAGGTACTGG GG[G/gap]CCTGT GGCAGCAAGATA GGGGGAGA | G | gap | Pro | Leu (9155) | FRAMES HIFT | kinase | Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa. | 7.8E-173 | 16 |
| 6985 | cg44000392 | 347 | CGGCATGGAGA AGGACGGCCTG TGC[gap]C/GCGC TGACCAGCAGTA CGAATGCCGT | gap | C | Arg | Pro (9156) | FRAMES HIFT | kinase | Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa. | 4.1E-172 | 7 |
| 6986 | cg43257282 | 1015 | ATGGCTGTGCGA GGCCGGGCTGC GC[C/gap]TGCTG CACTTCCTGTTC ATGTACGA | C | gap | Leu | Cys (9157) | FRAMES HIFT | kinase | Human Gene Homologous to SPTREMBL-ID:Q15130 CDC2-RELATED KINASE - HOMO SAPIENS (HUMAN), 316 aa. | 2.9E-147 | 16 |
| 6987 | cg44016530 | 578 | TGTAGTCTCTTT GGTGATCTCATC T[G/gap]CTTTTCT GCTCGAGTGATG ACAGCC | G | gap | Ala | Glu (9158) | FRAMES HIFT | kinase | Human Gene Homologous to SPTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment). | 1.7E-129 | 12 |
| 6988 | cg44016530 | 583 | TCTCTTTGGTGA TCTCATCTGCTT TT[gap]CTGCTC GAGTGATGACAG CCTTGAA | T | gap | Arg | Arg (9159) | FRAMES HIFT | kinase | Human Gene Homologous to SPTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment). | 1.7E-129 | 12 |
| 6989 | cg43022553 | 502 | TGCTGGGGCTG AGAGAGGGCTG CAA[G/gap]CTGC TCGTGCACGGCT TTGAGCTGC | G | gap | Leu | Leu (9160) | FRAMES HIFT | kinase | Human Gene Homologous to SPTREMBL-ID:Q90971 KINASE - GALLUS GALLUS (CHICKEN), 729 aa. | 1E-102 | |

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|------|------------|------|---|---|-----|-----|---------------|----------------|--------|--|---------|----|
| 6990 | cg43022553 | 754 | CATCCTGGAGCT TGCGGGCCCATG GC[C/gap]ACCCAC CTCATGGTCAGG AGGGTTGT | C | gap | Val | Val (9161) | FRAMES HIFT | kinase | Human Gene Homologous to SPTREMBL-ID:Q90971 KINASE - GALLUS GALLUS (CHICKEN), 729 aa. | 1E-102 | |
| 6991 | cg43952004 | 2215 | GCAGAGGAAATC AAACCCCTGCTT G[G/gap]CCACAG CCCCTAGTGTGT CAGCTAT | G | gap | Ala | Ala (9162) | FRAMES HIFT | kinase | Human Gene Similar to TREMBLNEW- ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa. | 6.3E-94 | 14 |
| 6992 | cg43966625 | 270 | TTCACCTTCCTC AGGCAGGAGCT GC[C/gap]TGTGC GCCTGGCCAAACA TCATGAAA | C | gap | Pro | Leu (9163) | FRAMES HIFT | kinase | Human Gene Similar to SWISSPROT- ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa. [pcis:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa. | 3.2E-89 | 17 |
| 6993 | cg43917718 | 694 | AAAGGTGGGT GGAATGCTGGCT CG[G/gap]CCCTG CCAGTCACTGGG TGGCAGCA | G | gap | Pro | Arg (9164) | FRAMES HIFT | kinase | Human Gene Similar to SPTREMBL- ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa. | 1.4E-79 | 17 |
| 6994 | cg41501665 | 381 | GCCAAGGCGC GCTGCTGGGA CCA[G/gap]CGGC CTCAAGCGCCG CTTCAGCCGC | G | gap | Ser | Thr (9165) | FRAMES HIFT | kinase | Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.7E-76 | |
| 6995 | cg43923082 | 257 | AGGAGACGGGT GCTTTGGCTGCG GC[C/gap]AAAGT CATTGAAACCAA GAGTGAGG | C | gap | Lys | Lys (9166) | FRAMES HIFT | kinase | Human Gene Similar to SPTREMBL- ID:O08815 PROTEIN KINASE - RATTUS NORVEGICUS (RAT), 1206 aa. | 9.4E-58 | |

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| 6996 | cg44021449 | 3311 | TTGCTGCTGCAG CAAGGGCTACTG C[C/gap]ACACAG TAGCTGTTAGCC CACAGGC | C | gap | Pro | His (9167) | FRAMES HIFT | kinaserec eptor | Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa. | 0 | 15 |
| 6997 | cg43322545 | 1486 | GTACCCCTGGAG GCCTGGCGCCC AG[G/gap]GGAAG CACAGCCAGTCC ACCAGCTG | G | gap | Gly | Gly (9168) | FRAMES HIFT | kinaserec eptor | Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. pcis:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. | 0 | 19 (19q13.1) |
| 6998 | cg43322545 | 1487 | TACCCCTGGAGG CCTGGCGCCCA GG[G/gap]GAAGC ACAGCCAGTCCA CCAGCTGG | G | gap | Glu | Lys (9169) | FRAMES HIFT | kinaserec eptor | Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. pcis:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. | 0 | 19 (19q13.1) |
| 6999 | cg43991478 | 544 | CACAGGGACATT TGTCGGGCCGT GG[C/gap]AGCCT CTCCCTCGTTC CAGCAACT | C | gap | Leu | Leu (9170) | FRAMES HIFT | kinaserec eptor | Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa. | 0 | |

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| 7000 | cg43998555 | 1379 | GGTCCGCGCCT GGCTGGAAGCC AAG[G/gap]CCTT CAGCCCGCGGA TCGTGGAGAA | G | gap | Ala | Pro (9171) | FRAMES HIFT | kinasereceptor | Human Gene Similar to SWISSPROT- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 - HOMO SAPIENS (HUMAN), 822 aa pcis: SPTREMBL- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE - HOMO SAPIENS (HUMAN), 822 aa | 1.2E-99 | 11 |
| 7001 | cg43942537 | 2552 | TTCTTAATTGTTT TGCCCTTTGGC [C/gap]AAATAAG AGGTAGATTTT GTTTCA | C | gap | Gly | Ala (9172) | FRAMES HIFT | kinesin | Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa pcis: SWISSPROT-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa | 0 | 10 |
| 7002 | cg43987378 | 830 | GAGCTGGAAGA GCGGCTGAGCA CGC[gap]CJAGGA GGCTTGGTGC AAGAGCTTCA | gap | C | Gln | Pro (9173) | FRAMES HIFT | kinesin | Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment). | 1.5E-254 | 6 |
| 7003 | cg43987378 | 931 | TAGAGGAGAAG GAGAGGAGGCT GCA[G/gap]ACAT CAGAAAGCAGCC CTGTCAAGCA | G | gap | Thr | His (9174) | FRAMES HIFT | kinesin | Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment). | 1.5E-254 | 6 |
| 7004 | cg43953676 | 552 | CTGTGTGCAGAC CGGGGTGACCG GG[G/gap]JTCACC AAGTCTGTTCAC CTGTGCGA | G | gap | Val | Ser (9175) | FRAMES HIFT | laminin | Human Gene SWISSPROT-ID:P11047 LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN) - HOMO SAPIENS (HUMAN), 1609 aa. | 0 | 1 (1q31) |

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|------|------------|------|--|-----|-----|---------------|-----|----------------|---------|---|---|----------|
| 7005 | cg43983535 | 1209 | CTGTTGCAAAAT CAGCATGATTGA T[G/gap]CGAGCC ATGTAAAAAGC AAGCCGG | G | gap | Arg (9176) | Arg | FRAMES HIFT | laminin | Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa. | 0 | 6 (6q22) |
| 7006 | cg43983535 | 338 | GCAAAATTAAACC TCCAGTGGCTTG C[C/gap]TGTGCC TTTGGTGAGCTT CAGGGAT | C | gap | Gln (9177) | Gln | FRAMES HIFT | laminin | Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa. | 0 | 6 (6q22) |
| 7007 | cg43983535 | 722 | GAAGAACTCCAG TCGTTGTAGTTG T[gap/C]GCGGAA TTCAAATTCTACA AGAAGG | gap | C | Thr (9178) | Asp | FRAMES HIFT | laminin | Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa. | 0 | 6 (6q22) |
| 7008 | cg43983535 | 726 | GAAGTCCAGTCG TTGTAGTTGTGC G[G/gap]AATTCA AATTCTACAAGA AGGTCCA | G | gap | Phe (9179) | Phe | FRAMES HIFT | laminin | Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa. | 0 | 6 (6q22) |
| 7009 | cg43296393 | 1540 | GGCCTACCTGG CTGCCCTCACCC AG[gap/C]TCCGC GCTCTGGTCTAC TACGCCCA | gap | C | Ala (9180) | Val | FRAMES HIFT | lipase | Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa. | 0 | |
| 7010 | cg43296393 | 1620 | TACTCTTCTTTGA GGGCGACGAGG G[G/gap]CTCACC GCCGACTTCCTC CGGGAGT | G | gap | Ser (9181) | Leu | FRAMES HIFT | lipase | Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa. | 0 | |
| 7011 | cg43296393 | 1636 | CGACGAGGGGC TCACCGCCGACT TC[C/gap]TCCGG GAGTATGTCACG CTGCATAA | C | gap | Ser (9182) | Leu | FRAMES HIFT | lipase | Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa. | 0 | |

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|------|------------|------|---|------------|------------|-----|---------------|----------------|------------------|---|---------------|----|
| 7012 | cg43296393 | 2183 | AACGGAGCCTG GAGCTGTGGCC GCG[<i>gap</i>][CCCC AGCAGGCACCC CGCTCGCGGT | <i>gap</i> | C | Arg | Arg (9183) | FRAMES HIFT | lipase | Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa. | 0 | 0 |
| 7013 | cg43921881 | 455 | GGGGAGCTGG ACCTGGCGGG GAG[C/ <i>gap</i>][CCCC TCAGCTGAGGAC TCGACATTG | C | <i>gap</i> | Ala | Leu (9184) | FRAMES HIFT | MHC | Human Gene Similar to SWISSPROT- ID:P46379 LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3) - HOMO SAPIENS (HUMAN), 1132 aa. | 2.6E-63 | 14 |
| 7014 | cg43921881 | 512 | GACGGAGCCAC GGATGAGGCCT GCC[C/ <i>gap</i>][AGGA CCAGGGGAAG GTGGCCTCTG | C | <i>gap</i> | Gly | Gly (9185) | FRAMES HIFT | MHC | Human Gene Similar to SWISSPROT- ID:P46379 LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3) - HOMO SAPIENS (HUMAN), 1132 aa. | 2.6E-63 | 14 |
| 7015 | cg43957213 | 580 | GTGGGGTTTCCC ACCCAAGTTCAA G[<i>gap</i>]/GJAGGAGG AGCAGACATCTG TGCTACT | <i>gap</i> | G | Leu | Pro (9186) | FRAMES HIFT | misc_cha nnel | Human Gene SWISSNEW-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa. ipcis:SWISSPROT-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa. ipcis:TREMBLNEW-ID:E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 669 aa. | 0 (1p36.1) | 1 |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|------------------|---|----------|-----------------|
| 7016 | cg43924981 | 481 | CCACCGCGTGC CCTTCCACCGTG TG[G/gap]ACACC ATCTCCGTCAAT GGCTCTGT | G | gap | Asp | Thr (9187) | FRAMES HIFT | misc_cha nnel | Human Gene Homologous to SPTREMBL-ID:P97840 URATE TRANSPORTER/CHANNEL - RATTUS NORVEGICUS (RAT), 322 aa. | 2.4E-130 | |
| 7017 | cg43309398 | 825 | TGGAGAAATGGGA GATTGTGAGTGC A[gap/A]CAGGGA GCAAAAGGAAACA GAACCGA | gap | A | Gln | Thr (9188) | FRAMES HIFT | misc_cha nnel | Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa. | 2.1E-67 | 15 (15q24) |
| 7018 | cg43991048 | 6715 | TTGCGAGGGTC GAGCAATTTGCT GG[G/gap]TTTCT GCCTCTGCGTTT CCCATAAAT | G | gap | Thr | Thr (9189) | FRAMES HIFT | nuc_rec pt | Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa. | 0 | 17 |
| 7019 | cg30421838 | 2225 | CTGGAGGAGGA GCCGCGGCTTG TCC[C/gap]GCCG GGGCGGCAGC AGGAGGCGTC | C | gap | Ala | Pro (9190) | FRAMES HIFT | nuc_rec pt | Human Gene SWISSNEW-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa. pcis:SWISSPROT-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa. | 0 | 11 (11q22) |
| 7020 | cg43249083 | 2410 | CAAGCTGCTGCT CAAGCTGCCGG AC[C/gap]TGCGG ACCTGAACAAC ATGCATTC | C | gap | Leu | Cys (9191) | FRAMES HIFT | nuc_rec pt | Human Gene SWISSPROT-ID:P20393 V- ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa. | 0 | 17 (17q11.2) |
| 7021 | cg43949686 | 1962 | TATGACATGATG GAGGGCCCGCT GG[G/gap]CAGAG CCATCTCCTCAG CCAGCATC | G | gap | Gly | Ala (9192) | FRAMES HIFT | nuc_rec pt | Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa. | 2.4E-167 | |

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|------|------------|------|---|---|-----|-----|---------------|----------------|---------------|---|----------|----|
| 7022 | cg43949686 | 2149 | GGGAGGCCAAG CTCCTAAAGCGG GA[G/gap]GGCAC GCCTCCGCCCC CACCGCCCT | G | gap | Gly | Ala (9193) | FRAMES HIFT | nuc_rec pt | Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa. | 2.4E-167 | |
| 7023 | cg43949686 | 2207 | CCTGACCGAGG CCTACAAGACGC AG[G/gap]CCCTG GGCCCCCTGAA GCTGAAGCC | G | gap | Ala | Pro (9194) | FRAMES HIFT | nuc_rec pt | Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa. | 2.4E-167 | |
| 7024 | cg43949686 | 2308 | ATGAGATCCCGC GCGAGGAGCTG CG[G/gap]CACAC GCCCCGAGCTGC CCCTGGCCCC | G | gap | His | Thr (9195) | FRAMES HIFT | nuc_rec pt | Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa. | 2.4E-167 | |
| 7025 | cg44128653 | 1705 | ATGAGTGCCCTG CCGTCCC GCCA GC[C/gap]TCCGG AGCTCTCGTCCA GATACTTG | C | gap | Gly | Ala (9196) | FRAMES HIFT | nuclease | Human Gene SWISSNEW-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.pclis:SWISSPROT- ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa. | 1.4E-203 | 19 |
| 7026 | cg43947341 | 295 | GCTCTTACTTTC TGAGGGCCCCAG GC[C/gap]TGGGC ATAAGGCCAGAT CTTCTCTT | C | gap | Gly | Ala (9197) | FRAMES HIFT | nuclease | Human Gene Homologous to SWISSPROT-ID:P07992 DNA EXCISION REPAIR PROTEIN ERCC-1 - HOMO SAPIENS (HUMAN), 297 aa. | 1.1E-115 | |

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| 7027 | cg43969123 | 2515 | CATCGGCAAGAA CCACGTGGCAGT G[C/gap]CCACAC ACTTCTTCAAGG TGCTGAT | C | gap | Pro | Pro (9198) | FRAMES HIFT | nuclease | Human Gene Similar to SWISSPROT- ID:P38447 ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G) - BOS TAURUS (BOVINE), 299 aa. | 1.2E-65 | 9 |
| 7028 | cg43969123 | 2517 | TCGGCAAGAACC ACGTGGCAGTG CC[C/gap]ACACA CTTCTTCAAGGT GCTGATCC | C | gap | Thr | His (9199) | FRAMES HIFT | nuclease | Human Gene Similar to SWISSPROT- ID:P38447 ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G) - BOS TAURUS (BOVINE), 299 aa. | 1.2E-65 | 9 |
| 7029 | cg43242829 | 570 | GCGTGCTCAGCT GGCTTCGTGGAC G[G/gap]CACAGC CCTGGCGGACC TCAGCCAT | G | gap | Gly | Ala (9200) | FRAMES HIFT | nuclease | Human Gene Similar to SWISSPROT- ID:Q17533 RIBONUCLEASE PH-LIKE PROTEIN B0564.1 - CAENORHABDITIS ELEGANS, 312 aa. | 2E-50 | |
| 7030 | cg43951535 | 1528 | ATCTGGTGGTGA ACTACAGCGAGT A[G/gap]CTTTTA GCCCTTTGCTTG GGCAAAC | G | gap | Ala | Leu (9201) | FRAMES HIFT | nuclease nhib | Human Gene SPTREMBL-ID:Q13181 RNASE L INHIBITOR - HOMO SAPIENS (HUMAN), 599 aa. | 2.5e-315 | 4 (4q31) |
| 7031 | cg43918816 | 581 | GGGACCCCATC CCCATCTCGAGG AG[G/gap]CCCCG CCCATTTGTCTT CCTCCGCC | G | gap | Pro | Leu (9202) | FRAMES HIFT | oncogen e | Human Gene SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa. | 0 | 19 |
| 7032 | cg44012756 | 5289 | TGCTGCTGTCCC GCAAGCGCCGG CG[G/gap]CAGCA TGCCACAGCTCTG GTTCCCTG | G | gap | Gln | Ser (9203) | FRAMES HIFT | oncogen e | Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa. | 0 | |
| 7033 | cg42732993 | 592 | CACTGGATTAA GCAGAGTTCAAA A[G/gap]CCCTTC AGCGCCAGTA GCATCTGA | G | gap | Ala | Pro (9204) | FRAMES HIFT | oncogen e | Human Gene Homologous to SPTREMBL-ID:Q13692 BCR/ABL FUSION PROTEIN - HOMO SAPIENS (HUMAN), 284 aa (fragment). | 6E-150 | |

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| 7034 | cg43918770 | 4789 | AGAGGATCTGGAG CAGCCAAGGAG AC[G/gap]GCAGC AGCCAGCCTGAT ACGATTTC | G | gap | Gly | Ala (9205) | FRAMES HIFT | oncogen e | Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa. | 1.6E-140 | 5 |
| 7035 | cg43918770 | 4790 | GAGGATCTGGAC AGCCAAGGAGA CG[G/gap]CAGCA GCCAGCCTGATA CGATTTC | G | gap | Gly | Ala (9206) | FRAMES HIFT | oncogen e | Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa. | 1.6E-140 | 5 |
| 7036 | cg43918770 | 4821 | GCCAGCCTGATA CGATTTCATCG C[C/gap]TCACGG ACGCTCTCAGAAC ACGCTGG | C | gap | Ser | His (9207) | FRAMES HIFT | oncogen e | Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa. | 1.6E-140 | 5 |
| 7037 | cg43297056 | 996 | AGACTTCCGGAC TTTCTTGATGGG G[gap/C]TCCGCC GCAGCCCAGGC TTCCTCTT | gap | C | Thr | Ser (9208) | FRAMES HIFT | oncogen e | Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa. | 1.9E-103 (20q13.1) | 20 |
| 7038 | cg43292762 | 1145 | AGACTACTGTAT CAGGGACCCGAG AG[G/gap]CAGGC TCCCTGGGTACA GCAGGCCG | G | gap | Ala | Gln (9209) | FRAMES HIFT | oncogen e | Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa. | 3E-84 7 (7q31) | 7 (7q31) |
| 7039 | cg43307658 | 1767 | AGACTTCCCTCCC CAACCCGGCCAC GC[C/gap]ACACC TGGGAGTGGCA CAGCTGCCA | C | gap | His | Thr (9210) | FRAMES HIFT | oxidase | Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa. | 0 | 15 |

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| 7040 | cg43307658 | 1853 | ACGACCTACTGG ATGCAGCCACAG G[C/gap]AAGAAG GTGCCGAGGG CCACAAGG | C | gap | Lys | Arg (9211) | FRAMES HIFT | oxidase | Human Gene SPTREMBL-ID:Q8397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa. | 0 | 15 |
| 7041 | cg44028217 | 584 | CCATGGAGTAGA TCTGCAGGCGGT A[gap/G]CTGCCG TTGTGGCCCCAG GGGTTCT | gap | G | Tyr | Leu (9212) | FRAMES HIFT | oxidase | Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa. | 0 7 (7q31) | |
| 7042 | cg43969851 | 1187 | CAGAGGCCCCAC ATCTCCAGCTGC AA[G/gap]CTGGG CCCCCAGGTGTC ACTGGACC | G | gap | Leu | Trp (9213) | FRAMES HIFT | oxidase | Human Gene TREMBLNEW- ID:G1890108 LYSYL OXIDASE- RELATED PROTEIN - HOMO SAPIENS (HUMAN), 774 aa. | 0 | |
| 7043 | cg43972840 | 929 | AGACAAAGGTGC CCTGGAGGGCA GC[A/gap]GCTGT CCCTTCCGAACA GCTATGGC | A | gap | Ser | Ala (9214) | FRAMES HIFT | oxygenase | Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa. | 4.6E-168 (16p13.3) | 16 (16p13.3) |
| 7044 | cg43972840 | 953 | CAGCTGTCCCTT CCGAACAGCTAT G[G/gap]CTGTGC TGAGGAAGCCCA GCCTCCA | G | gap | Ala | Leu (9215) | FRAMES HIFT | oxygenase | Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa. | 4.6E-168 (16p13.3) | 16 (16p13.3) |
| 7045 | cg43972840 | 1002 | CAGTTCATCCTG GCCGCTGGTGT GG[C/gap]CCTAG CTGCTGGACTCT TGGCCTGG | C | gap | Ala | Ala (9216) | FRAMES HIFT | oxygenase | Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa. | 4.6E-168 (16p13.3) | 16 (16p13.3) |

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| 7046 | cg43972840 | 753 | AAGACCAAGAG AGGATCGTGA GG[A/gap]GGCCA ACAAGGCTTTTG AGTATAAC | A | gap | Glu | Gly (9217) | FRAMES HIFT | oxygenase | Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa. | 4.6E-168 | 16 (16p13.3) |
| 7047 | cg43972840 | 913 | TCTACGCTGCTG AACAAAGACAAAG GT[gap]GCCCTG GAGGGCAGCAG CTGTCCCT | T | gap | Ala | Pro (9218) | FRAMES HIFT | oxygenase | Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa. | 4.6E-168 | 16 (16p13.3) |
| 7048 | cg44010395 | 718 | GGGAGCGGGTG TTGAGTGGGG CTT[C/gap]CCTC TGGGAGTCTCCA CGGGGGCAG | C | gap | Gly | Gly (9219) | FRAMES HIFT | oxygenase | Human Gene SWISSNEW-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.[pcis:SWISSPROT-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa. | 5.2E-151 | 22 (22q12) |
| 7049 | cg44010395 | 772 | CTTGCACTTTGT TGCTGGCCCCGCT G[G/gap]CGAAGC CCTGGTGCCCCGT GAGGGGC | G | gap | Arg | Arg (9220) | FRAMES HIFT | oxygenase | Human Gene SWISSNEW-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.[pcis:SWISSPROT-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa. | 5.2E-151 | 22 (22q12) |
| 7050 | cg43916857 | 776 | GCGCCCTCATCG AGTGGATCCGCA G[G/gap]AACAAAG TTTGCTTTCT GGAAATC | G | gap | Asn | Thr (9221) | FRAMES HIFT | peptidase | Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa. | 3.4E-96 | 17 |
| 7051 | cg43254736 | 692 | CATCTGGGGCTG TGCTGATGTCGT G[G/gap]CGAATG CCTTTGACTGAG ATCCGGG | G | gap | Arg | Arg (9222) | FRAMES HIFT | peptidase | Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa. | 1.1E-67 | |

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| 7052 | cg42691989 | 846 | CGAAGCCACATT CTCAATCAGCAC G[G/gap]CCCTGC CCCGGAACGTAT TGAAATC | G | gap | Ala | Ala (9223) | FRAMES HIFT | peroxidase | Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa. | 8.9E-101 | 14 (14q24.1) |
| 7053 | cg40084915 | 4336 | CTCAGCAAAAAGC CAGGCCTTTGGG G[G/gap]CCCTCA TGGGCTCTGCG CATTGGT | G | gap | Ala | Ala (9224) | FRAMES HIFT | phosphatase | Human Gene SPTREMBL-ID:O00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR - HOMO SAPIENS (HUMAN), 1436 aa. | 0 | 1 |
| 7054 | cg42548845 | 2808 | TGCGAGAACTGC TGAAAAATTCAG C[A/gap]AAAAAAT CATTGGATGAG AATATT | A | gap | Gln | Gln (9225) | FRAMES HIFT | phosphatase | Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment). | 0 | |
| 7055 | cg42548845 | 2814 | AACTGCTGAAAA ATTCAGCAAAA A[A/gap]TCATTG GATGAGAAATATT CTAGCT | A | gap | Asn | Ile (9226) | FRAMES HIFT | phosphatase | Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment). | 0 | |
| 7056 | cg43139469 | 885 | TGGATAGCGACA ATCAATGACATA A[A/gap]ACTTCTC AATCAGACCCCTG GAACCTT | A | gap | Phe | Phe (9227) | FRAMES HIFT | phosphatase | Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa. | 7E-259 | 5 (5q31) |
| 7057 | cg43139469 | 886 | GGATAGCGACAA TCAATGACATAA A[A/gap]CTTCTCA ATCAGACCCCTGG AACTTC | A | gap | Phe | Phe (9228) | FRAMES HIFT | phosphatase | Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa. | 7E-259 | 5 (5q31) |

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|------|------------|------|---|-----|-----|---------------|----------------|-------------|---|-----------------------|----------|
| 7058 | cg43988365 | 2487 | ACCATTTGCACT CGGGGAAGTAG TC[C/gap]TGGGG AAACTTCTCCTT CTCCAGCA | C | gap | Gln (9229) | FRAMES HIFT | phosphatase | Human Gene SWISSPROT-ID:Q14642 TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 412 aa.lpcis:SPTREMBL-ID:Q14642 INOSITOL 1,4,5-TRIPHOSPHATE 5- PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa. | 2.6E-227 | 10 |
| 7059 | cg43307302 | 949 | TGGAAGAAGCTT TCTAAGGAAGAC T[gap]/TACCTCCT GCGTTTGATCAT TCACCA | gap | T | Leu (9230) | FRAMES HIFT | phosphatase | Human Gene SWISSPROT-ID:P17706 T- CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) (TCPTP) - HOMO SAPIENS (HUMAN), 415 aa. | 8.7E-218 (18p11.3) | 18 |
| 7060 | cg42921141 | 90 | CCTCCTCCTGGC CAGGGCAGCAA GC[C/gap]TTAGC CTTGGCTTCTTG TTTCIGCT | C | gap | Leu (9231) | FRAMES HIFT | phosphatase | Human Gene SWISSPROT-ID:P15309 PROSTATIC ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) - HOMO SAPIENS (HUMAN), 386 aa. | 6.8E-213 | 3 (3q21) |
| 7061 | cg43269274 | 1194 | GAGACTGTTGAG TGGGTAGGCAC CG[G/gap]TGCCA GCACCGAGCA GGGAATGTG | G | gap | Arg (9232) | FRAMES HIFT | phosphatase | Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa. | 3.2E-151 | 10 |
| 7062 | cg43272594 | 663 | GTCCAGTTCCTC CTGGTGGCCTTT G[C/gap]CCTCTA CGTGGGCTACAC CCGCGTG | C | gap | Ala (9233) | FRAMES HIFT | phosphatase | Human Gene Similar to SPTREMBL- ID:Q61469 PHOSPHATIDIC ACID PHOSPHATASE - MUS MUSCULUS (MOUSE), 283 aa. | 1.4E-79 | 19 |

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| 7063 | cg43985274 | 612 | AAGGCCAAGTTC TGTGAGGCCCC CG[G/gap]CAGCT GCGTGGCTGTG CACTGCGTG | G | gap | Gly | Ala (9234) | FRAMES HIFT | phosphatase | Human Gene Similar to SPTREMBL-ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa. pcis:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa. pcis:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa. | 7.8E-70 | |
| 7064 | cg43985274 | 650 | TGTGCACTGCGT GGCGGGCCTGG GC[C/gap]GGGCT CCAGTCCTTGTG GCGCTGGC | C | gap | Arg | Gly (9235) | FRAMES HIFT | phosphatase | Human Gene Similar to SPTREMBL-ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa. pcis:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa. pcis:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa. | 7.8E-70 | |
| 7065 | cg43985274 | 675 | CGGGCTCCAGT CCTTGCGGCGCT GG[C/gap]CCTTA TTGAGAGCGGG ATGAAGTAC | C | gap | Ala | Ala (9236) | FRAMES HIFT | phosphatase | Human Gene Similar to SPTREMBL-ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa. pcis:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa. pcis:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa. | 7.8E-70 | |
| 7066 | cg43948077 | 1428 | GGGGCAAGTTT GGGTATGGCATG G[G/gap]CAAGCC ACCGATGAGTGC TGTCCTCA | G | gap | Pro | Pro (9237) | FRAMES HIFT | phosphatase inhibitor | Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa. | 2.1E-146 | 1 |

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|------|------------|------|--|---|-----|-----|---------------|----------------|----------------------|---|----------|----|
| 7067 | cg44005370 | 384 | GACAGCCGGAG CGCCCGGCAAT GGC[G/gap]GCCT CGACGGCCTCG CACCGGCCCCA | G | gap | Ala | Pro (9238) | FRAMES HIFT | phosphat aseinhib | Human Gene Homologous to SWISSPROT-ID:P41236 PROTEIN PHOSPHATASE INHIBITOR 2 (IPP-2) - HOMO SAPIENS (HUMAN), 204 aa. | 1.5E-105 | |
| 7068 | cg43301213 | 490 | CAAGGCTGGGC ACCTCTGGGACA GC[A/gap]AAAA AACTGCAGAAAT GCATCCCT | A | gap | Lys | Lys (9239) | FRAMES HIFT | phosphat aseinhib | Human Gene Similar to SWISSPROT- ID:Q13522 PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (-1) - HOMO SAPIENS (HUMAN), 171 aa. | 7.8E-70 | 12 |
| 7069 | cg43301213 | 498 | GGCACCTCTGG GACAGCAAAAAA AA[A/gap]CTGCA GAATGCATCCCT AAAACCTCA | A | gap | Asn | Thr (9240) | FRAMES HIFT | phosphat aseinhib | Human Gene Similar to SWISSPROT- ID:Q13522 PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (-1) - HOMO SAPIENS (HUMAN), 171 aa. | 7.8E-70 | 12 |
| 7070 | cg43988162 | 295 | ATGAAGTAGCTC ACCAGCCGCTG CG[G/gap]CCTCT GCTGGTACTCGC TGAGCACAC | G | gap | Pro | Arg (9241) | FRAMES HIFT | phosphor ylase | Human Gene SWISSPROT-ID:Q16831 URIDINE PHOSPHORYLASE (EC 2.4.2.3) (UDRPASE) - HOMO SAPIENS (HUMAN), 310 aa. | 1.8E-164 | 7 |
| 7071 | cg43988162 | 448 | AGGACTCCATCT CGATATTGCGGA C[G/gap]CCGGCT GCATAGGCTGCC TCCAGAT | G | gap | Gly | Gly (9242) | FRAMES HIFT | phosphor ylase | Human Gene SWISSPROT-ID:Q16831 URIDINE PHOSPHORYLASE (EC 2.4.2.3) (UDRPASE) - HOMO SAPIENS (HUMAN), 310 aa. | 1.8E-164 | 7 |
| 7072 | cg43996195 | 1251 | GAACCTGCCCTG CATCATCACACA G[G/gap]CCCTGC CATTGAGGAACC CAAACAC | G | gap | Ala | Ala (9243) | FRAMES HIFT | phosphor ylase | Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa. | 2.4E-155 | |

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| 7073 | cg44022214 | 144 | GTCCAGGGGGT CCGAAGCGCCG CAG[gap]AGCT GCTCCTGGTCTT CCAGGTCCT | G | gap | Leu | Leu (9244) | FRAMES HIFT | polymera se | Human Gene SWISSNEW-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.lpcis:SWISSPROT- ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa. | 0 | 19 (19q13.3) |
| 7074 | cg44022214 | 281 | ACTGCGTCCAGA GGCGCGAGAAG CG[gap/C]TCCTC CAGGGCATTTCAG ATGGGATA | gap | C | Arg | Ala (9245) | FRAMES HIFT | polymera se | Human Gene SWISSNEW-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.lpcis:SWISSPROT- ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa. | 0 | 19 (19q13.3) |
| 7075 | cg43923788 | 547 | CCTTTGTCTGAA TTCATTAGTGAT G[C/gap]TTTCAG CAAGTGGTGGC CTTGGTAA | C | gap | Ser | Thr (9246) | FRAMES HIFT | polymera se | Human Gene SWISSNEW-ID:P56282 DNA POLYMERASE EPSILON SUBUNIT B (EC 2.7.7.7) (DNA POLYMERASE II SUBUNIT B) - HOMO SAPIENS (HUMAN), 527 aa.lpcis:TREMBLNEW- ID:G2832260 DNA POLYMERASE EPSILON SMALL SUBUNIT - HOMO SAPIENS (HUMAN), 527 aa. | 1.2E-288 | |
| 7076 | cg43968632 | 236 | CTTTTTGAGTC AGGGGCCACG CC[gap/C]AGGCC TCCCAGGTCATC GTCCTCTG | gap | C | Leu | Leu (9247) | FRAMES HIFT | polymera se | Human Gene SWISSNEW-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.lpcis:SWISSPROT-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa. | 6E-237 | 7 |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|----------------|---|--------------------|---|
| 7077 | cg43968632 | 295 | CCCAGAAAGCT GATGGCTGGC AGG[C/gap]CAGG CTGCGCAGGTTC ACAAGGCAG | C | gap | Ala | Pro (9248) | FRAMES HIFT | polymera se | Human Gene SWISSNEW-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.lpcis:SWISSPROT-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa. | 6E-237 | 7 |
| 7078 | cg43968632 | 296 | CCGAGAAGCTGA TGGGCTGGCAG GC[C/gap]AGGCT GCGCAGGTTTAC AAGGCAGG | C | gap | Leu | Leu (9249) | FRAMES HIFT | polymera se | Human Gene SWISSNEW-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.lpcis:SWISSPROT-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa. | 6E-237 | 7 |
| 7079 | cg43968623 | 1667 | CCTGCCCTTGTA ACCTGCGCAGC CT[G/gap]GCCTG CCAGCCCATCAG CTTCTCGG | G | gap | Ala | Pro (9250) | FRAMES HIFT | polymera se | Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.lpcis:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa. | 7E-199 | |
| 7080 | cg43968623 | 529 | GCGCAGCTTTAG CCGGCAGTATGC C[C/gap]ACATTTA TGCCACCCGCCT CATCCA | C | gap | His | Thr (9251) | FRAMES HIFT | polymera se | Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.lpcis:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa. | 7E-199 | |
| 7081 | cg43993893 | 579 | GAACACCACAGT AATACTGATCTTT [gap]TJGGGTATC AACCTGATATCA ATTCTT | gap | T | Lys | Lys (9252) | FRAMES HIFT | polymera se | Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.lpcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa. | 5E-178 (8p11.2) | 8 |

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|------|------------|------|---|---|-----|-----|---------------|----------------|---------------------------|---|----------|---------------|
| 7082 | cg43993893 | 586 | CACAGTAATACT GATCTTTGGTA TTC/gap/AACCTG ATATCAATTCTTC TGTGTG | C | gap | Leu | Leu (9253) | FRAMES HIFT | potassiu se | Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa. pcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa. | 5E-178 | 8 (8p11.2) |
| 7083 | cg4333426 | 1585 | CAGCCACCTGGA CCTGGAGCGCAT G[C/gap]AGGCTT CCCTCCCGCTG GACAACAT | C | gap | Gln | Arg (9254) | FRAMES HIFT | potassiu m_chann el | Human Gene SWISSNEW-ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa. pcis:SWISSPROT- ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa. | 4.4E-241 | |
| 7084 | cg43008113 | 670 | CGCATCACCGTG CAGGTCACCCGC A[G/gap]GCCGGT CCTCTACTTCCA CATCCGC | G | gap | Arg | Ser (9255) | FRAMES HIFT | potassiu m_chann el | Human Gene SPTREMBL-ID:O00180 POTASSIUM CHANNEL KCNO1 - HOMO SAPIENS (HUMAN), 336 aa. pcis:TREMBLNEW-ID:G281120 TWO P DOMAIN POTASSIUM CHANNEL SUBUNIT - HOMO SAPIENS (HUMAN), 336 aa. | 1.8E-180 | 1 |

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| 7085 | cg44131493 | 1304 | GAAGAGTACTGC ATGGCCGTGTGT G[G/gap]CAGCGC CATGTCCCAAG TTTACTC | G | gap | Gly | Ala (9256) | FRAMES HIFT | protease | Human Gene SWISSNEW-ID:P05067 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II) (PN-II) (APPI) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)] - HOMO SAPIENS (HUMAN), 770 aa. pcis:SWISSPROT-ID:P05067 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II) (PN-II) (APPI) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)] - HOMO SAPIENS (HUMAN), 770 aa. | 0 | 21 |
| 7086 | cg43916732 | 1058 | GCCCAAGCAGT GCCGCCGGACA GG[C/gap]ACCTT GCAGAGCAACTT CTGTGCCA | C | gap | Thr | Pro (9257) | FRAMES HIFT | protease | Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa. | 1.2E-247 (7q21.3) | 7 |
| 7087 | cg43916732 | 773 | GAGCCGTGAGC GACGACTCCCG GAG[G/gap]CTGG GGAAATTCTGCG GCGACGCAG | G | gap | Leu | Trp (9258) | FRAMES HIFT | protease | Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa. | 1.2E-247 (7q21.3) | 7 |
| 7088 | cg43916732 | 914 | ACAAGACCCCTGC CGCGGGGCACT GC[C/gap]AAAGA AGGCAAGGGC CCGGCCCCA | C | gap | Lys | Lys (9259) | FRAMES HIFT | protease | Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa. | 1.2E-247 (7q21.3) | 7 |
| 7089 | cg42538037 | 1038 | TCTGCCATGGAT GAAACTCAGAG A[gap/A]GAAAAG GAAGAGGGCCA TCAAACTC | gap | A | Arg | Lys (9260) | FRAMES HIFT | protease | Human Gene SWISSPROT-ID:P55085 PROTEINASE ACTIVATED RECEPTOR 2 PRECURSOR (PAR-2) - HOMO SAPIENS (HUMAN), 397 aa. | 2.6E-207 | 5 |

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| 7090 | cg43921678 | 459 | CTGGCTCCATG GATTGAGGCCTC T[G/gap]GCCGGA GCTGCCTGGTCC CAGAGTG | G | gap | Gln | Arg (9261) | FRAMES HIFT | protease | Human Gene SPTREMBL-ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment). | 8.2E-185 | 15 |
| 7091 | cg43921678 | 460 | TGGCTCCATGG ATTGAGGCCTCT G[G/gap]CCGGAG CTGCCTGGTCCC AGAGTGG | G | gap | Gly | Gly (9262) | FRAMES HIFT | protease | Human Gene SPTREMBL-ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment). | 8.2E-185 | 15 |
| 7092 | cg43306871 | 642 | ATCTGGGTGTAG ACAGCTGGATGC T[G/gap]GGCAGA GCCACAGGGGT AAACACCC | G | gap | Gln | Ser (9263) | FRAMES HIFT | protease | Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.[pcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa. | 3.1E-153 | 19 |
| 7093 | cg43306871 | 644 | CTGGGTGTAGAC AGCTGGATGCTG G[G/gap]CAGAGC CACAGGGGTAAA CACCCCA | G | gap | Ala | Ala (9264) | FRAMES HIFT | protease | Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.[pcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa. | 3.1E-153 | 19 |
| 7094 | cg43310246 | 2053 | CTGGAGCTGGG ATTGTGGGCAG CG[C/gap]CCCGC AGAAGGGGGTG CTGAAGGAG | C | gap | Ala | Ala (9265) | FRAMES HIFT | protease | Human Gene Homologous to SWISSPROT-ID:P21662 NEUROENDOCRINE CONVERTASE 1 PRECURSOR (EC 3.4.21.93) (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) (PROTEIN CONVERTASE 1) (PC3) (FURIN HOMOLOG) (PROPEPTIDE PROCESSING PROTEASE) - MUS MUSCULUS (MOUSE), AND MUS COCKII, 753 aa. | 1.1E-141 (20p11.2) | 20 |

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| 7095 | cg43930253 | 923 | GAAAGACTGGCT AACTACACCGGA G[G/gap]CATCTA TGCCGAATACCA GGACACC | G | gap | Gly | Ala (9266) | FRAMES HIFT | protease | Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa. | 2.9E-102 | 20 |
| 7096 | cg43930253 | 383 | GACGGGCTGGC TCCGCTGGGGC GCA[G/gap]CACA TACCCCGGCCT CATGAGTAC | G | gap | Ser | Thr (9267) | FRAMES HIFT | protease | Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa. | 2.9E-102 | 20 |
| 7097 | cg43930253 | 644 | GGTAACGCTGG CTCCTGTGAAGG GG[G/gap]TAATG ACCTGTCCGTGT GGGACTAC | G | gap | Gly | Val (9268) | FRAMES HIFT | protease | Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa. | 2.9E-102 | 20 |
| 7098 | cg44032168 | 1468 | TTCTGGTGGGC CTGGTGAGCTG GG[G/gap]TGAGG GCTGTGGGCTC CTTCACAAC | G | gap | Gly | Val (9269) | FRAMES HIFT | protease | Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa. | 2.4E-82 2 (2q13) | |
| 7099 | cg43921680 | 187 | CTTACGCCAGAC TTCAGCCCTGCG G[G/gap]AGCTGC TGCCGCCAAAGA AAGCGGG | G | gap | Glu | Ser (9270) | FRAMES HIFT | protease | Human Gene Similar to SPTREMBL- ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment). | 4.6E-77 | 15 |
| 7100 | cg43511784 | 115 | CTCGTGGGGCAT CCTCCTGCTGGC A[G/gap]GCCGTG GCTGCCGTGTCC CTGTCTC | G | gap | Gly | Ala (9271) | FRAMES HIFT | protease nhib | Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1- ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa. | 9.2E-212 | |
| 7101 | cg43511784 | 116 | TCGTGGGGCATC CTCCTGCTGGCA G[G/gap]CCTGTG CTGCCCTGGTCCC TGCTCTCC | G | gap | Gly | Ala (9272) | FRAMES HIFT | protease nhib | Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1- ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa. | 9.2E-212 | |

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|------|------------|------|---|---|-----|-----|---------------|----------------|------------------|---|-----------------------|--|
| 7102 | cg43511784 | 126 | TCCTCCTGCTGG CAGGCCTGTGCT G[C/gap]CTGGTC CCTGTCTCCCTG GCTGAGG | C | gap | Leu | Trp (9273) | FRAMES HIFT | protease nhib | Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1-PROTEASE INHIBITOR) (ALPHA-1-ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa. | 9.2E-212 | |
| 7103 | cg43511784 | 272 | GCCTTCAGCCTA TACCGCCAGCTG G[C/gap]ACACCA GTCCAACAGCAC CAATATC | C | gap | Ala | Asp (9274) | FRAMES HIFT | protease nhib | Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1-PROTEASE INHIBITOR) (ALPHA-1-ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa. | 9.2E-212 | |
| 7104 | cg43268468 | 1212 | CGCTCCCAGCG AGAGGCCGAG AGG[G/gap]CCGT GGCCACACTGA GAGGAGACAG | G | gap | Ala | Ala (9275) | FRAMES HIFT | protease nhib | Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa. | 2.8E-188 (17p13.3) | |
| 7105 | cg43059041 | 1118 | GACACGATTAAC AGGTGTCGCG AG[G/gap]CCTGA CCAGCAGCCAG GTGGACCTG | G | gap | Gly | Ala (9276) | FRAMES HIFT | protease nhib | Human Gene Similar to SWISSPROT- ID:P17475 ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1-PROTEINASE INHIBITOR) - RATTUS NORVEGICUS (RAT), 411 aa. | 4.4E-83 (14q32.1) | |
| 7106 | cg43969711 | 1380 | CAATTCATCCCA ATGAGCTTCACA G[G/gap]CAAGGC CTCAGTGAGGAA CTCCTGT | G | gap | Pro | Leu (9277) | FRAMES HIFT | reductas e | Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa. | 1.9E-208 2 (2p25) | |
| 7107 | cg43969711 | 1599 | AAATACGACGCA AAAGAACCGGAA A[A/gap]GAAAT GCCTTCCACTGC AGCAAAAG | A | gap | Phe | Phe (9278) | FRAMES HIFT | reductas e | Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa. | 1.9E-208 2 (2p25) | |
| 7108 | cg43941472 | 659 | CCCGCACCAAGA CGGGAGTGGGG TA[C/gap]CCCCA GCTGAGTGCCGT CATTGAGT | C | gap | Pro | Pro (9279) | FRAMES HIFT | reductas e | Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa. | 7.4E-184 X (Xq28) | |

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|------|------------|-----|--|---|-----|-----|---------------|----------------|---------------|---|----------|----------|
| 7109 | cg43982619 | 411 | GATGTGCTCTTC CTGGCTGTGAAG C[C/gap]ACACAT CATCCCTTCAT CCTGGAT | C | gap | Pro | His (9280) | FRAMES HIFT | reductas e | Human Gene SWISSPROT-ID:P32322 PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE) - HOMO SAPIENS (HUMAN), 319 aa. | 4.2E-158 | 17 |
| 7110 | cg43286949 | 965 | CCTCATCCGCAC GGAGCCGGCTC GG[C/gap]CAACA CCAACCCACCACG ACGCCAAA | C | gap | Gly | Ala (9281) | FRAMES HIFT | reductas e | Human Gene SWISSNEW-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.jpds:SWISSPROT-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa. | 1.3E-152 | 7 |
| 7111 | cg43948290 | 866 | AATCATGGAGTG GTGTGGCTATGC C[C/gap]TGGCCA GCTGGTCTGTCC AAGGCGC | C | gap | Leu | Trp (9282) | FRAMES HIFT | reductas e | Human Gene Homologous to SWISSPROT-ID:P18405 3-OXO-5- ALPHA-STEROID 4-DEHYDROGENASE 1 (EC 1.3.99.5) (STEROID 5-ALPHA- REDUCTASE 1) (SR TYPE 1) - HOMO SAPIENS (HUMAN), 259 aa. | 2.9E-141 | 5 (5p15) |
| 7112 | cg43921583 | 275 | AGTGCCATTCTT TGGGGCATTCT G[C/gap]CACTGC AGCCCTCAGGC CTGCTGCA | C | gap | Ala | Ala (9283) | FRAMES HIFT | reductas e | Human Gene Homologous to SWISSNEW-ID:P30048 MITOCHONDRIAL THIOREDUXIN- DEPENDENT PEROXIDE REDUCTASE PRECURSOR (ANTIOXIDANT PROTEIN 1) (AOP-1) (MER5 PROTEIN HOMOLOG) (HBC189) - HOMO SAPIENS (HUMAN), 256 aa.jpds:SWISSPROT-ID:P30048 MITOCHONDRIAL THIOREDUXIN- DEPENDENT PEROXIDE REDUCTASE PRECURSOR (ANTIOXIDANT PROTEIN 1) (AOP-1) (MER5 PROTEIN HOMOLOG) (HBC189) - HOMO SAPIENS (HUMAN), 256 aa. | 1.2E-135 | 10 |

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|------|------------|-----|--|-----|-----|---------------|----------------|-----------|--|--------|---|
| 7113 | cg43918176 | 911 | CCACAAAGTCGCT CCGCCGTGGCC AG[gap]CCCAG GCCCAGGCTC CTCCGGTTA | gap | Gly | Gly (9284) | FRAMES HIFT | reductase | Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa. | 2E-133 | X |
| 7114 | cg43918176 | 917 | GTGCTCCGCC GTGGCCAGGCC CAG[gap]CCCG AGGCTCCTCCG GTTATTACCG | gap | Gly | Gly (9285) | FRAMES HIFT | reductase | Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa. | 2E-133 | X |
| 7115 | cg43918176 | 928 | GTGGCCAGGCC CAGGCCCGAGG CTC[C/gap]TCCG GTTATTACCGCC ACCAGGCC | gap | Gly | Glu (9286) | FRAMES HIFT | reductase | Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa. | 2E-133 | X |

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|------|------------|-----|---|-----|-----|---------------|----------------|---------------|--|-----------------------|---|
| 7116 | cg43918176 | 943 | CCCGAGGCTCCT CCGGTTATTACC G[C/gap]CACCAG GCCCTTCACGCT CCGACAC | gap | Ala | Arg (9287) | FRAMES HIFT | reductas e | Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa. | 2E-133 | X |
| 7117 | cg43918176 | 450 | ATCCCGAGCAAT GGGCAGTGTCTAT G[C/gap]CCACTA TTCCCCCCTTGG AAGCAGA | gap | Gly | Ala (9288) | FRAMES HIFT | reductas e | Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa. | 2E-133 | X |
| 7118 | cg43927549 | 728 | GCGCTCCTTTCC GTAACACACGGGA G[G/gap]CACCAGC CGAGATGTACAC GAAGACA | gap | Gly | Ala (9289) | FRAMES HIFT | reductas e | Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT- DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIOLONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa. | 1.6E-124 6 (6pter) | |
| 7119 | cg43332645 | 364 | GACGTCCTGTTT CTGGCTGTGAAG C[C/gap]ACATAT CATCCCCCTTCAT CCTGGAT | gap | Pro | His (9290) | FRAMES HIFT | reductas e | Human Gene Similar to SWISSPROT- ID:P32322 PYRROLINE-5- CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE) - HOMO SAPIENS (HUMAN), 319 aa. | 4.6E-65 | 1 |

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| 7120 | cg43936108 | 1407 | AGAGGCCGGCG GGGGAGCAGA GTC[C/gap]TGGC GGCTTGGAACT CCGGCCTAG | C | gap | Arg (9291) | Arg (9291) | FRAMES HIFT | ribosomal prot | Human Gene SWISSPROT-ID:P49406 PUTATIVE 60S RIBOSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 280 aa. | 2.5E-151 | 2 |
| 7121 | cg43930758 | 566 | TCGAATGACCAC TGCTGGATGTAC C[T/gap]TTTTCT GAGCTCTGGTT GCCTTT | T | gap | Lys | Arg (9292) | FRAMES HIFT | ribosomal prot | Human Gene Similar to SWISSNEW- ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND SUS SCROFA (PIG), 140 aa.jpds:SWISSPROT-ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 140 aa. | 2.3E-70 | 17 |
| 7122 | cg43930758 | 722 | GTTGTCAGCACA ATTGATTACAGC TTC[gap]CTACCG GAAGACCCAAAG GAAATCCG | C | gap | Gly | Glu (9293) | FRAMES HIFT | ribosomal prot | Human Gene Similar to SWISSNEW- ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND SUS SCROFA (PIG), 140 aa.jpds:SWISSPROT-ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 140 aa. | 2.3E-70 | 17 |
| 7123 | cg43930758 | 723 | TTGTCAGCACAA TTGATTACAGCT C[C/gap]TACCGG AAGACCCAAAG AATCCGG | C | gap | Gly | Glu (9294) | FRAMES HIFT | ribosomal prot | Human Gene Similar to SWISSNEW- ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND SUS SCROFA (PIG), 140 aa.jpds:SWISSPROT-ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 140 aa. | 2.3E-70 | 17 |
| 7124 | cg43255045 | 5827 | AATCCCAAGAAG GGAAGGGCCAT GG[G/gap]CGGCT TCTGGAGCCCG GCACTCATC | G | gap | Arg | Gly (9295) | FRAMES HIFT | struct | Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa. | 0 | 1 |

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|------|------------|------|---|---|-----|-----|---------------|----------------|--------|---|---|---|
| 7125 | cg43927378 | 6235 | AAGGGAAGGC CCGGCCCCCG AGC[C]gap]GCTC AGCTCCAAGCG CCCCTGCCC | C | gap | Arg | Ala (9296) | FRAMES HIFT | struct | Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa. | 0 | 2 |
| 7126 | cg43927378 | 6288 | GAAGCCGCTTCT GCAGAGCTTCAC G[C]gap]TCCCGC ACCAGCCCGC CCCCCGCA | C | gap | Ser | Pro (9297) | FRAMES HIFT | struct | Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa. | 0 | 2 |
| 7127 | cg43927378 | 715 | CGCGTGAACCA GTGCATCGTGTA TC[T]gap]CGGGT GAGAGCGGCTC CGCAAGAC | T | gap | Ser | Arg (9298) | FRAMES HIFT | struct | Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa. | 0 | 2 |
| 7128 | cg43944016 | 2870 | GGCTTGGCATTG CCCATGGGCTTC A[A]gap]GGGTCT CGGCAGGCTTG GCGTTGCC | A | gap | Leu | End (9299) | FRAMES HIFT | struct | Human Gene SWISSPROT-ID:Q15746 MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) (CONTAINS: TELOKIN) - HOMO SAPIENS (HUMAN), 1913 aa. | 0 | 3 |
| 7129 | cg43944016 | 642 | CAAGGAAAGCTT GGGACACATCTT C[T]gap]TCAGATT CTAGTTTTCTG CATTGA | T | gap | Glu | Glu (9300) | FRAMES HIFT | struct | Human Gene SWISSPROT-ID:Q15746 MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) (CONTAINS: TELOKIN) - HOMO SAPIENS (HUMAN), 1913 aa. | 0 | 3 |
| 7130 | cg43944016 | 643 | AAGGAAAGCTTG GGACACATCTTC TTT]gap]CAGATT TAGTTTTCTGC ATTGAG | T | gap | Glu | Glu (9301) | FRAMES HIFT | struct | Human Gene SWISSPROT-ID:Q15746 MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) (CONTAINS: TELOKIN) - HOMO SAPIENS (HUMAN), 1913 aa. | 0 | 3 |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|--------|--|---|---------------|
| 7131 | cg43996806 | 3139 | AACGCTCCCTCC CATATGGACCG C[C/gap]ATGGAA AAAGCTCAGCTC AAGCCTC | C | gap | Met | Trp (9302) | FRAMES HIFT | struct | Human Gene SWISSNEW-ID:P08648 FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-F) (INTEGRIN ALPHA-5) (VLA-5) (CD49E) - HOMO SAPIENS (HUMAN), 1049 aa. pcds:SWISSPROT-ID:P08648 FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-F) (INTEGRIN ALPHA-5) (VLA-5) (CD49E) - HOMO SAPIENS (HUMAN), 1049 aa. | 0 | 12 (12q11) |
| 7132 | cg44033566 | 2968 | GTGGACTCAGCC CTCCGAGTGCAC A[C/gap]ACTATG CGTAGATTGCGA GGAGACC | C | gap | Thr | Asn (9303) | FRAMES HIFT | struct | Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa. pcds:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa. | 0 | 14 (14q22) |
| 7133 | cg44033566 | 2972 | CTCAGCCCTCCG AGTGCACACACT A[gap]/CTGCGTA GATTGCGAGGA GACCAGCA | gap | C | Cys | Leu (9304) | FRAMES HIFT | struct | Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa. pcds:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa. | 0 | 14 (14q22) |
| 7134 | cg42693827 | 2323 | TGTGAACGTCAG AGTCTTGGACAC G[G/gap]CCAGGC CCAGTCCTCAAC CTGCGGC | G | gap | Ala | Pro (9305) | FRAMES HIFT | struct | Human Gene SPTREMBL-ID:Q10466 TTIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 26926 aa. | 0 | 2 (2q24.3) |
| 7135 | cg44001078 | 2033 | AAGTTGAGCTTG GCCGAGAGCGA AC[C/gap]AAGGG CGTAGCCGTCAG GCACAAAC | C | gap | Gly | Val (9306) | FRAMES HIFT | struct | Human Gene TREMBLNEW- ID:G2920823 CARDIAC MYOSIN BINDING PROTEIN-C - HOMO SAPIENS (HUMAN), 1274 aa. | 0 | |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|--------|---|----------|----------|
| 7136 | cg43916919 | 297 | TGCATGCGCGA GATGAAGCCCTC GG[C/gap]CAGCT GCAGGGCTGCC TGCCGCTCC | C | gap | Ala | Pro (9307) | FRAMES HIFT | struct | Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.[pcis:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa. | 4.3E-188 | 2 (2cen) |
| 7137 | cg43304066 | 2303 | TCAGTCCCAGTA ACCGGCGCTGG GG[gap]CJACCTC CAGCTCCAGCC GATAGGACA | gap | C | Val | Val (9308) | FRAMES HIFT | struct | Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa. | 2.2E-186 | 2 |
| 7138 | cg43304066 | 2325 | GGGGACCTCCA GCTCCAGCCGAT AG[G/gap]ACAGG TTCCTCAGGGTG CACACGCA | G | gap | Ser | Ser (9309) | FRAMES HIFT | struct | Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa. | 2.2E-186 | 2 |
| 7139 | cg43918346 | 684 | TGCAGTCAGAAG AGACTCGTGTGT G[G/gap]CACCGC CGGGATGGAAA GTGGCAGA | G | gap | His | Thr (9310) | FRAMES HIFT | struct | Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa. | 2.4E-130 | |
| 7140 | cg43980282 | 3863 | CCTGGGCAGCA CCTCCGGGACT GAC[gap]CJTTCG GCAGTGGCTGG GGGACTGCTT | gap | C | Thr | Thr (9311) | FRAMES HIFT | struct | Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa. | 3.9E-113 | 22 |

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| 7141 | cg43981852 | 662 | CCGCAGTGAGAT GAGGATCGGT CG[G/gap]CATCC CGCCCGCTCAC CCACTCCTC | G | gap | Ala | Ala (9312) | FRAMES HIFT | struct | Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa. | 7.8E-113 | |
| 7142 | cg43981852 | 812 | GGCTCATGCAG TTTGTAGAACCG G[G/gap]CGATCT CGCACTTGCTGA CCTCCAG | G | gap | Ala | Ala (9313) | FRAMES HIFT | struct | Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa. | 7.8E-113 | |
| 7143 | cg42887734 | 249 | CTGAAGAGCCTG ATGCTGGCCAAG G[C/gap]CAAGGA ATGCTGGGAGCA GGAGCAC | C | gap | Ala | Ala (9314) | FRAMES HIFT | struct | Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa. | 2.6E-94 | 1 (1q31.3) |
| 7144 | cg42887734 | 250 | TGAAGAGCCTGA TGCTGGCCAAG GC[C/gap]AAGGA ATGCTGGGAGCA GGAGCAC | C | gap | Lys | Arg (9315) | FRAMES HIFT | struct | Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa. | 2.6E-94 | 1 (1q31.3) |
| 7145 | cg42887734 | 313 | CTGAGAAAGTGCT GCTACCTGGCAG A[G/gap]CGCATC CCCACGCTGCA GACCCGTG | G | gap | Arg | Ala (9316) | FRAMES HIFT | struct | Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa. | 2.6E-94 | 1 (1q31.3) |
| 7146 | cg42887734 | 538 | GTCGAGTCCGTG TCTCGGCTGACG C[C/gap]ATGCTC CGGGCCCTGCT GGGCTCCA | C | gap | Met | Cys (9317) | FRAMES HIFT | struct | Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa. | 2.6E-94 | 1 (1q31.3) |
| 7147 | cg42896604 | 695 | ACTCCTCATTCT TCACATTGAGGC G[G/gap]CCCCATG GCTGCGAAGGT GTCCCCGAA | G | gap | Gly | Gly (9318) | FRAMES HIFT | struct | Human Gene Similar to SPTREMBL- ID:Q14843 MYOSIN LIGHT CHAIN 2 - HOMO SAPIENS (HUMAN), 170 aa. | 8.6E-87 | 12 (12q23) |

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|------|------------|------|---|---|-----|---------------|-----|----------------|--------|---|---------|---------------|
| 7148 | cg42898003 | 516 | CTCGTCCGTCAC GTGCTCCCGG AG[G/gap]CCCTG AAATCTCAGCC AGCTCCTC | G | gap | Ala (9319) | Ala | FRAMES HIFT | struct | Human Gene Similar to SWISSPROT- ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa. | 1.5E-80 | 20 (20q12) |
| 7149 | cg42898003 | 539 | AGGCCCTGAAAA TCTCAGCCAGCT C[C/gap]TCCGGG TCGATGTAGCCG TCTGCAT | C | gap | Glu (9320) | Glu | FRAMES HIFT | struct | Human Gene Similar to SWISSPROT- ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa. | 1.5E-80 | 20 (20q12) |
| 7150 | cg43962741 | 1591 | TATTGGCGTAAT GCTCTGAAAGAC G[C/gap]CCCCGG CCGTGGCTGCC CAGACGTA | C | gap | Ala (9321) | Gly | FRAMES HIFT | struct | Human Gene Similar to SWISSNEW- ID:P35080 PROFILIN II - HOMO SAPIENS (HUMAN), 139 aa. pcls:SWISSPROT-ID:P35080 PROFILIN II - HOMO SAPIENS (HUMAN), 139 aa. | 6.6E-73 | 3 (3q25.1) |
| 7151 | cg44014373 | 749 | CAGTTCTGGGAT GTCACCTTGCT G[C/gap]TCTGCA CAGTGGCTGGA CTGGCTGC | C | gap | Thr (9322) | Ser | FRAMES HIFT | struct | Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa. | 6.1E-70 | 17 |
| 7152 | cg43936426 | 729 | TCAAGTAGTTTC CATCCAGCCGCA G[G/gap]TAGCGC AGGTGTGGCAC GTTCTCCA | G | gap | Tyr (9323) | Tyr | FRAMES HIFT | struct | Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa. | 5.6E-67 | 1 (1q32) |
| 7153 | cg43927885 | 422 | GTGCAGATGCAC TCCAGGCGGGG GC[C/gap]TCCCA GTTTGAACAAG CGCAGCCA | C | gap | Pro (9324) | Ser | FRAMES HIFT | struct | Human Gene Similar to SWISSPROT- ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa. | 1.2E-55 | 17 |
| 7154 | cg43961860 | 1112 | AATGCTGCTTTT CCCCACATTTGG G[A/gap]AACCAC TTACTCCAACCC GAATGGC | A | gap | Ser (9325) | Phe | FRAMES HIFT | struct | Human Gene Similar to SPTREMBL- ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment). | 3.5E-51 | |

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| 7155 | cg43961860 | 1137 | AAACCAATTACT CCAACCCGAATG G[C/gap]TTTGCT GCAAGTTTCCTG AAAAACCT | C | gap | Ala | Pro (9326) | FRAMES HIFT | struct | Human Gene Similar to SPTREMBL- ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment). | 3.5E-51 | |
| 7156 | cg43248320 | 2488 | TTTGATTACAGAA GTGGCGCCCCG GC[G/gap]GGCAG CAGCCCTCTTGC CCAAAGCC | G | gap | Arg | Arg (9327) | FRAMES HIFT | sulfotran sferase | Human Gene SWISSPROT-ID:P52848 HEPARAN SULFATE N- DEACETYLASEN- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARAN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N-DEACETYLASEN- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 882 aa. | 0 | 5 (5q32) |
| 7157 | cg44005661 | 2103 | TTTCCACACCA GAAGTTGGGG TG[G/gap]CCGAG CCCACTCAATGA AAGGATGG | G | gap | Pro | His (9328) | FRAMES HIFT | sulfotran sferase | Human Gene SPTREMBL-ID:O00338 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 296 aa. lpcis: TREMBLNEW-ID:G2828824 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 296 aa. | 5.4E-165 | |
| 7158 | cg43972499 | 256 | ATATCTAAGTGT GCTGCCCCCGTA G[G/gap]AGGCAC TGGAATTCCTTG CCCAGCA | G | gap | Pro | Leu (9329) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa. | 0 | 2 |
| 7159 | cg43972499 | 588 | GTCAATGTAGAGC ACATCAGTGTC G[G/gap]CAGCGC CTCCTCAATGCT CTCGAAT | G | gap | Pro | Leu (9330) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa. | 0 | 2 |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|----------|--|---|-----------------|
| 7160 | cg40388639 | 1224 | TGGCTCACTCCC CCATGCCAACGG C[C/gap]TGGCCC CCAGGCCCCCA GGCCAGGA | C | gap | Leu | Trp (9331) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa. | 0 | 12 (12q24.2) |
| 7161 | cg40388639 | 1232 | TCCCCCATGCCA ACGGCCTGGCC CC[C/gap]AGGCC CCCAGGCCAGG ACCCCGCGA | C | gap | Arg | Gly (9332) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa. | 0 | 12 (12q24.2) |
| 7162 | cg40388639 | 1245 | CGGCCTGGCCC CCAGGCCCCCA GGC[C/gap]AGGA CCCCGCGAAGA AAGCAACCAG | C | gap | Gln | Arg (9333) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa. | 0 | 12 (12q24.2) |
| 7163 | cg43987111 | 2284 | GCATGCTTTCTA TGTCCTCCACGG T[gap]TCCACCA AGCTCAATAACA CACACTT | gap | T | Thr | Asn (9334) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP-- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa. | 0 | 18 (1p34.1) |
| 7164 | cg43981333 | 403 | GTCACATATCCAC CAGGCCCCCGCG CA[G/gap]CAGGG TAGATGGGAGAG AGGGAGAG | G | gap | Ala | Val (9335) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P18858 DNA LIGASE I (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) - HOMO SAPIENS (HUMAN), 919 aa. | 0 | 19 (19q13.2) |

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|------|------------|-----|---|-----|-----|---------------|----------------|----------|--|----------|---------------------|
| 7165 | cg43948262 | 649 | GCATTTTTCATT CCACTTTTGGAC[A/gap]AAGGGGC CAGAAAGAAATTC TCATGA | gap | Phe | Leu (9336) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P22102 PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE) / PHOSPHORIBOSYLFORMYLGLYCINA MIDINE CYCLO-LIGASE (EC 6.3.3.1) (AIRS) (PHOSPHORIBOSYL- AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2) (GART) (GAR TRANSFORMYLASE) (5'- PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE) - HOMO SAPIENS (HUMAN), 1010 aa. | 0 | 21 (21q22.1) |
| 7166 | cg43918681 | 911 | CCACATCACACA GCTCTTCCAGTG G[G/gap]CACACC GCCCATCCATT GAATGGA | gap | Cys | Cys (9337) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P13196 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA- AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa. | 0 | 3 (3p21.1) |
| 7167 | cg43918681 | 750 | GATGTACCCTCC AACACAACCAA G[G/gap]CTTTGC CAAGTGTTCCAG AAATGAT | gap | Ala | Ala (9338) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P13196 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA- AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa. | 0 | 3 (3p21.1) |
| 7168 | cg43976335 | 475 | GCCCTCACACAG GGTATGGGTTGT C[C/gap]AGGACT GCCACTCCCGCT GCCACAC | gap | Leu | Leu (9339) | FRAMES HIFT | synthase | Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa. | 5.3E-240 | 20 (20q11.2) |

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|------|------------|-----|---|---|-----|-----|---------------|----------------|----------|---|---------|---------------------|
| 7169 | cg43959826 | 605 | CATGGGGCTGG AGAGCCTTCCTG AT[G/gap]CCAGT GGCCAGGGCTT GTGGCGTGG | G | gap | Gly | Gly (9340) | FRAMES HIFT | synthase | Human Gene Homologous to SWISSPROT-ID:P10746 UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75) (UROS) (UROPORPHYRINOGEN- III COSYNTHETASE) (HYDROXYMETHYLBILANE HYDROLYASE (CYCLIZING)) (UROIIIS) HOMO SAPIENS (HUMAN), 265 aa. | 7E-140 | 10 (10q25.2) |
| 7170 | cg43959826 | 692 | CGGCCAGCGCG CGAGCCGTAGT GGG[G/gap]CCGA TGGCTGCAAACT TAATTTGAT | G | gap | Gly | Gly (9341) | FRAMES HIFT | synthase | Human Gene Homologous to SWISSPROT-ID:P10746 UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75) (UROS) (UROPORPHYRINOGEN- III COSYNTHETASE) (HYDROXYMETHYLBILANE HYDROLYASE (CYCLIZING)) (UROIIIS) HOMO SAPIENS (HUMAN), 265 aa. | 7E-140 | 10 (10q25.2) |
| 7171 | cg43933068 | 500 | CAAGGCTGGCTT GGTGGATGACTT T[G/gap]AGAAGA AGTTTAATGCGC TGAAGGT | G | gap | Glu | Arg (9342) | FRAMES HIFT | synthase | Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa. | 1.9E-75 | 12 |
| 7172 | cg43933068 | 502 | AGGCTGGCTTG GTGGATGACTTT GA[G/gap]AAGAA GTTTAATGCGCT GAAGGTTT | G | gap | Lys | Arg (9343) | FRAMES HIFT | synthase | Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa. | 1.9E-75 | 12 |
| 7173 | cg43963566 | 109 | CAAGCCACACCC TCACCTGGCCTT G[C/gap]CCTGGG CAGCCACAGCCT CCATGGC | C | gap | Gly | Ala (9344) | FRAMES HIFT | synthase | Human Gene Similar to SWISSPROT- ID:P07952 BISPHOSPHOGLYCERATE MUTASE (EC 5.4.2.4) (2,3- BISPHOSPHOGLYCERATE MUTASE, ERYTHROCYTE) (2,3- BISPHOSPHOGLYCERATE SYNTHASE) (BPGM) (EC 5.4.2.1) (EC 3.1.3.13) (BPG-DEPENDENT PGAM) - ORYCTOLAGUS CUNICULUS (RABBIT), 258 aa. | 9.3E-74 | |

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|------|------------|------|---|---|-----|-----|---------------|----------------|----------|---|----------|--|
| 7174 | cg43963566 | 577 | TTCTGCCTTGTT GAGGCCTGTGA GG[C/gap]CCCCG TAATGCCGCTCA TTGAGGCG | C | gap | Gly | Ala (9345) | FRAMES HIFT | synthase | Human Gene Similar to SWISSPROT- ID:P07952 BISPHOSPHOGLYCERATE MUTASE (EC 5.4.2.4) (2,3- BISPHOSPHOGLYCERATE MUTASE, ERYTHROCYTE) (2,3- BISPHOSPHOGLYCERATE SYNTHASE) (BPGM) (EC 5.4.2.1) (EC 3.1.3.13) (BPG-DEPENDENT PGAM) - ORYCTOLAGUS CUNICULUS (RABBIT), 258 aa. | 9.3E-74 | |
| 7175 | cg44017251 | 1064 | CTGTGGGTGAG GGCTGGGGCAG CGG[C/gap]TGCC GCATCCAGCAGT GCCCCGGCA | C | gap | Cys | Ala (9346) | FRAMES HIFT | tgf | Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa. | 6.5e-315 | |
| 7176 | cg44017251 | 1118 | AGACAGCTGAGT ACCAGTCATTGT G[C/gap]CCTCAC GGCCGGGGCTA CCTGGCGC | C | gap | Pro | Leu (9347) | FRAMES HIFT | tgf | Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa. | 6.5e-315 | |
| 7177 | cg44017251 | 1120 | ACAGCTGAGTAC CAGTCATTGTGC C[C/gap]TCACGG CCGGGGCTACC TGGCGCCC | C | gap | Pro | Leu (9348) | FRAMES HIFT | tgf | Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa. | 6.5e-315 | |
| 7178 | cg44017251 | 1161 | CCTGGCGGCCA GTGGAGACCTGA GC[C/gap]TCCGG AGAGACGTGGA CGAATGTCA | C | gap | Leu | Ser (9349) | FRAMES HIFT | tgf | Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa. | 6.5e-315 | |

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|------|------------|-------|--|-----|-----|-----|---------------|----------------|-----|--|---------------------------|----|
| 7179 | cg44017251 | 1521 | CAGCCACCCCTCG GCTGGACCGTCA G[G/gap]CCACCT ACACAGAGTGCT GCTGCCT | G | gap | Ala | Pro (9350) | FRAMES HIFT | tgf | Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa. | 6.5e-315 | |
| 7180 | cg44017251 | 887 | CTGCTAGCCCG TTCTGCCCCGCA G[G/gap]CCACCT CCGCCACCCCT GCCCCGCC | G | gap | Pro | His (9351) | FRAMES HIFT | tgf | Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa. | 6.5e-315 | |
| 7181 | cg44017251 | 937 | CGACCCAGCACA CCTAGGCAGGG CC[C/gap]TGTGG GGAGTGGGCGC CGGGAGTGC | C | gap | Pro | Leu (9352) | FRAMES HIFT | tgf | Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa. | 6.5e-315 | |
| 7182 | cg43931248 | 1787 | TGGAAGTGGATC CACGAGCCCAA GG[G/gap]CTACC ATGCCAACTTCT GCCTCGGG | G | gap | Gly | Ala (9353) | FRAMES HIFT | tgf | Human Gene SWISSPROT-ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa. | 9.7E-214 | 19 |
| 7183 | cg43980446 | 10250 | CTTCACGTTCCC AGCCTCCAAAT G[gap/G]CGTCCG CCCCATGGCTCG TGTAGGA | gap | G | Arg | Arg (9354) | FRAMES HIFT | tgf | Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa. | 1.3E-166 (15q21.1) | 15 |
| 7184 | cg43980446 | 2708 | AGGTGAAGCTTC CAGGAGTGTCT G[G/gap]CAAAATG CCCTTAGACCG CACAGAT | G | gap | Cys | Cys (9355) | FRAMES HIFT | tgf | Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa. | 1.3E-166 (15q21.1) | 15 |

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| 7185 | cg43272560 | 829 | ACAGGAGGTGC ATGTCCTGAATC TC[C/gap]GCACT GCAGGCCAGGG GCTGGCCAG | C | gap | Arg | Ala (9356) | FRAMES HIFT | tgfrecept or | Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa. | 0 | 1 (1p33) |
| 7186 | cg43272560 | 837 | TGCATGTCCTGA ATCTCCGCACTG C[A/gap]GGCCAG GGGCTGGCCAG CTACAGAG | A | gap | Arg | Gly (9357) | FRAMES HIFT | tgfrecept or | Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa. | 0 | 1 (1p33) |
| 7187 | cg43982633 | 1191 | TGATTTTGTGGT TATGTGGCTGGA A[G/gap]CACCGA GACCTTCTTTT CATAATT | G | gap | Ala | Val (9358) | FRAMES HIFT | tgfrecept or | Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa. | 1.5E-254 | |
| 7188 | cg43918322 | 1060 | GTCGTGACCAAG ACGCTACGGAG GT[gap/C]CCCAG GGGATCGCCG CGGTCGCCA | gap | C | Asp | Gly (9359) | FRAMES HIFT | thioester ase | Human Gene Similar to SPTREMBL- ID:Q19781 SIMILAR TO ACYL-COA THIOESTERASE. NCBI GI: 1213545 - CAENORHABDITIS ELEGANS, 343 aa. | 1.1E-53 | 20 |
| 7189 | cg36988276 | 790 | GCATTCATGGA ACCCAACTAGAT G[C/gap]AGTGAA TCTAAGCGATAA TAATAAT | C | gap | Ala | Glu (9360) | FRAMES HIFT | tm7 | Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa. | 0 | 2 (2p21) |
| 7190 | cg36988276 | 792 | TTCAATGGAACC CAACTAGATGCA G[gap/C]TGAATC TAAGCGATAATA ATAATT | gap | C | Val | Ala (9361) | FRAMES HIFT | tm7 | Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa. | 0 | 2 (2p21) |

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| 7191 | cg43300806 | 1000 | CCAAGGCCAGC CGCAGCTCTGAG AA[G/gap]TCGCT GGCGCTGCTCAA GACCGTAA | G | gap | Ser | Arg (9362) | FRAMES HIFT | tm7 | Human Gene SWISSPROT-ID:P21453 PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1 - HOMO SAPIENS (HUMAN), 381 aa. pcis:TREMBLNEW- ID:G2668608 G PROTEIN-COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 381 aa (fragment). | 9.4E-200 | 22 (22q13) |
| 7192 | cg43967090 | 1249 | TTTCTTAAGCAC TTTTCAGAGCGA G[G/gap]CCGAGC CCCAGTCTAAGT CCCAGTC | G | gap | Ala | Pro (9363) | FRAMES HIFT | tm7 | Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa. | 5.1E-195 | 2 |
| 7193 | cg43967090 | 923 | CAGATTCGGAGG ATCATGGCTGCG G[C/gap]CAAACC CAAGCAGGACTG GACGAGG | C | gap | Ala | Ala (9364) | FRAMES HIFT | tm7 | Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa. | 5.1E-195 | 2 |
| 7194 | cg43967090 | 924 | AGATTCGGAGG TCATGGCTGCGG C[C/gap]AAACCC AAGCACGACTGG ACGAGGT | C | gap | Lys | Asn (9365) | FRAMES HIFT | tm7 | Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa. | 5.1E-195 | 2 |
| 7195 | cg42908704 | 924 | CGCGGGAGGAG GTCAGCAGGACA AG[gap/A]GTGCG GGGGCCGCAAG GATAGCAAG | gap | A | Arg | Arg (9366) | FRAMES HIFT | tm7 | Human Gene SWISSPROT-ID:P46663 B1 BRADYKININ RECEPTOR (BK-1 RECEPTOR) - HOMO SAPIENS (HUMAN), 353 aa. | 7E-188 | 14 (14q32.1) |
| 7196 | cg43040271 | 1239 | TACGTGAACAAG AGGACGCCCCCG GC[G/gap]CGCCG CTGCGCTCATCT CGCTCACT | G | gap | Arg | Pro (9367) | FRAMES HIFT | tm7 | Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. pcis:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. | 2.9E-74 | |

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| 7197 | cg43040271 | 1243 | TGAACAAGAGGA CGCCCCGGCGC GC[C/gap]GCTGC GCTCATCTCGCT CACTTGGC | C | gap | Ala | Leu (9368) | FRAMES HIFT | tm7 | Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. pcds:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. | 2.9E-74 | |
| 7198 | cg43040271 | 1245 | AACAAGAGGACG CCCCGGCGCGC CG[C/gap]TGCGC TCATCTCGCTCA CTTGCTT | C | gap | Ala | Val (9369) | FRAMES HIFT | tm7 | Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. pcds:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. | 2.9E-74 | |
| 7199 | cg43962131 | 2093 | GTGGCCACACTG CGCCTGGAAGG GC[C/gap]TGCGG AGGACGTTTCTG CAGGCGGA | C | gap | Arg | Ser (9370) | FRAMES HIFT | tnfirecept or | Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa. | 9.2E-257 | 9 |
| 7200 | cg42700065 | 108 | TGAAGGAGCGCT TCCTACCGTTAG G[G/gap]AACTCT GGGACAGAGC GCCCCGGC | G | gap | Asn | Thr (9371) | FRAMES HIFT | tnfirecept or | Human Gene TREMBLNEW- ID:G2957264 TNF RELATED TRAIL RECEPTOR - HOMO SAPIENS (HUMAN), 299 aa. | 2.3E-164 | 8 |
| 7201 | cg43988937 | 768 | TTCTGGCTCGTC CTTGCCCCCTTG G[G/gap]AGCCAA GAGACCCCTTCC CTTCTT | G | gap | Ser | Ser (9372) | FRAMES HIFT | traffic | Human Gene SPTREMBL-ID:Q99408 PUTATIVE NUCLEOLAR TRAFFICKING PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 1410 aa. | 0 5 (5q32) | |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|----------------------|---|----------|---------------|
| 7202 | cg43934374 | 2836 | AGGTTTCATCTA GAGGCAGAACAA G[C/gap]AGTACT AATGAAGATGAG GATTGA | C | gap | Ser | Val (9373) | FRAMES HIFT | transcript factor | Human Gene SWISSNEW-ID:Q99081 (TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.lpcis:SWISSPROT-ID:Q99081 (TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa. | 0 | 15 (15q21) |
| 7203 | cg43321351 | 2475 | CAGGGCCTCCG GAGGGGCCCGC TGG[G/gap]CAGG CCTTCTGAATCT TGTGCTGAA | G | gap | Ala | Ala (9374) | FRAMES HIFT | transcript factor | Human Gene SPTREMBL-ID:O00146 P120E4F TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 783 aa. | 1E-290 | |
| 7204 | cg43321351 | 538 | CAGTGCCCTCGC TGATGGCCGAG GC[C/gap]AGCGT CATGGCCACCTG CTCTGTCA | C | gap | Leu | Leu (9375) | FRAMES HIFT | transcript factor | Human Gene SPTREMBL-ID:O00146 P120E4F TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 783 aa. | 1E-290 | |
| 7205 | cg42896335 | 318 | GCTCGGGGCC CCAGCAAGTCCC CC[G/gap]GTCGT CCCCGCAGGCC GCCTTCACC | G | gap | Arg | Arg (9376) | FRAMES HIFT | transcript factor | Human Gene TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa. | 2.1E-285 | 12 |
| 7206 | cg43947662 | 505 | TGATATGATAGC TATCATTGGTTT C[gap/C]TGCTTT CATTGTGTCCAG AATAAAA | gap | C | Glu | Gly (9377) | FRAMES HIFT | transcript factor | Human Gene TREMBLNEW-ID:G545525 LBP-1C=TRANSCRIPTION FACTOR ALPHA-GLOBIN CP2 HOMOLOG {ALTERNATIVELY SPLICED} - HOMO SAPIENS, 502 aa. | 3.7E-276 | 12 |
| 7207 | cg43917801 | 840 | ACGGAAGCGCT GCTGGCCGGCG AGA[gap/G]CTCG GACTCGGGCGC CGGCCTCGAG | gap | G | Asp | Glu (9378) | FRAMES HIFT | transcript factor | Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa. | 1.3E-249 | 6 (6p22.3) |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|----------------------|--|----------|-----------------|
| 7208 | cg43920700 | 1283 | TGCTTGCTGGAG TCAGACCAGGGA G[C/gap]CCCCGG GCCACAGCATCA GCCCTGC | C | gap | Pro | Pro (9379) | FRAMES HIFT | transcript factor | Human Gene SWISSPROT-ID:Q14938 NUCLEAR FACTOR 1X (NFI-X) (NF-IX) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGCA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 441 aa. | 2.1E-243 | 19 (19p13.3) |
| 7209 | cg21646034 | 870 | TCCAATTCTTCA GAAACTCCAGTA GT[gap]GGCCAC AGAAAGAGTAGT TACTGCA | T | gap | Val | Gly (9380) | FRAMES HIFT | transcript factor | Human Gene SWISSPROT-ID:Q06545 GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-47) (GAPBP2) - HOMO SAPIENS (HUMAN), 347 aa. | 9E-179 | 15 |
| 7210 | cg43950592 | 97 | CGCAGCAAACTT CGGGGGCGGC GG[C/gap]GGCAA CTCCACCGCG CGCGGGCCG | C | gap | Gly | Ala (9381) | FRAMES HIFT | transcript factor | Human Gene SWISSPROT-ID:P48431 TRANSCRIPTION FACTOR SOX-2 - HOMO SAPIENS (HUMAN), 317 aa. | 4.7E-173 | 3 (3q26.3) |
| 7211 | cg43929348 | 739 | GATGAAGGCCA GGGATAAATTC AA[G/gap]AGTTG CTTCGGACACT TCCCTTTC | G | gap | Leu | Leu (9382) | FRAMES HIFT | transcript factor | Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa. | 6.5E-169 | 2 |
| 7212 | cg43929348 | 746 | CCAGGGATAAAT TTCAAGAGTTGC T[gap]CTTCGGA CACTCCCTTTC TGCTCTT | gap | C | Lys | Arg (9383) | FRAMES HIFT | transcript factor | Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa. | 6.5E-169 | 2 |
| 7213 | cg43935763 | 742 | CAGGCAGACACT TTCAGTTCTTTT T[gap]CTTGCT TTCAGCACTGGA GGCAGA | T | gap | Lys | Lys (9384) | FRAMES HIFT | transcript factor | Human Gene SPTREMBL-ID:Q13889 BASIC TRANSCRIPTION FACTOR 2, 35 KD SUBUNIT - HOMO SAPIENS (HUMAN), 303 aa. | 1E-161 | |
| 7214 | cg43982109 | 1793 | GTCGACTCCAC AGCCGGTGCAC AG[C/gap]CTGC TCCAGACCTCC CAGGGCAC | C | gap | Glu | Asp (9385) | FRAMES HIFT | transcript factor | Human Gene Homologous to SWISSPROT-ID:Q00059 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1) - HOMO SAPIENS (HUMAN), 246 aa. | 5.6E-131 | 10 (7p) |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|----------------------|---|----------|----|
| 7215 | cg44028769 | 482 | GGTGCTCACAA CCACCGTCCGCA G[G]gapJAGGCAA ACTTCAGGGACA GCACGCA | G | gap | Ser | Ser (9386) | FRAMES HIFT | transcript factor | Human Gene Homologous to SWISSPROT-ID:Q02482 TRANSCRIPTION FACTOR UNC-37 - CAENORHABDITIS ELEGANS, 612 aa. | 4.6E-119 | 1 |
| 7216 | cg43918209 | 1675 | AGCGACAGCTG CAGACTCCGGTG CA[G]gapJCCGCA GGCCACCGCGC TGCAATGCGG | G | gap | Leu | Cys (9387) | FRAMES HIFT | transcript factor | Human Gene Homologous to SPTRMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa. | 2.7E-115 | 19 |
| 7217 | cg43297584 | 707 | TCCGCTGGCAAC AGTGCTCCCAAT A[gap]A]GCCCCA TGCCCATGCTGC ACATTGG | gap | A | Ser | Lys (9388) | FRAMES HIFT | transcript factor | Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa. | 2.6E-90 | |
| 7218 | cg43297584 | 785 | TGTCATTGACAA CATTATGCGTCT G[G]gapJACGATG TCCTTGGCTACA TCAATCC | G | gap | Asp | Thr (9389) | FRAMES HIFT | transcript factor | Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa. | 2.6E-90 | |
| 7219 | cg43297584 | 793 | CAACATTATGCG TCTGGACGATGT C[gap]T]CTTGGC TACATCAATCCT GAAATGC | gap | T | Leu | Ser (9390) | FRAMES HIFT | transcript factor | Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa. | 2.6E-90 | |
| 7220 | cg43917302 | 1568 | ACCAGGCGGTG CACACTGGCAGC CG[C]gapJCCCCA CGCCTGCGCCG TCTGCGCCC | C | gap | Pro | Pro (9391) | FRAMES HIFT | transcript factor | Human Gene Similar to SWISSNEW- ID:Q81751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcds:SWISSPROT- ID:Q81751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 3.9E-68 | 7 |

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|------|------------|------|---|---|-----|-----|---------------|----------------|----------------------|---|---------|---|
| 7221 | cg43917302 | 1572 | GGCGGTGCACA CTGGCAGCCGC CCC[C/gap]ACGC CTGGCCCGTCTG CGCCCGCAG | C | gap | His | Thr (9392) | FRAMES HIFT | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 3.9E-68 | 7 |
| 7222 | cg43917302 | 1590 | CCGCCCCACG CCTGCGCGTCT GC[G/gap]CCCGC AGCTTCAGCTCC AAAACCAA | G | gap | Ala | Pro (9393) | FRAMES HIFT | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 3.9E-68 | 7 |
| 7223 | cg43917302 | 1652 | ACCAGGCGATCC ACACAGGCTCCC G[C/gap]CCCTTC TCCTGCCCCGAG TGCGGAA | C | gap | Pro | Pro (9394) | FRAMES HIFT | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 3.9E-68 | 7 |
| 7224 | cg29214653 | 587 | CCGGGACGGTT CTCTGCTAGCTC CC[T/gap]AACTG CTTCTGGCCAGG AGTCCAGT | T | gap | Leu | Gln (9395) | FRAMES HIFT | transcript factor | Human Gene Similar to SWISSPROT- ID:P50548 ETS-DOMAIN TRANSCRIPTION FACTOR ERF - HOMO SAPIENS (HUMAN), 548 aa. | 4.9E-68 | 1 |
| 7225 | cg43917396 | 2229 | CATGCGTTTGGG CATCTCAGGGTC G[G/gap]CCTTGC CCGCCACCATCC AGCGCGA | G | gap | Ala | Ala (9396) | FRAMES HIFT | transcript factor | Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa. | 6.9E-68 | |

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|------|------------|------|---|---|-----|---------------|----------------|----------------------|--|----------|----|
| 7226 | cg43944978 | 1414 | AACAGGCCCGC AGATGCCCGCAG GTC[C/gap]TTCCG GCACCGTCTCCA GGGCCATCT | C | gap | Lys (9397) | FRAMES HIFT | transcript factor | Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa. | 3.4E-60 | 17 |
| 7227 | cg43946772 | 3292 | CATGAACCTGGTA CTTTTAGTTTTT [T/gap]CACATAA CTCTCTAAAGGC CTTTTC | T | gap | Lys (9398) | FRAMES HIFT | transfe se | Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1, O N-ACETYLGLACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa. | 0 | 18 |
| 7228 | cg43935558 | 3108 | ACAGTATGCACA AAACATGGGCCT G[C/gap]CCCAGA ACCGTATCATTT TTTCACC | C | gap | Pro (9399) | FRAMES HIFT | transfe se | Human Gene SWISSNEW-ID:P56558 UDP-N-ACETYLGLUCOSAMINE-- PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERAS E 110 KD SUBUNIT (EC 2.4.1.-) (O- GLCNAC TRANSFERASE P110 SUBUNIT) - RATTUS NORVEGICUS (RAT), 1036 aa. pcis: TREMBLNEW- ID:G1931579 O-GLCNAC TRANSFERASE, P110 SUBUNIT - RATTUS NORVEGICUS (RAT), 1036 aa. | 0 | |
| 7229 | cg43916882 | 1905 | ACCAAAAGAGGG CCCAAGCCCGG GC[C/gap]GCGGT GCTGGGCTCCAT CTTCCTCC | C | gap | Ala (9400) | FRAMES HIFT | transfe se | Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa. | 5.3E-245 | 1 |

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|------|------------|------|---|---|-----|-----|---------------|----------------|-------------|---|----------|-----------------|
| 7230 | cg2537639 | 258 | CACCTAGGAAGG ATGTCCTCGTGG T[G/gap]ACCCCT TGGCTGGCTCCC ATTGTCT | G | gap | Thr | Pro (9401) | FRAMES HIFT | transferase | Human Gene SWISSPROT-ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA-N- ACETYL GALACTOSAMINYLTRANSFER ASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa. | 6.5E-192 | 9 (9q34) |
| 7231 | cg43258046 | 1453 | GCCACAGCCTGT GCACCTGCTGCC C[C/gap]TGCACG GGATACAGCATC TCAACAT | C | gap | Leu | Cys (9402) | FRAMES HIFT | transferase | Human Gene Homologous to TREMBLIN-NEW-ID:G2673984 LEGITHIN:CHOLESTEROL ACYL TRANSFERASE - AKODON TORQUES, 294 aa (fragment). | 3.2E-146 | 16 (16q22.1) |
| 7232 | cg43949162 | 1194 | CTCCGTTGGGA TAGTGGAGCTTG G[G/gap]CCTTGC TGCCATGATAGC TTTTCAG | G | gap | Pro | Pro (9403) | FRAMES HIFT | transferase | Human Gene Homologous to TREMBLIN-NEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa. | 1.3E-115 | 6 |
| 7233 | cg43933127 | 1862 | CTGGATCTGTGA TACTTGCTGTGT G[A/gap]CTGCCG TCTGGAGCTGTT CATTTTG | A | gap | Val | Ala (9404) | FRAMES HIFT | transport | Human Gene SWISSPROT-ID:P41541 GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP) - BOS TAURUS (BOVINE), 961 aa. | 0 | 4 |
| 7234 | cg40351913 | 1680 | TCCAGCAGATGA CCGGGCAGCGG CC[C/gap]AGCCT GTACTGGCGGCT GTGCTGGA | C | gap | Ser | Ala (9405) | FRAMES HIFT | transport | Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa. | 0 | 5 (5p15.3) |
| 7235 | cg43993573 | 252 | GACGTCAGAATG ATTCCTTGCGA G[C/gap]CGCGCT GACCTTTGCCCG ATGTCTG | C | gap | Ala | Ala (9406) | FRAMES HIFT | transport | Human Gene SWISSPROT-ID:P52569 LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2) - HOMO SAPIENS (HUMAN), 658 aa. | 0 | 8 (8p22) |

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|------|------------|------|---|-----|-----|---------------|---------------|-----------------|-----------|--|----------|---|
| 7236 | cg44011204 | 1168 | CAGGATGAAACG GCTGATGTGCTT G[G]gap]CCACGC CATTATTCTCCT CCACGCA | G | gap | Ala (9407) | Ala (9407) | IFRAMES HIFT | transport | Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.[pcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.[pcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa. | 6.9E-197 | |
| 7237 | cg44025532 | 678 | CTGTGCACGCG GCTGGCCATCAT GG[gap]G]TGAAC GGTCGCCTGCG GTGCCTGGG | gap | G | Val | Gly (9408) | IFRAMES HIFT | transport | Human Gene SWISSPROT-ID:P41234 ATP-BINDING CASSETTE TRANSPORTER 2 - MUS MUSCULUS (MOUSE), 1472 aa (fragment). | 6.8E-174 | |
| 7238 | cg43945806 | 307 | AAACTCTGGTCT GGAAGATCAGT C[A]gap]CCTGAG CAAGGCTTCCGG AAGTAGA | A | gap | Gly | Gly (9409) | IFRAMES HIFT | transport | Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa. | 2.2E-145 | 6 |
| 7239 | cg43945806 | 432 | AGATCTGAGGGC AGTCCGTTCCGG G[G]gap]TACCCA ATAGGCAATTGC TGTGTAG | G | gap | Pro | Pro (9410) | IFRAMES HIFT | transport | Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa. | 2.2E-145 | 6 |
| 7240 | cg43928832 | 1562 | CGGTGCGGACA TGGCAACAGCC GCA[G]gap]CACC GGTGCTGTAGA ACCGGTCAC | G | gap | Cys | Cys (9411) | IFRAMES HIFT | transport | Human Gene Homologous to SWISSPROT-ID:Q15012 GOLGI 4- TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108) - HOMO SAPIENS (HUMAN), 233 aa. | 2E-126 | 2 |
| 7241 | cg43061328 | 262 | CTGCAACAGGAA AACATTGTTCC C[C]gap]AGATGC TGGAGATGCAA GTAAGGC | C | gap | Trp | Trp (9412) | IFRAMES HIFT | transport | Human Gene Homologous to TREMBLNEW-ID:E315451 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 552 aa. | 5.6E-125 | |

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|------|------------|------|--|---|-----|---------------|-----|----------------|-----------|---|---------|----|
| 7242 | cg43331724 | 414 | GTGCCCTTGGAC TTGCAGACCGTG A[G/gap]GACAGT ATTGGCTGTGTT TGGGAAG | G | gap | Arg (9413) | Arg | FRAMES HIFT | transport | Human Gene Similar to SPTRMBL- ID:Q61185 KIDNEY-SPECIFIC TRANSPORT PROTEIN - MUS MUSCULUS (MOUSE), 545 aa. | 1.2E-55 | |
| 7243 | cg43990999 | 427 | TTCCCTATCCCA GCTATGGTGTGT G[G/gap]CACTGC CTTCTTCATCAAT TTCATA | G | gap | Gly (9414) | Gly | FRAMES HIFT | transport | Human Gene Similar to SWISSPROT- ID:P32802 ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 667 aa. | 7.5E-55 | 10 |
| 7244 | cg43986426 | 1241 | TAAGCAGTGCAA GGTGTCTTGAGC C[C/gap]TATGGT GGCCATGCTGG GTGCAGTA | C | gap | Tyr (9415) | Met | FRAMES HIFT | ubiquitin | Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa. | 0 | 1 |
| 7245 | cg43986426 | 1251 | AAGGTGTCTTGA GCCCTATGGTGG C[C/gap]ATGCTG GGTGCAGTAGCT GCCCAGG | C | gap | His (9416) | Met | FRAMES HIFT | ubiquitin | Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa. | 0 | 1 |
| 7246 | cg43986426 | 1261 | GAGCCCTATGGT GGCCATGCTGG GT[G/gap]CAGTA GCTGCCCAGGA AGTGCTGAA | G | gap | Cys (9417) | Ser | FRAMES HIFT | ubiquitin | Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa. | 0 | 1 |
| 7247 | cg43986426 | 2004 | TAGCACAGCCGA GCACACCCCTGCA G[T/gap]TGGGCC CGGCATGAGTTT GAAGAAC | T | gap | Trp (9418) | Gly | FRAMES HIFT | ubiquitin | Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa. | 0 | 1 |

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|------|------------|------|--|---|-----|-----|---------------|----------------|-----------|---|----------|----|
| 7248 | cg43986426 | 2361 | ACCTCCTCTACG TACTGGCAGCTG C[C/gap]AACCTG TATGCCCCAGATG CATGGGC | C | gap | Asn | Thr (9419) | FRAMES HIFT | ubiquitin | Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa. | 0 | 1 |
| 7249 | cg43986426 | 2761 | AGCAGCTGTGG CAGGCCTGTTGG GC[C/gap]TGGAG CTGTATAAGGTG GTGAGTGG | C | gap | Leu | Trp (9420) | FRAMES HIFT | ubiquitin | Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa. | 0 | 1 |
| 7250 | cg43291895 | 702 | TCATCCGGAAGC AGGTCCTGGGG AC[C/gap]AAGGT GGACGCGGAGC GTGACGGCG | C | gap | Lys | Arg (9421) | FRAMES HIFT | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa. | 3.5E-129 | |
| 7251 | cg44923887 | 2517 | AGAGTATTCTTC AGCTAGGTCAGC C[C/gap]GAAGCG GGTGCTCAGGCT GGGGGTC | C | gap | Arg | Arg (9422) | FRAMES HIFT | ubiquitin | Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa. | 4E-82 | 22 |
| 7252 | cg44923887 | 2870 | CTTCAAGCTCCT TCATCAGCCTCC TTG[gap]CTGGCC GCCATCTTGGAT TTGGTGC | G | gap | Ser | Arg (9423) | FRAMES HIFT | ubiquitin | Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa. | 4E-82 | 22 |

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|------|------------|------|--|---|-----|-----|---------------|----------------|-----------|---|---------|----|
| 7253 | cg43939935 | 2099 | GCAATGACCACA TGAAATAACGG G[C/gap]GTTGCT CTCATCTGGTC GGCTTTG | C | gap | Ala | Pro (9424) | FRAMES HIFT | ubiquitin | Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.[pcds:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa. | 7.7E-79 | 12 |
| 7254 | cg43939935 | 2173 | CAAACGCTGGGT TTCCCTTGATGAT C[C/gap]TGCGGG GCAGCCCGGCC ATCTTGTC | C | gap | Arg | Arg (9425) | FRAMES HIFT | ubiquitin | Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.[pcds:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa. | 7.7E-79 | 12 |
| 7255 | cg43974851 | 1430 | GTGGGGGAGTT GAGCAGGTGCC GCA[G/gap]GATG ATGGAGCGGTC CATGATGGTG | G | gap | Leu | Cys (9426) | FRAMES HIFT | ubiquitin | Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa. | 1E-70 | 1 |
| 7256 | cg43974851 | 1431 | TGGGGGAGTTG AGCAGGTGCCG CAG[G/gap]ATGA TGGAGCGGTC ATGATGGTGC | G | gap | Ile | Ile (9427) | FRAMES HIFT | ubiquitin | Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa. | 1E-70 | 1 |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|------------------|---|---|---|
| 7257 | cg43921289 | 1307 | CAGCTGGCAGC CAAGGAGGCGA AAG[C/gap]TTCG AGACCTGGAGG ACTCACTGGC | C | gap | Leu | Phe (9428) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa. | 0 | 1 |
| 7258 | cg43921289 | 1794 | GGAGATGATCCC TTGCTGACTTAC C[G/gap]GTTCCC ACCAAAGTTCAC CCTGAAG | G | gap | Arg | Arg (9429) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa. | 0 | 1 |
| 7259 | cg43921289 | 1795 | GAGATGATCCCT TGCTGACTTACC G[G/gap]TTCCTCA CCAAAGTTCACC CTGAAGG | G | gap | Phe | Ser (9430) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa. | 0 | 1 |
| 7260 | cg43921289 | 1856 | GGTGACGATCTG GGCTGCAGGAG CT[G/gap]GGGCC ACCCACAGCCCC CCTACCGA | G | gap | Gly | Gly (9431) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa. | 0 | 1 |
| 7261 | cg43921289 | 2045 | TGGAGATGACCT GCTCCATCACCA C[C/gap]ACGTGA GTGGTAGCCGC CGCTGAGG | C | gap | His | Thr (9432) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa. | 0 | 1 |
| 7262 | cg43929067 | 2129 | GTAGGACACTGC TGGAGCTGAGTG G[C/gap]TTCACA GCGGCAATGACA GCAGCGT | C | gap | Lys | Asn (9433) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa. | 0 | 1 |
| 7263 | cg43929067 | 4145 | GTCGCCCTTGGT ACATGTGGAATA G[gap/A]AAAAA AATAGCAGTCTT CTCCTTG | gap | A | Phe | Phe (9434) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa. | 0 | 1 |

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| 7264 | cg43929067 | 4153 | TGGTACATGTGG AATAGAAAAA A[ap/A]TAGCAG TCTTCTCCTTGA TTAGGCA | gap | A | Phe | Phe (9435) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa. | 0 | 1 |
| 7265 | cg43969426 | 2748 | GACCAAGTCTCA TTAGGCCAAGGC C[C/gap]ACAAC GCTCCTATCACC ATCTCCT | C | gap | Thr | Gln (9436) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O15463 PTPL1-ASSOCIATED RHOGAP - HOMO SAPIENS (HUMAN), 1261 aa. | 0 | 1 |
| 7266 | cg43924236 | 986 | GCTTTCAAGCTG CATACGGTGGCC C[C/gap]AGTGGG GAGCGAGTCC ACGGACAA | C | gap | Leu | Leu (9437) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q16632 TFIIIC2 SUBUNIT - HOMO SAPIENS (HUMAN), 911 aa. | 0 | 2 |
| 7267 | cg43925699 | 1687 | CCCGGCCACTT CCTGGCCACCG CA[G/gap]GCCCC TCGCCATGGCC GCTGGCCT | G | gap | Gly | Ala (9438) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q03989 MODULATOR RECOGNITION FACTOR I - HOMO SAPIENS (HUMAN), 614 aa (fragment). | 0 | 2 |
| 7268 | cg44927137 | 1868 | AGAGGAGTCTGA TGATGAAATAGC A[ap/A]GATAAG GATTCTGAAGAT AATTGGG | gap | A | Asp | Arg (9439) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment). | 0 | 2 |
| 7269 | cg44927137 | 1880 | TGATGAAATAGC AGATAAGGATTC T[ap/T]GAAGAT AATTGGGATGAA GATGAGG | gap | T | Glu | End (9440) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment). | 0 | 2 |
| 7270 | cg43918935 | 306 | AGGGACAGACG CACCGATCGCC GGA[G/gap]GGAC AGACACACGACC ACGGGGCGC | G | gap | Gly | Gly (9441) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment). | 0 | 3 |

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|------|------------|------|---|---|-----|-----|---------------|----------------|------------------|---|---|---|
| 7271 | cg43918935 | 308 | GGACAGACGCA CCGATCGCCGG AGG[G/gap]ACAG ACACACGACCAC GCGGCGCCA | G | gap | Thr | Gln (9442) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment). | 0 | 3 |
| 7272 | cg43918935 | 337 | GACACACGACCA CGCGCGCCAC CG[C/gap]CCACG CTCCACCCACC GCGGCCCA | C | gap | Ala | Ala (9443) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment). | 0 | 3 |
| 7273 | cg43918935 | 415 | TGGCACAAACTT TCCTCCCGGGAC G[G/gap]AACACG CTGCCTCAGGGA GCCCGCG | G | gap | Gly | Glu (9444) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment). | 0 | 3 |
| 7274 | cg43918935 | 443 | CACGCTGCCTCA GGAGCCCGCG AC[C/gap]GCGCC TTCTCCTCCGCC GGTCCCAT | C | gap | Ala | Arg (9445) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment). | 0 | 3 |
| 7275 | cg43939697 | 414 | AGATCCGCATGA AGGAGCTGGAG CG[G/gap]CACAG AAGGAGGTAGAA GAGAGACC | G | gap | Ala | His (9446) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa. | 0 | 3 |
| 7276 | cg43940975 | 1352 | CATCACCAGCTT CATCCGCTAGTGT G[G/gap]CCTCGC CCTCTGAAAACCT TGCCCTT | G | gap | Ala | Ala (9447) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa. | 0 | 3 |

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| 7277 | cg43940975 | 381 | ACAGAGCAGTCC ACTAATGCTGCA T[C/gap]CACCAC GTGTAGTGATGC CAGGTTC | C | gap | Asp | Met (9448) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa. | 0 | 3 |
| 7278 | cg43940975 | 382 | CAGAGCAGTCCA CTAATGCTGCAT C[C/gap]ACCACG TGTAGTGATGCC AGGTTC | C | gap | Val | Val (9449) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa. | 0 | 3 |
| 7279 | cg44917921 | 3496 | CCAGCCCCCAAA ACCAGCCTGGA GG[C/gap]ACTCA CTTCACAGGGTC CTGCCACA | C | gap | Ala | Asp (9450) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75162 KIAA0675 PROTEIN - HOMO SAPIENS (HUMAN), 1208 aa. | 0 | 3 |
| 7280 | cg43930961 | 1504 | ATCTTTAACTCA TTTTTTTTTTTTT gap/AAAAGGAGG ACATTGTAAACA AGTG | T | gap | Lys | Lys (9451) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa. | 0 | 4 |
| 7281 | cg43935402 | 1165 | AGCAACTCTTAC AGAGGGCAAAA A[gap/A]GGGGC TCAAAAGAAAAT TGAAAA | gap | A | Lys | Lys (9452) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa. | 0 | 4 |
| 7282 | cg43935402 | 412 | ATCGGCACCAAC CTGCGCCGGTTC C[G/gap]GGCCGT GTTTGGGGAGA GCGCGGGG | G | gap | Arg | Arg (9453) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa. | 0 | 4 |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|------------------|--|---|---|
| 7283 | cg43935402 | 973 | ACAGAAAGGATA AAGACCCCTTCG G[G/gap]TCTCCT CATTAAATCTGA ACTGGAA | G | gap | Gly | Val (9454) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa. | 0 | 4 |
| 7284 | cg43924112 | 1967 | TGTTGTTCAAGA AACTAAAACTG G[C/gap]TTTGCT GCACCTTGATCA GCTGTAG | C | gap | Lys | Asn (9455) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa. | 0 | 6 |
| 7285 | cg43925091 | 228 | ACCCCAAGTCTA GGGCTACCGGA AG[G/gap]TAGAG AAGCTCTGGTG GCAGTGCA | G | gap | Thr | Thr (9456) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14999 HYPOTHETICAL PROTEIN KIAA0076 (HA0936) - Homo sapiens (Human), 1698 aa. | 0 | 6 |
| 7286 | cg43929503 | 1035 | GCTGCGGGTC GCAGGCTTTGCC GG[gap/C]CTTCC ACGCAGGAGCA GACCCACG | gap | C | Ala | Gly (9457) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)- METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa. | 0 | 6 |
| 7287 | cg43929503 | 1349 | CCAGTGCCGAG GCTCCATTCCGC AC[C/gap]TCCGG CAGGTCGGACAT CGTGCTC | C | gap | Glu | Glu (9458) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)- METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa. | 0 | 6 |
| 7288 | cg44036171 | 2202 | TGGAGTGATTCA GCACACAGGCG CA[G/gap]CAGCT GAAGAATTTAAT GATGATAC | G | gap | Ala | Gln (9459) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75485 MULTIPLE MEMBRANE SPANNING RECEPTOR TRC8 - HOMO SAPIENS (HUMAN), 664 aa. | 0 | 8 |

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| 7289 | cg43958488 | 1801 | GCAGGTGCTCAT CCTTGGCGGAG GC[C/gap]AACAA ATGTTACATTTT GCTTCCC | C | gap | Leu | Leu (9460) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA31649 KIAA0674 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment). | 0 | 9 |
| 7290 | cg43923753 | 3157 | TATGGTCCAGAC CTTCTGGGGT G[G/gap]CTGCTG CCTTCTCCTCCT CTGAGTC | G | gap | Ala | Ala (9461) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment). | 0 | 10 |
| 7291 | cg43923753 | 3690 | CTTCGCTCTGG GACCTTGGCAGA C[gap/C]TTGAGC CAGAAAGCTATAG ATGTCTA | gap | C | Asn | Lys (9462) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment). | 0 | 10 |
| 7292 | cg43923753 | 3733 | GATGTCTAAGAG GGAAGAGGCATT G[G/gap]CATCCT GCTGTGTAGCTC CTGTGCGC | G | gap | Ala | Ala (9463) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment). | 0 | 10 |
| 7293 | cg43925880 | 769 | CACCTTGCAGCT CAGGAGCCGGG CC[C/gap]TTCCG GCTCATAACCGT GGACATGT | C | gap | Lys | Lys (9464) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q13435 SPICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150) - Homo sapiens (Human), 872 aa. | 0 | 11 |
| 7294 | cg43966967 | 1484 | GGGCGTCGGGC GGGACAGTGGA AGA[G/gap]AGAG GGACTTTGCCTA CGTAGCTCG | G | gap | Glu | Arg (9465) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa. | 0 | 11 |

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| 7295 | cg43966967 | 1486 | GCCTCGGGCGG GACAGTGAAGA GA[G/gap]AGGA CTTGCCTACGT AGCTCGTG | G | gap | Arg | Gly (9466) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa. | 0 | 11 |
| 7296 | cg43966967 | 1490 | CGGCGGGACA GTGGAAGAGAG AGG[G/gap]ACTT TGCCTACGTAGC TCGTGATAA | G | gap | Asp | Thr (9467) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa. | 0 | 11 |
| 7297 | cg43334182 | 5146 | AGGGGCTGTCT GCTGTATCCCT GCTT/gap]GCACA CTTGAGGGTGGA TATACCCC | T | gap | Gln | Arg (9468) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O15052 KIAA0344 - HOMO SAPIENS (HUMAN), 1246 aa. | 0 | 12 |
| 7298 | cg43916884 | 993 | AAACCTTCCTG GCCAAAGTCTAG G[C/gap]CCGTGG GCACCAGTCGCA CATTCTCT | C | gap | Gly | Ala (9469) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa. | 0 | 12 |
| 7299 | cg43916884 | 287 | GAGACACAGTG GGAGGCTGAGG CCC[C/gap]TTGG GGGTATCATTCT GTTCTGGA | C | gap | Lys | Lys (9470) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa. | 0 | 12 |
| 7300 | cg43932638 | 324 | TGCCTCCATCCA CCGGGGCTATG GC[C/gap]GCAGA AGAGGTATTGCA GACGGTGG | C | gap | Ala | Gln (9471) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O43892 BICAUDAL-D - HOMO SAPIENS (HUMAN), 975 aa. | 0 | 12 |

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| 7301 | cg44918447 | 608 | AAATCTTTTCAGG CTATGGCTTTTTT [gap/T]GTCICTT GGCCTTATATCC TGGACG | gap | T | Gln (9472) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa. | 0 | 12 |
| 7302 | cg43961443 | 539 | CGCCGCCTCGT CCAGGTCACGCA GC[C/gap]TCCGG TTGACCTCCAGT GTCATGCA | C | gap | Arg (9473) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14393 GROWTH-ARREST-SPECIFIC PROTEIN - HOMO SAPIENS (HUMAN), 678 aa. | 0 | 13 |
| 7303 | cg43968223 | 774 | GCTGCCTGGCA GTGCAGATGAGC CG[G/gap]CTGAT GCCCTCAATGCA CTGGCTCT | G | gap | Ser (9474) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment). | 0 | 14 |
| 7304 | cg44022133 | 3698 | GAGAGGGACAG GGAGAGAGAGA GAG[gap/A]AAGG GAGCGGGACAG GGGGACCGA | gap | A | Arg (9475) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75158 KIAA0670 PROTEIN - HOMO SAPIENS (HUMAN), 1280 aa (fragment). | 0 | 14 |
| 7305 | cg43055918 | 485 | AGGGGGCCTGG GCTTTGGAGGG GCC[C/gap]GCAG AGCGCTGGCATA GGACATGGC | C | gap | Arg (9476) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa. | 0 | 17 |
| 7306 | cg43949150 | 887 | AGATGAACCTCT TAAGCACATTCT T[G/gap]GGAAGG ATGTAGGTGTAG CCAGTCT | G | gap | Pro (9477) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75965 SPLICING FACTOR PRP8 - HOMO SAPIENS (HUMAN), 2335 aa. | 0 | 17 |
| 7307 | cg44023800 | 352 | GCCTGGACGCT CAGCCACTCACT CT[gap/C]TCCGC CATTGCTGAGGC TGCACCCC | gap | C | Glu (9478) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14521 GIANT LARVAE HOMOLOGUE - HOMO SAPIENS (HUMAN), 1015 aa. | 0 | 17 |

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| 7308 | cg44001797 | 3902 | GCTATCTTCCTG AAAGGCTGCATA G[C/gap]CTTCAG TCCTCTTTTCCTT TTTCCT | C | gap | Gly | Ala (9479) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa. | 0 | 18 |
| 7309 | cg43917942 | 1322 | GGGGTTCAGG CATGCCCCCGG GGG[G/gap]CCGA GGCCGAGGAAG AGGCCAAGGC | G | gap | Gly | Ala (9480) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa. | 0 | 18 |
| 7310 | cg43917942 | 1491 | TAGAGATCTCCC GGCAGCTGCCA CC[C/gap]AACGG GGACCCCAACTT CAAGTTGT | C | gap | Asn | Thr (9481) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa. | 0 | 18 |
| 7311 | cg43917942 | 1498 | CTCCCGGCAGCT GCCACCCAACG GG[G/gap]ACCCG AACTTCAAGTTG TTCATCAT | G | gap | Asp | Thr (9482) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa. | 0 | 18 |
| 7312 | cg43917942 | 1616 | TGCCCAGTTGGA CCAGGCCCAGG TG[G/gap]CCCAG GCCCTGCTGGC CCAATGGGG | G | gap | Gly | Ala (9483) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa. | 0 | 18 |
| 7313 | cg43917942 | 1641 | GCCCAGGCCCT GCTGGCCCAATG GG[G/gap]CCCTT CAATCCTGGGCC CTTCAACC | G | gap | Pro | Pro (9484) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa. | 0 | 18 |

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| 7314 | cg43917942 | 1892 | CCCCGGCCCCGC ACCGGCCCTG CGG[C/gap]CCCCA CCGGCTCAGGG TGAGCCCCCT | C | gap | Ala | Ala (9485) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa. | 0 | 19 |
| 7315 | cg43917942 | 1912 | TGCGGCCCCAC CGGCTCAGGGT GAG[C/gap]CCCC TCAGCCCCCACC CACCGGCCA | C | gap | Pro | Pro (9486) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa. | 0 | 19 |
| 7316 | cg43917942 | 1916 | GCCCCACCGGC TCAGGGTGAGC CCC[C/gap]TCAG CCCCCACCACC GGCCAGTCG | C | gap | Pro | Leu (9487) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa. | 0 | 19 |
| 7317 | cg43917942 | 2077 | GAAGCAAGCGC AAGTGGCCACC GGA[G/gap]GGG GTCCAGGAGCTC CCCCAGGCTC | G | gap | Gly | Gly (9488) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa. | 0 | 19 |
| 7318 | cg43975166 | 820 | GGAGTGGGTATT CTGGTAGCCTGC T[G/gap]GGCTTG GCGCCACCTGG TGGTAGCT | G | gap | Pro | Gln (9489) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00267 SUPT5H PROTEIN - HOMO SAPIENS (HUMAN), 1087 aa. | 0 | 19 |
| 7319 | cg43991657 | 1308 | CTCTGGGCTGG GGCTGAGGATTG CG[G/gap]CCCTG GGCAGCTTCTC CTTCCCA | G | gap | Pro | Arg (9490) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa. | 0 | 19 |

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| 7320 | cg43991657 | 335 | CCTGAGGGCGTG CCCAGGGCTCTG GCC[C/gap]GGGC AGCAGGGGTGA GGCAGGGGGCT | C | gap | Arg | Arg (9491) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa. | 0 | 19 |
| 7321 | cg43991657 | 443 | CTGCTCCCAGG GGCCCTGGCGG GCG[G/gap]CCTG GGCCGGCCCTG CCCAGACAGC | G | gap | Ala | Ala (9492) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa. | 0 | 19 |
| 7322 | cg43991657 | 568 | GAGTAGGGGTTT CTGGGCGCTTGA G[C/gap]CGCCTT TGCAGTCGGAG GGCAGGCC | C | gap | Arg | Arg (9493) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa. | 0 | 19 |
| 7323 | cg43919691 | 1070 | GGCAAGCTCATC GCTCTGTTTCTG G[G/gap]CTTCGC TCTTGGCGGCAT CGAGCTG | G | gap | Ala | Ala (9494) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa. | 0 | 20 |
| 7324 | cg43919691 | 701 | CTTCAGAAAGCTC CTGCAGTCTCGT G[G/gap]CGGGCG GCCCCAGGTCA CTTGTTAA | G | gap | Ala | Ala (9495) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa. | 0 | 20 |
| 7325 | cg43919691 | 709 | GCTCCTGCAGTC TCGTGGCGGCG CG[C/gap]CCCAG GTCAC TTGTTAA CTTCTTCT | C | gap | Gly | Gly (9496) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa. | 0 | 20 |
| 7326 | cg43921598 | 1826 | ACAAGGACTGG GAGCGGCACCA CCG[C/gap]CTCT GTGGTCAGAACCC TGCATGGCC | C | gap | Leu | Ser (9497) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O43439 MTG8-LIKE PROTEIN (MTG8 RELATED PROTEIN) (EHT) - HOMO SAPIENS (HUMAN), 604 aa. | 0 | 20 |

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| 7327 | cg43919155 | 1307 | GTAAAGAAAGAG AAGGACAGAGA GG[G/gap]CAGCA GCCTGAAGAAGA AGTGTTTG | G | gap | Gly | Ala (9498) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14241 ELONGIN A - HOMO SAPIENS (HUMAN), 772 aa. | 0 | 1 (1p36.1) |
| 7328 | cg43968854 | 893 | CAATGTC TTGAC AATAGCAAAAA A[gap/A]TAAATCT CCCTTTTGAAG CTTTAT | gap | A | Asn | Lys (9499) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa. | 0 | 10 (10q25) |
| 7329 | cg43973740 | 1103 | GATTGCTATTTT TAGAGCTTTTIT T[gap]AGGCACTC CATTACCCTCTT GCCTC | T | gap | Leu | Leu (9500) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q61123 MATERNAL EMBRYONIC MESSAGE 3 (MEM3) - MUS MUSCULUS (MOUSE), 754 aa. | 0 | 16 (12q12) |
| 7330 | cg44928323 | 4878 | TTGAGGAATTTA TGACTAGGCATC A[gap/T]GGTACA TGAAAAAGAAAGA ATTCAAG | gap | T | Gln | His (9501) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa. | 0 | 17 (17q11.2) |
| 7331 | cg43948022 | 921 | CTGTCACGGTGT CCCCAGGCCCC CA[G/gap]GTGGC TGCGCACTGCAT CCTCAGTG | G | gap | Leu | Trp (9502) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa. | 0 | 3 (3p21.33) |
| 7332 | cg43948022 | 922 | GTCACGGTGTCC CCAGCCCCCA GG[gap/G]TGGCT GCGCACTGCATC CTCAGTGT | gap | G | His | His (9503) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa. | 0 | 3 (3p21.33) |
| 7333 | cg43948022 | 703 | GGGGCACAAAC AAGGTCAACTGA GG[G/gap]CCCCG GGCTGGCCAATA GCGGCCAA | G | gap | Gly | Gly (9504) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa. | 0 | 3 (3p21.33) |

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| 7334 | cg43948022 | 713 | CAAGGTCAACTG AGGGCCCCGGG CT[G/gap]GCCAA TAGCGGCCAAG GTAAAGCC | G | gap | Pro | Gln (9505) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa. | 0 | 3 (3p21.33) |
| 7335 | cg43955232 | 838 | AGCAGCAGCAG CAGCAGCAGCA GCA[G/gap]CACC TCAGCAGGGCTC CGGGGCTCA | G | gap | His | Thr (9506) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P54253 ATAXIN-1 (SPINOCEREBELLAR ATAXIA TYPE 1 PROTEIN) - Homo sapiens (Human), 816 aa. | 0 | 6 (6p23) |
| 7336 | cg42907760 | 1681 | CATCCCCCTCAC CTTCGGCGGAC CG[G/gap]CGGCG CCAGCTTCGTGC CCCTGGAG | G | gap | Arg | Gly (9507) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa. | 0 | 9 (9p12) |
| 7337 | cg43311566 | 1080 | CCAACCTCCACC CTGACGGCCGC GC[C/gap]ATGGC CACCAAGTTTGC ACACTTGA | C | gap | Met | Trp (9508) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment). | 0 | X |
| 7338 | cg43311566 | 856 | CAAGGATGTACT GCGCACTGACC GG[G/gap]CCCAC CCCTACTATGCG GGGCCTGA | G | gap | Ala | Pro (9509) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment). | 0 | X |
| 7339 | cg43921793 | 1032 | CTCGCAGGGAG CTGATAGGCTGG AA[G/gap]CTATTT TTGAAGTTTCTT TTTGT | G | gap | Ser | Ser (9510) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment). | 0 | X |
| 7340 | cg43921793 | 1318 | CTGGGGGTCTATA GTAGTAGCCGGA G[G/gap]TCTCAT CGTACTGGTAGG TAGAGAC | G | gap | Thr | Thr (9511) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment). | 0 | X |

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| 7341 | cg43921793 | 364 | GCCCCCGTGCAC CCAGGCCCGGAG CCC[C/gap]GCAC CCGTGTTGGGC CTCGATAGG | C | gap | Arg (9512) | Arg (9512) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment). | 0 | X |
| 7342 | cg42682094 | 289 | CATAGTAGAGAA GGGGGCCCCCT GG[gap/G]CCTGC TCCAAGCCAGCC TTGCAGCA | gap | G | Gly (9513) | Gly (9513) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14674 KIAA0165 PROTEIN - HOMO SAPIENS (HUMAN), 1795 aa. | 0 | |
| 7343 | cg42682094 | 3085 | GACAGACTGCTG TGAGGACAGGG CT[gap/C]GGCGC AGAGCGAGCAG TCACAGGTG | gap | C | Ser (9514) | Glu (9514) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14674 KIAA0165 PROTEIN - HOMO SAPIENS (HUMAN), 1795 aa. | 0 | |
| 7344 | cg43032555 | 1098 | AGAGCTTGGCC GTCTCTTGGGG TC[C/gap]TTCCG GTCATTACCTC AAAGTGCC | C | gap | Lys (9515) | Lys (9515) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa. | 0 | |
| 7345 | cg43032555 | 189 | CCACTGGCACCC TTCTGCCCCAGGG G[C/gap]TGACCC TCGGGCCCCATC CCCAGCA | C | gap | Gln (9516) | His (9516) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa. | 0 | |
| 7346 | cg43303383 | 1243 | ACAGACTTTATT GTGGGGGGGT CC[C/gap]ACCTG GGACCCACCTC TTAAATAA | C | gap | Trp (9517) | Trp (9517) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa. | 0 | |

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| 7347 | cg43303383 | 1383 | GGGCTGGAGGG GTGGAGGCAGG GCC[C/gap]TTGT CACCTGCATGCC CACATCCAC | C | gap | Lys (9518) | IFRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa. | 0 | |
| 7348 | cg43303383 | 1455 | AGATGCTCTGGG AGGGGCTAGGG AG[gap/C]CCCCA GGCTAGGGGCA AGATGGCAG | gap | C | Gly (9519) | IFRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa. | 0 | |
| 7349 | cg43303383 | 664 | CTGAGGCCGAG TCGCTCGCCGCT GC[G/gap]GGCTC TGATTGAGATGG TGGTGGCA | G | gap | Pro (9520) | IFRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa. | 0 | |
| 7350 | cg43927175 | 134 | AGCATCTTCTGG AATAGGCGGATG G[C/gap]CTCATC CACCTTCCTGAG CTCTGCT | C | gap | Pro (9521) | IFRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD21819 G7A - HOMO SAPIENS (HUMAN), 1264 aa. | 0 | |
| 7351 | cg43932090 | 1755 | CCATGTCGGACA CTTCCTCCTCCT C[C/gap]TCTAAAT CTTCTAGGTCCT CCTTGT | C | gap | Glu (9522) | IFRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment). | 0 | |
| 7352 | cg43932090 | 1757 | ATGTCGGACACT TCCTCCTCCTCC T[C/gap]TAAATCT TCTAGGTCCTCC TTGTCA | C | gap | Arg (9523) | IFRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment). | 0 | |
| 7353 | cg43940146 | 354 | ATGCCGAGATAC TTCAGGGCATCA G[C/gap]CTGGCT GTATCTGTAATC AAAAAC | C | gap | Leu (9524) | IFRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q15910 ENHANCER OF ZESTE HOMOLOG 2 (ENX-1) - Homo sapiens (Human), 746 aa. | 0 | |

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| 7354 | cg43940465 | 5447 | CTGAGGGCTCG GTCATGCTGGTT TC[C/gap]TTCGG CTGCTCAGAGAC TTCACATA | C | gap | Lys | Lys (9525) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60300 KIA0553 PROTEIN - HOMO SAPIENS (HUMAN), 1095 aa (fragment). | 0 | |
| 7355 | cg43966585 | 1546 | CAAGCACCTGCG CCTGTCCCTGAA C[G/gap]GCCACG GCCAGTGTACAG TACAGCA | G | gap | Gly | Ala (9526) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa. | 0 | |
| 7356 | cg43966585 | 1547 | AAGCACCTGCGC CTGTCCCTGAAC G[G/gap]CCACGG CCAGTGTACAGT ACAGCAT | G | gap | Gly | Ala (9527) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa. | 0 | |
| 7357 | cg43966585 | 1643 | CACCCCATCCCA CTGGAGTCAGG GG[G/gap]CTCGG CCGACATCACCC TTCCGAGC | G | gap | Gly | Ala (9528) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa. | 0 | |
| 7358 | cg43966585 | 1701 | GGCCCCAGGAC CCCCACCAGA GCC[G/gap]GGCC CCACGCCCCCT GCCGGCCCCG | G | gap | Gly | Ala (9529) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa. | 0 | |
| 7359 | cg43966585 | 1703 | GCCCAGGACCC CCCACCAGAGC CGG[G/gap]CCCC ACGCCCCCTGC CGCGCCCCGG | G | gap | Gly | Ala (9530) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa. | 0 | |
| 7360 | cg43966585 | 867 | TC TTCGTGCCGC CCAAAGCCTCCA G[G/gap]CCCAAG GTCAGCATCCCA CTGTCAG | G | gap | Pro | Pro (9531) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa. | 0 | |

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| 7361 | cg44003855 | 393 | CTCCTGGGTGGT GCCACCGGAGC CC[C/gap]GGCCC AGCTTCTTCTCC ATCTCCCC | C | gap | Arg | Gly (9532) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P49841 ALPHA-MANNOSIDASE IIX (EC 3.2.1.114) (MANNOSYL- OLIGOSACCHARIDE 1,3-1,6-ALPHA- MANNOSIDASE) (MAN IIX) - Homo sapiens (Human), 1139 aa. | 0 | |
| 7362 | cg44011100 | 566 | CAAGCTCCTGGG GAGGGGGCCCT GC[C/gap]GCAGG GCITTCCTCCTC CCTCTCCA | C | gap | Ala | Ala (9533) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O15450 P160 - HOMO SAPIENS (HUMAN), 1251 aa. | 0 | |
| 7363 | cg44016445 | 1446 | GGGCTCCCTGC CCCGCTGCAGC CCC[gap]CTGCT TGGGAGGCACT GGACTTAGGC | gap | C | Arg | Arg (9534) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75427 LEUCIN RICH NEURONAL PROTEIN - HOMO SAPIENS (HUMAN), 832 aa. | 0 | |
| 7364 | cg44024279 | 1732 | ATGCCAACAGGA GGCCATGCTTCA G[C/gap]AGCTTG GTGGTGGATGAA ACATATG | C | gap | Ser | Ala (9535) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa. | 0 | |
| 7365 | cg44024279 | 1850 | CTGCAACGATG AAGCAAGAGTTT C[gap]CTCATTAA CCTTGTAAGCA AAAGCC | gap | C | Leu | Pro (9536) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa. | 0 | |
| 7366 | cg44024279 | 1941 | TTCTCAGGCCTG TTGGAGAAATGC T[G/gap]CCAAGG CCAGGAACAGG AAGTCTGC | G | gap | Cys | Ser (9537) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa. | 0 | |

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| 7367 | cg44932543 | 319 | TGTTGATCTGTC CCTCCTGGATTT C[C/gap]TGCCGG GTCTCGGCAGG CAGATGGT | C | gap | Gln (9538) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75341 BRCA1-ASSOCIATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 600 aa. | 0 | |
| 7368 | cg43957199 | 1189 | CCGAGGAAATAT CAGGCTGATGG CT[G/gap]GGGCA GGCCCGGAGCT GGTAGTGTG | G | gap | Pro (9539) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa. | 1 | 1.0e-313 |
| 7369 | cg44002959 | 4273 | GGCTGCCTCGTC CGGGGTCTCAG GG[G/gap]CCAGT GGCGGGGGGCT TTCAGGGGT | G | gap | Ala (9540) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92513 MYELOBLAST KIAA0239 - HOMO SAPIENS (HUMAN), 571 aa (fragment). | 5 | 1.4e-316 |
| 7370 | cg43937128 | 832 | CTGGTTTTTCATT CCATTCTTGCT[G/gap]CCTTTTGG CTGTATCTCTCC ACGAG | G | gap | Glu (9541) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa. | X | 4.0e-317 |
| 7371 | cg43937128 | 504 | TGTGAAAGGTGC TTATCTCGTTGT C[C/gap]TTCGGA GTTGCCCTGCTGA CTGTTTC | C | gap | Lys (9542) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa. | X | 4.0e-317 |
| 7372 | cg44015618 | 837 | AGGACAGAGGA CAGTGAGGGAC AGG[G/gap]CTGG GGCCAAAAGAAAT TAACAGATC | G | gap | Ser (9543) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment). | 11 | 8.7e-312 |

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| 7373 | cg43923376 | 1635 | CCCCAGGCTCTG GCCCAGAGCAG GG[G/gap]CTGTT GCCGAAAGGCT GTGGAGCAA | G | gap | Ala | Leu (9544) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P06865 BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N- ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 529 aa. | 9.2E-297 | 15 |
| 7374 | cg43981656 | 1518 | AGTCTCTTTCCG TTTGCCACCAGA A[A/gap]GGCTT TGTCCTCGCTC TTGGGAT | A | gap | Leu | Leu (9545) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa. | 1.6E-292 | 10 |
| 7375 | cg44128920 | 1189 | ATGAGAAGACAC CTCAGATGGG GA[C/gap]CCCCG CAGCTTGAGGC CCAGATCG | C | gap | Pro | Pro (9546) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa. | 1E-290 | 19 |
| 7376 | cg44128920 | 1418 | GGACACCAGG AGAGCTCTGAAG AG[C/gap]CTCCC TCAGAAAGAGAGC CAGGACAC | C | gap | Pro | Leu (9547) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa. | 1E-290 | 19 |
| 7377 | cg44128920 | 1520 | CATAGGTCAC TG TGTGGCCATCTA C[C/gap]ACTTTG AAGGTCCAGC GAGGGCAC | C | gap | His | Thr (9548) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa. | 1E-290 | 19 |
| 7378 | cg43949262 | 1272 | GGGTCCCGCTG AAGCTGCCCAG GGC[C/gap]TGCG GGTCGCTCTGAA TGCCCTTCA | C | gap | Gln | Gln (9549) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa. | 9E-290 | |

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| 7379 | cg43949262 | 770 | CAGCAGGCACC AGGCTGGGGCA CCA[G/gap]CTGG GGCCTGGGTAC GCCCAGAAAG | G | gap | Leu | Trp (9550) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa. | 9E-290 | |
| 7380 | cg43931799 | 2153 | GCTGGGGGTCT GAACCCGAACCA GG[G/gap]CCTGA ACAGGCTGATGC TGGCTGTG | G | gap | Gly | Ala (9551) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA83001 KIAA1049 PROTEIN - HOMO SAPIENS (HUMAN), 550 aa (fragment). | 7.6E-289 | 22 |
| 7381 | cg44010409 | 1496 | GACGAGCAGAA CTGCGAGTGGT GGG[G/gap]CGGT AGCCAGGCAAG CTGAGCAGGG | G | gap | Arg | Arg (9552) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q14981 NUMA PROTEIN - HOMO SAPIENS (HUMAN), 2101 aa. | 2.1E-281 | 11 |
| 7382 | cg43930921 | 1135 | CAATCTCAAAGA AGGAGATGGTG CC[C/gap]TTGCG GTAATCTCATT GCCTGGAG | C | gap | Lys | Lys (9553) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa. | 2.4E-280 | 11 |
| 7383 | cg43930921 | 877 | CATAGCTGAAC CGATCAGCAGCT TT[G/gap]CCGTAG CCCCGGCGCTG GTAGGGAG | G | gap | Gly | Gly (9554) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q92893 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa. | 2.4E-280 | 11 |
| 7384 | cg44001088 | 352 | GGTCACACACA GTGACCGGACG AA[G/gap]TTGTT CCAATTGGTTTT CCAATGCA | G | gap | Leu | Phe (9555) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa. | 2.2E-279 | X |
| 7385 | cg44001088 | 489 | TTTGCCTCTTTAT TTTTGCGGATAG[C/gap]AGTTTGAA TGGCCTTCTTCT GTTTG | C | gap | Ala | Leu (9556) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa. | 2.2E-279 | X |

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| 7386 | cg44022026 | 1703 | CCCAGGGGTGTG CTGGAGCACCAC AC[C/gap]TACGG CGCCCTGCTCTT CCCACTGC | C | gap | Tyr | Thr (9557) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O43292 HGAA1 - HOMO SAPIENS (HUMAN), 621 aa. | 1.2E-278 | 8 |
| 7387 | cg43252100 | 1461 | TCTAACATTTTC ATCAGCCTATGG [C/gap]AAGTGGT TTTGTGGATTTT CTAAA | C | gap | Ala | Glu (9558) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BA83037 KIAA1085 PROTEIN - HOMO SAPIENS (HUMAN), 584 aa (fragment). | 4.9E-278 | |
| 7388 | cg43922691 | 188 | GGCCGGACTGG AAAGCCGGAGC GGG[G/gap]CCAG GCGGGCCTCCC CAAAAGCCTG | G | gap | Pro | Gln (9559) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa. | 8.5E-278 | 17 |
| 7389 | cg43922691 | 324 | GCTCCGGCAGC GGAACCGCCTG AGG[C/gap]TGGA GGAGGACAAAC CGGCCGTGGA | C | gap | Leu | Trp (9560) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa. | 8.5E-278 | 17 |
| 7390 | cg43922691 | 353 | AGGAGGACAAAC CGGCCGTGGAG CG[G/gap]TGCTT GGAGGAGCTGG TCTTCGGCG | G | gap | Cys | Ala (9561) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa. | 8.5E-278 | 17 |
| 7391 | cg43988211 | 1246 | ACCCAAATCGAA TCCATAGGCTGC G[C/gap]CAGGGG CCTGTTATCATG TAATAGG | C | gap | Trp | Cys (9562) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIC63 - HOMO SAPIENS (HUMAN), 519 aa. | 6.2E-275 | |
| 7392 | cg43958878 | 131 | GGTGATGGGTTG GTCTCAGCGGA T[G/gap]CCTTGG TGGATGAGGCTG CTTTTGG | G | gap | Gly | Gly (9563) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa. | 3E-269 | 9 |

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| 7393 | cg43958878 | 1461 | TTTGCCAGGAGT TCGGCCCCGAG TC[C/gap]TGCCG GCGCTGTGGA TCGGTTGGC | C | gap | Arg (9564) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa. | 3E-269 | 9 |
| 7394 | cg43958878 | 1510 | CGGCCCGCATG GGTGAGGGGC CGG[gap/G]CCTG CGGCTTCCCTGG CTTCGCTG | gap | G | Pro (9565) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa. | 3E-269 | 9 |
| 7395 | cg43958878 | 1530 | GCCGGCCTGCG GCTTCCCTGGCT TT[gap/G]CGCTG CCAGCGCGCAG GGGTGCAT | gap | G | Glu (9566) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa. | 3E-269 | 9 |
| 7396 | cg43958878 | 247 | AGGGTCTCATCT GCTGCTGCGGAT G[C/gap]CACTGT GGCCCATCTG GGCTCATG | C | gap | Ala (9567) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa. | 3E-269 | 9 |
| 7397 | cg43153237 | 244 | CCAGCCCTGGT GCTGGGGGTGG CCC[C/gap]TTGTG CCTGGGTTGTGG CCAGCCCCCT | C | gap | Leu (9568) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60540 HYALURONIDASE - HOMO SAPIENS (HUMAN), 463 aa. | 1E-267 | |
| 7398 | cg43967058 | 536 | CCTTCCAGGAGG GCGCGCGGGC CC[gap/C]GTTGG AACAAATTTCGT GGATAGGC | gap | C | Arg (9569) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60788 DJ32F7.1 - HOMO SAPIENS (HUMAN), 506 aa (fragment). | 6.5E-264 | X |

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| 7399 | cg43967058 | 541 | CAGAAAGGGCGC GGCGGGCCCGT TGG[gap]/G/AACA AATTTCGTGGAT AGGCTGCCT | gap | G | Asn | Glu (9570) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60788 DJ32F7.1 - HOMO SAPIENS (HUMAN), 506 aa (fragment). | 6.5E-264 | X |
| 7400 | cg43967058 | 570 | AATTTCGTGGAT AGGCTGCCTCAG G[gap]/C/JAGTTAG AAATCGTGTGCA AGCGCTT | gap | C | Gly | Gly (9571) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60788 DJ32F7.1 - HOMO SAPIENS (HUMAN), 506 aa (fragment). | 6.5E-264 | X |
| 7401 | cg43980328 | 1085 | CTGAAAGAGATC ATCATCACTGCT G[G/gap]/CCTCGC CTAGAGCAGGAA ACATGGG | G | gap | Ala | Ala (9572) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment). | 3.7E-262 | 10 |
| 7402 | cg43922182 | 1381 | GCTGCTGCTCGA CAGCCCCACGTC G[C/gap]/GCACGC CGCCGCCGCC TCCTGCTC | C | gap | Arg | Ala (9573) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa. | 1.1E-261 | 2 |
| 7403 | cg43922182 | 1570 | CCTGCTGGCGC CGGGGGCCCCG TGC[G/gap]/CGGC CTGCTCGTCGGC CTCGTGCGC | G | gap | Ala | Arg (9574) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa. | 1.1E-261 | 2 |
| 7404 | cg43922182 | 1958 | TCTGAGTCTCCG AGCCTCGACCCT G[G/gap]/CCGCCG CCTGCCAATCTT CAGCCCGC | G | gap | Gly | Ala (9575) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa. | 1.1E-261 | 2 |
| 7405 | cg43922648 | 2335 | GCCAGTAATGGA CACCTGTCTGTT G[G/gap]/CTTTGC CCAGAGCAGCA GTCCCTTT | G | gap | Ala | Ala (9576) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q15054 HYPOTHETICAL PROTEIN KIAA0039 - Homo sapiens (Human), 491 aa (fragment). | 3.3E-260 | 11 |

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| 7406 | cg43980777 | 1028 | CAATCTGGGGTC GTGAGCAAGTG GC[gap]CJTCTT GGCCCTCCTTTT CATCATTT | gap | C | Ala | Gly (9577) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa. | 6.2E-259 | 2 |
| 7407 | cg43929959 | 195 | AAGAAACATGT CAGGACACAAAT G[gap]CJTATCC CTGGGACTTACA GGATCGA | gap | C | Cys | Cys (9578) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:P78506 DIABETES MELLITUS TYPE I AUTOANTIGEN (ISLET CELL AUTOANTIGEN P69) - HOMO SAPIENS (HUMAN), 483 aa. | 2.1E-258 | 7 |
| 7408 | cg43254094 | 1287 | CCGGCTCCAGCT AGGAATGCTGCA G[C/gap]AAGCAC AGTGTGGCCTTG ATCTTCG | C | gap | Gln | Lys (9579) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P78539 SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa. | 6.4E-257 | X |
| 7409 | cg43254094 | 287 | CCGGCTCTGCTG CTGCTGCTGCTG C[gap]TGCGTCC CGCCCAGCCGC AGCTTCCC | gap | T | Arg | Leu (9580) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P78539 SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa. | 6.4E-257 | X |
| 7410 | cg43254094 | 803 | CCAACAACTGA CAGTCCGGGTGT C[C/gap]TGGGAG ACACCCGAAGGA AGAGACA | C | gap | Trp | Gly (9581) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P78539 SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa. | 6.4E-257 | X |
| 7411 | cg43986498 | 1366 | GCTACATCTACC ACAGTGACATCG TG[gap]CAGTCC CTGCCACCGGAT CTGCCGC | G | gap | Gln | Ser (9582) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa. | 1.3E-255 | 19 |
| 7412 | cg43986498 | 1519 | AGATCGAGCGCA AATTCGACAAAT G[gap]CAGGAG CCGCCGCCTGT GAAGCAGG | G | gap | Gln | Arg (9583) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa. | 1.3E-255 | 19 |

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| 7413 | cg43986498 | 1950 | CGGCAGAGAAG AAGGTGGCTGA GGC[C/gap]AACC AGAAATATTTCT CCAGCATGG | C | gap | Asn | Thr (9584) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa. | 1.3E-255 | 19 |
| 7414 | cg43986498 | 961 | GCACGGTCAAG GAGCTGGGCAA CAG[C/gap]CTGG ACAAAGTCAAGA ACAATGAGA | C | gap | Leu | Trp (9585) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa. | 1.3E-255 | 19 |
| 7415 | cg43978430 | 1070 | TACGACGCCACA TCTCTGCCCGCA G[G/gap]TGCAGA CCCACAGCAAGT GATCAAT | G | gap | Gly | Val (9586) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75879 CYTOCHROME OXIDASE ASSEMBLY FACTOR - HOMO SAPIENS (HUMAN), 557 aa. | 2.8E-255 | 4 |
| 7416 | cg44034555 | 470 | GCGGAGTCTCAT GGGCAAGGGCT GGG[C/gap]CAAG GGGCTCCTTCCC GAAGTCCAC | C | gap | Gly | Ala (9587) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa. | 3.8E-252 | 1 |
| 7417 | cg44034555 | 471 | CGGAGTCTCATG GGCAAGGGCTG GGC[C/gap]AAGG GGCTCCTTCCCG AAGTCCACC | C | gap | Gly | Ala (9588) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa. | 3.8E-252 | 1 |
| 7418 | cg39711096 | 893 | CCGGGAGGCCCC ACAGTTACTGCC TC[C/gap]AGCTG CAGCAGTGACAT CGCTGACC | C | gap | Ser | Ala (9589) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa. | 1E-251 | |

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| 7419 | cg43254830 | 1275 | CATTCCAAAGCT CTGACCCAGAAC A[G/gap]ATGCGA CAGAGTTTGCTG ACTGCCAA | G | gap | Met | Cys (9590) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA78821 KIAA0977 PROTEIN - HOMO SAPIENS (HUMAN), 1166 aa. | 1.3E-251 | 2 |
| 7420 | cg43254830 | 1323 | CAATCCGTTCCG GAGAGGCTGCT GC[C/gap]AAATT GAAAAGGGTTAC CATTCCAT | C | gap | Lys | Asn (9591) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA78821 KIAA0977 PROTEIN - HOMO SAPIENS (HUMAN), 1166 aa. | 1.3E-251 | 2 |
| 7421 | cg44910581 | 2889 | CAAACTCTGAAG TGAACCTCATGAT C[gap]/AJGTAGA ATACCAGATCCT TATACTC | gap | A | Cys | Met (9592) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa. | 5.8E-251 | |
| 7422 | cg43945969 | 303 | GGAGGCCCTGC GCGCGCTCAGC GCG[C/gap]TCTT CAAAGAGCAGC GGAACCGAGA | C | gap | Leu | Ser (9593) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB43383 HYPOTHETICAL 53.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 475 aa. | 4.1E-246 | 22 |
| 7423 | cg43980318 | 142 | CAACGGCGATTG CGGCCGCCCA GG[G/gap]CGCG GCCCGGAGGAA ACCGGGTGAC | G | gap | Ala | Arg (9594) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCLINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa. | 1.6E-244 | 1 (1cen) |
| 7424 | cg43980318 | 150 | ATTGCGGCCGC CCCAGGCGCG GCC[C/gap]GGAG GAAACCGGGTG ACGGTGGTGC | C | gap | Gly | Glu (9595) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCLINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa. | 1.6E-244 | 1 (1cen) |
| 7425 | cg43980318 | 231 | GGAAGGTGGTG GACCTGCTGCG GCA[G/gap]GACG CCGACATCGTGT GCCGCTGCC | G | gap | Asp | Thr (9596) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCLINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa. | 1.6E-244 | 1 (1cen) |

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| 7426 | cg43980318 | 232 | GAAGGTGGTGG ACCTGCTGGCG CAG[G/gap]ACGC CGACATCGTGTG CCGCTGCCA | G | gap | Asp | Thr (9597) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa. | 1.6E-244 | 1 (1can) |
| 7427 | cg43980318 | 237 | TGGTGGACCTGC TGGCGCAGGAC GC[C/gap]GACAT CGTGTGCCGCT GCCAGGGAG | C | gap | Asp | Thr (9598) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa. | 1.6E-244 | 1 (1can) |
| 7428 | cg43980318 | 87 | GCGTCACTGGA GCCATGGCGTTC GC[C/gap]GAGAC CTACCCGGCGG CATCCTCCC | C | gap | Glu | Arg (9599) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa. | 1.6E-244 | 1 (1can) |
| 7429 | cg43994815 | 358 | GTCAGTGTCCAC CCCTGGCTGGG AG[G/gap]CAGAG CCGGACCTTCCT CGTGGACC | G | gap | Gln | Arg (9600) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O43632 SPINDLE POLE BODY PROTEIN SPC97 HOMOLOG - HOMO SAPIENS (HUMAN), 902 aa. | 3E-236 | 10 |
| 7430 | cg43994815 | 729 | AGCCTGTCCAC GACAGGAGCTTC A[G/gap]CTACAC AGGGACAGCC AGGCGCAG | G | gap | Ser | Thr (9601) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O43632 SPINDLE POLE BODY PROTEIN SPC97 HOMOLOG - HOMO SAPIENS (HUMAN), 902 aa. | 3E-236 | 10 |
| 7431 | cg43932322 | 327 | TGGTCCAGCCGT GGAAGGGCGG CA[gap]GICCGAT GCCTCGCCCATC GCGGTAC | gap | G | Cys | Leu (9602) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q88941 GLYCOPROTEIN PROCESSING GLUCOSIDASE I - RATTUS NORVEGICUS (RAT), 834 aa. | 6.5E-236 | 2 |
| 7432 | cg43330158 | 1330 | GAAGTCGCACAA GACCCGCAACCA G[gap]/C/JACAGGA CGAGGGGATCC TGCCCTCG | gap | C | Arg | Ser (9603) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa. | 2.1E-235 | |

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| 7433 | cg43330158 | 1332 | AAGTCGCACAAG ACCCGCAACCAG A[C/gap]AGGACG AGGGGATCCTG CCCTCGGG | C | gap | Gln | Arg (9604) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa. | 2.1E-235 | |
| 7434 | cg43330158 | 1333 | AGTCGCACAAGA CCCGCAACCAGA C[A/gap]GGACGA GGGGATCCTGC CCTCGGGC | A | gap | Gln | Arg (9605) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa. | 2.1E-235 | |
| 7435 | cg43930174 | 1376 | CAGTGCTGCGG GGCCGCATGGT GCG[G/gap]TACC TGATGCGCTCGC GTGAGATCA | G | gap | Tyr | Thr (9606) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14742 NUCLEOLAR PROTEIN - HOMO SAPIENS (HUMAN), 462 aa. | 2.4E-234 | 12 |
| 7436 | cg43948360 | 2451 | CTCCATGTTGAG GGCCAGTCCTC G[C/gap]TCTGCA GGGAGCCATCT GTGGCTTT | C | gap | Ser | Thr (9607) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa. | 5.1E-234 | 22 |
| 7437 | cg43952917 | 1353 | TGGGCATTGACA GCAACCTGGGT C[C/gap]TAACGG TTTGGTTAACAC CAGCACG | C | gap | Gly | Glu (9608) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q99611 SELENIDE;WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2) (SELENIUM DONOR PROTEIN 2) - Homo sapiens (Human), 448 aa. | 1.5E-232 | |
| 7438 | cg43940463 | 852 | GTGCTCTTGGTA GTACTCCAGGAA G[G/gap]CGCGGC CCACACTCTGCG CCACCGG | G | gap | Ala | Ala (9609) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa. | 3.1E-232 | |

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| 7439 | cg43947107 | 781 | CCATGCGCACCC GCTGCCTCAGCT C[C/gap]TGCCGG CTCACCTCCTCC TTTGCCA | gap | Gln (9610) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75528 ADA3-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 432 aa. | 2.8E-231 | 3 |
| 7440 | cg43948144 | 1163 | TAAAAAGGCCAA GTTTCACCACTC T[G/gap]ATTGCC TTTCAACCTGGC TACTTCA | gap | Asp (9611) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA74901 KIAA0878 PROTEIN - HOMO SAPIENS (HUMAN), 611 aa. | 4.6E-231 | 5 |
| 7441 | cg43986279 | 2340 | CTACCCGCTTCC GCGGCCCGAC TG[G/gap]CTGTG CCGCGTGGTGA AGCACCTGC | gap | Leu (9612) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P37288 VASOPRESSIN V1A RECEPTOR (VASCULAR/HEPATIC-TYPE ARGININE VASOPRESSIN RECEPTOR) (ANTIDIURETIC HORMONE RECEPTOR 1A) (AVPR V1A) - Homo sapiens (Human), 418 aa. | 7.5E-231 | 12 (12q14) |
| 7442 | cg43986279 | 2588 | GTCACCAAGGCC C GCGACTGCTG GG[C/gap]CACCT TCATCCAGCCCT GGGGTTCT | gap | Ala (9613) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P37288 VASOPRESSIN V1A RECEPTOR (VASCULAR/HEPATIC-TYPE ARGININE VASOPRESSIN RECEPTOR) (ANTIDIURETIC HORMONE RECEPTOR 1A) (AVPR V1A) - Homo sapiens (Human), 418 aa. | 7.5E-231 | 12 (12q14) |
| 7443 | cg43916785 | 3222 | GATCTGGATGCC CTTCTGCCAGAA G[G/gap]CGCTGC CTGATTTCCTCA AGCTCCT | gap | Arg (9614) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment). | 2.5E-230 | 14 |
| 7444 | cg43933074 | 1068 | CAGCTCCACCCCT C GAAGTCGCTGCT G[C/gap]GCCCCC ACTTCTCAACA CGCCTGA | gap | Ala (9615) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa. | 3.2E-228 | 19 |

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| 7445 | cg43933074 | 115 | GTGCAGTTCTAC AAGGTGTGCGTG A[G/gap]CGTGGT GAGCGAGAAGT GCCGTATC | G | gap | Ser | Thr (9616) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa. | 3.2E-228 | 19 |
| 7446 | cg43933074 | 967 | TCCACCCGGATC CTGGCCATGAAG G[C/gap]CTCGCT CTGCAAGCTGTC GCCCTGC | C | gap | Ala | Ala (9617) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa. | 3.2E-228 | 19 |
| 7447 | cg43978295 | 756 | TGCCAGGGATGA ATAGCCACTGGG G[C/gap]CCTGGC CATAGCTGGACT GTCTCTT | C | gap | Gly | Gly (9618) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa. | 1.4E-227 | 6 |
| 7448 | cg43978295 | 758 | CCAGGGATGAAT AGCCACTGGG CC[C/gap]TGGCC ATAGCTGGACTG TCTCTTC | C | gap | Gly | Gly (9619) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa. | 1.4E-227 | 6 |
| 7449 | cg43918561 | 603 | AGAGGACGTGC GCAGCCCCGCG GGG[G/gap]CCCCA AGTCCCCCTGGT TCCCAAGAA | G | gap | Pro | Pro (9620) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa. | 2.1E-224 (11p15.5) | 11 |
| 7450 | cg43994204 | 674 | CGCACGTCAAGA CTGTCTGCGACG C[A/gap]GCAGAG AAGGGAGTGAG GACCCCTCA | A | gap | Ala | Gln (9621) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa. | 5.4E-221 | 19 |
| 7451 | cg44032871 | 637 | TGTGGTGGGGT CTCCTCGGAGCT GG[G/gap]CCCTT GGCGGGGCAGC TGCAGAAAT | G | gap | Pro | Pro (9622) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment). | 1.1E-220 | 5 |

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|------|------------|------|--|---|-----|-----|---------------|----------------|------------------|---|----------|----|
| 7452 | cg43960557 | 741 | CAGGCTCTAGAA AGTCATCTGCTG C[C/gap]CCCCAG GTCCTCCAGGGA ATCCTCC | C | gap | Gly | Ala (9623) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa. | 2.7E-220 | 22 |
| 7453 | cg43062833 | 1042 | CTGGCCCCCAGAA AGGGGCTTTTGG C[C/gap]ACCAGC TTCAGAAAAACA TGGCAGC | C | gap | Pro | His (9624) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q83088 BETAINE--HOMOCYSTEINE S- METHYLTRANSFERASE (EC 2.1.1.5) - Homo sapiens (Human), 406 aa. | 2.1E-219 | 5 |
| 7454 | cg43934903 | 894 | CTGGAGCAAAAC CTCCCTGAAGTC C[C/gap]TGAGGG GCAATGTTCCAG GCAAGGT | C | gap | Gln | Gln (9625) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa. | 3.1E-218 | 1 |
| 7455 | cg43251548 | 233 | AGCTTCCTATGG ATCTGCGGGACC G[C/gap]TTCACG GAAATGCGCGA GATGGACC | C | gap | Phe | Ser (9626) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60394 PAC CLONE DJ0872F07 FROM 7Q31, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 408 aa (fragment). | 2.7E-217 | |
| 7456 | cg43251548 | 274 | GAGATGGACCTG CAGGTGCAGAAT G[C/gap]AATGGA TCAACTAGAACA AAGAGTC | C | gap | Ala | Glu (9627) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60394 PAC CLONE DJ0872F07 FROM 7Q31, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 408 aa (fragment). | 2.7E-217 | |
| 7457 | cg43990581 | 262 | CAGATCCTCAGC CACCGCTTCAAA G[C/gap]CTGTGC CCAGCAGGTC CAGTGAGC | C | gap | Ala | Ala (9628) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60651 RAP2 INTERACTING PROTEIN 8 - HOMO SAPIENS (HUMAN), 405 aa. | 1.6E-214 | 17 |
| 7458 | cg43990581 | 263 | AGATCCTCAGCC ACCGCTTCAAAG C[C/gap]TG TGCC CCAGCAGGTCCA GTGAGCT | C | gap | Cys | Val (9629) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60651 RAP2 INTERACTING PROTEIN 8 - HOMO SAPIENS (HUMAN), 405 aa. | 1.6E-214 | 17 |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|------------------|--|----------|---------------|
| 7459 | cg43062448 | 1362 | GAATCCATAAAA TGGTGAAGTCCC A[gap]TGGAGCT CCACAAATGTAG CCAAATT | gap | T | Leu | His (9630) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa. | 9.9E-213 | 3 (3q21.3) |
| 7460 | cg43969195 | 156 | TGGAGGAGCTG CTCGCAAAAGGCA GA[G/gap]CAGGA CGAGGCAGAGA AGTTGCAAC | G | gap | Gln | Arg (9631) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:Q15050 HYPOTHETICAL PROTEIN KIAA0112 (HA0609) - Homo sapiens (Human), 399 aa (fragment). | 2.8E-211 | 8 |
| 7461 | cg43332618 | 619 | GTCACAGGGCA CCTCGAAGCTGA AA[G/gap]CTTCG TTGTAATAGGGG TTCAGAGT | G | gap | Ala | Val (9632) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:O00445 SYNAPTOTAGMIN V - Homo sapiens (Human), 386 aa. | 5.8E-208 | 19 |
| 7462 | cg43932174 | 464 | CACACTTCTTAT TCCTGGGCTTTA[G/gap]CTCTTCGG CTGCATTACGCA GGAAA | G | gap | Leu | End (9633) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa. | 4.1E-207 | 20 |
| 7463 | cg43986867 | 1174 | GAAGAACTTGTA GAACATTACAAA A[A/gap]GGCACC AATTTTACAAGT GAACAA | A | gap | Lys | Arg (9634) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa. | 8.5E-207 | 3 (3q21) |
| 7464 | cg43920365 | 922 | TGCTTTGTGAAT GGTGCTGGGCT CG[C/gap]CATGG CTACTGTGATA TCATTTTC | C | gap | Ala | Ala (9635) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa. | 6E-206 | 3 |
| 7465 | cg43968205 | 508 | AGGGCCACGGA GACACACTGTAC GT[G/gap]GGGAC CACCCGCAATTC CATCCTGC | G | gap | Gly | Gly (9636) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB46373 HYPOTHETICAL 71.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 653 aa (fragment). | 6.9E-206 | |

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|------|------------|------|---|---|-----|-----|---------------|----------------|------------------|--|----------|---------------|
| 7466 | cg43999733 | 1292 | GGCCCGGCGCT GACACGGCCAG CTC[G/gap]GGCT CGCCCCGAAC TCCTCCCGGA | G | gap | Pro | Pro (9637) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa. | 8.8E-205 | 17 (17q24) |
| 7467 | cg43999733 | 1310 | CCAGCTCGGC TCGGCCCCGAA CTC[C/gap]TCCC GGAAGGCTCGC CGGGCCTCGG | C | gap | Glu | Glu (9638) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa. | 8.8E-205 | 17 (17q24) |
| 7468 | cg43999733 | 1327 | CCGAACCTCTCC CGGAAGGCTCG CC[G/gap]GGCCT CGGCCAGCAGC TCCGCGACC | G | gap | Arg | Gly (9639) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa. | 8.8E-205 | 17 (17q24) |
| 7469 | cg43999733 | 464 | AGCGGTGGCTCT CCACCATGAGGC G[G/gap]CCAAAG GCTCTGTAGTCG CCACGTC | G | gap | Gly | Gly (9640) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa. | 8.8E-205 | 17 (17q24) |
| 7470 | cg43999733 | 614 | GCTCTCCAGTT GTACCTCCCCGA G[G/gap]CTTTCC TTGCCACGCGCC CGGGCCA | G | gap | Ser | Ser (9641) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa. | 8.8E-205 | 17 (17q24) |
| 7471 | cg43999733 | 659 | GGGCCACTTCTT CACATTGGCGCC G[C/gap]CGCACA GGGTACTCGCTG GAGGCCA | C | gap | Arg | Arg (9642) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa. | 8.8E-205 | 17 (17q24) |

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|------|------------|------|---|-----|---------------|----------------|------------------|---|----------|---------------|
| 7472 | cg43999733 | 660 | GGCCACTTCTTC ACATTGGCGCCG C[C/gap]GCACAG GGTACTCGCTGG AGGCCAG | gap | Arg (9643) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa. | 8.8E-205 | 17 (17q24) |
| 7473 | cg43302693 | 632 | GCAGCTGGCTTC GGCAGGCCGTC AG[G/gap]ACCCA GGAGGTGGCG CAGGGGTCA | gap | Pro (9644) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa. | 2.7E-204 | 16 |
| 7474 | cg43302693 | 671 | GCGCAGGGGTC ATCCAGGATTG AG[G/gap]CCCTG GCCCCACCTGA GTGACAATG | gap | Pro (9645) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa. | 2.7E-204 | 16 |
| 7475 | cg43302693 | 678 | GGTCATCCAGGA TTTGAGGCCCTG G[C/gap]CCCACC TGAGTGACAATG ATGTATT | gap | Gly (9646) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa. | 2.7E-204 | 16 |
| 7476 | cg43302693 | 681 | CATCCAGGATT GAGGCCCTGGC CC[C/gap]ACCTG AGTGACAATGAT GTATTGA | gap | Val (9647) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa. | 2.7E-204 | 16 |
| 7477 | cg43950996 | 2126 | GTAGCTGATCCA GTCCAGAACCTG C[G/gap]TCCTCG ACCAGAACTGGG GCTGTTC | gap | Thr (9648) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa. | 6.2E-204 | 1 |

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|------|------------|------|--|-----|-----|---------------|-----|----------------|------------------|--|--------------------|----|
| 7478 | cg43942842 | 2011 | CATGAGGCCGAA CATGTTTCCGCA G[G/gap]CCTTGC TCACCGCAGCCA TCTTGGC | G | gap | Ala (9649) | Ala | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P49903 SELENIDE,WATER DIKINASE 1 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) - Homo sapiens (Human), 383 aa. | 1.9E-203 | 17 |
| 7479 | cg43942842 | 2730 | GAATGACACAAG TATCCATTCCAA T[G/gap]CCAAGC CTTGGCATAACG GCTCCCA | G | gap | Gly (9650) | Gly | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P49903 SELENIDE,WATER DIKINASE 1 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) - Homo sapiens (Human), 383 aa. | 1.9E-203 | 17 |
| 7480 | cg43959472 | 990 | TGAGGTAGATGA TGACCACATTGT C[C/gap]TCCGGC CCTGATGGCTGC ACCTCGT | C | gap | Glu (9651) | Glu | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa. | 2.4E-203 | 15 |
| 7481 | cg43918848 | 2198 | ACGGCCTGTTGG TGACCTCAGCTC C[G/gap]GGCAGG GAATCCGTTGCA GTGCCGG | G | gap | Pro (9652) | Pro | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa. | 5.6E-202 | 2 |
| 7482 | cg43918848 | 2200 | GGCCTGTTGGTG ACCTCAGCTCCG G[G/gap]CAGGGA ATCCGTTGCAGT GCCGGTC | G | gap | Pro (9653) | Pro | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa. | 5.6E-202 | 2 |
| 7483 | cg44128902 | 825 | CCTAGGAAAGG GAATACTCTCTA TG[gap]ATATATG GAGAAAGACATGA CACCCAC | gap | A | Asp (9654) | Val | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa. | 1E-201 (1p36.2) | 1 |
| 7484 | cg43940298 | 804 | GTCACCTGAATGA TAGGTGATTATG G[G/gap]CCCCGG GCACCTCCGCTT CTTATGA | G | gap | Pro (9655) | Pro | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q15906 YL-1 PROTEIN - Homo sapiens (Human), 364 aa. | 3.7E-197 | 1 |

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| 7485 | cg44015472 | 1167 | ACTTGGATGTTG TCGGGCGGCGT TG[gap]CACAG GGCCAGCGCTC ACCGCCAGG | G | gap | Pro | Gln (9656) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa. | 8.9E-196 | 9 (9q32) |
| 7486 | cg44015472 | 618 | CCTTCCTCTTCT TGGGGTAGCACA G[C/gap]CCTCCG GACTCTCGGGAT TAAGATG | C | gap | Ala | Leu (9657) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa. | 8.9E-196 | 9 (9q32) |
| 7487 | cg44015472 | 716 | GGTGAAGATGGA GTCCTCAGGGAT G[C/gap]CCACAC CCTGGGCAACCA CTCTGAA | C | gap | Gly | Ala (9658) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa. | 8.9E-196 | 9 (9q32) |

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| 7488 | cg44015472 | 771 | TGCAGGAGAGT TCCCTCAGCTGC G[G/gap]CGCCCG CCCGTAGAGCTT GGCAGTA | G | gap | Pro | Arg (9659) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P02760 AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa. | 8.9E-196 | 9 (9q32) |
| 7489 | cg43287442 | 765 | CTGGGCAGAGT TTTGTCACAAA A[gap]/JTTCATTA TGCTGCAAGGCC GTAAAT | gap | A | Phe | Phe (9660) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD09188 PLACENTA-SPECIFIC ATP-BINDING CASSETTE TRANSPORTER - HOMO SAPIENS (HUMAN), 655 aa. | 3.1E-193 | 4 |
| 7490 | cg43970111 | 1377 | CCTGGCTGAGTC AGCTGGGGCTG AC[C/gap]TCCGG AGTCAGCCATCT TGAGGAAC | C | gap | Gly | Val (9661) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD43131 SYLD709613 PROTEIN HOMO SAPIENS (HUMAN), 357 aa. | 6.5E-193 | 14 |
| 7491 | cg43935935 | 284 | TTAGTCTTACG GCGTCAATAACA A[A/gap]TGCTTC AACATCATCAGC TCCAATC | A | gap | Phe | Leu (9662) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O60735 GA17 PROTEIN - HOMO SAPIENS (HUMAN), 374 aa. | 1.7E-192 | X |
| 7492 | cg43973314 | 638 | ATGATCTGACTA ACTTCACTGATA TTT[gap]CCCCCT GGTGGAGTAGA GGAGAAAG | T | gap | Pro | Pro (9663) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:O75521 DBI-RELATED PROTEIN 1 (DRS-1) - Homo sapiens (Human), 364 aa. | 3.6E-192 | 6 |
| 7493 | cg43964795 | 1267 | TGTTTCTTTTC AGCTCTTCAAAC[C/gap]TCCGGGA AAGATCATCAAA GTCAAT | C | gap | Arg | Ser (9664) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa. | 5.8E-192 | 16 |

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| 7494 | cg439968431 | 235 | TCGTCGTCGCTG CCCTCGCCGCC CG[C/gap]GCCGC CCATCCGCTCCT CTCTGCTC | C | gap | Ala | Arg (9665) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa. | 1E-191 | 11 |
| 7495 | cg439968431 | 438 | CACGCCTTGAC ATCTTCTTCATG G[gap/G]CCTTGG GAGCCAGGAACT GAGAAGA | gap | G | Ala | Ala (9666) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa. | 1E-191 | 11 |
| 7496 | cg439968431 | 500 | CCACTTGGGTAA GGAGCCTTTGG GG[gap/G]TCCAC CTGGGCCAGGT AGGTGATGA | gap | G | Asp | Asp (9667) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa. | 1E-191 | 11 |
| 7497 | cg43920610 | 924 | CAGGCCACCTGT TTCTTCCAAACA G[C/gap]TTTCAG CAACATGAACCT TCCCAT | C | gap | Ser | Thr (9668) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD22381 QUINONE OXIDOREDUCTASE HOMOLOG-1 - HOMO SAPIENS (HUMAN), 349 aa. | 5.9E-191 | 21 |
| 7498 | cg43996402 | 1046 | GGAAGAGGAGG AGGAGGAGGAA GAT[G/gap]AGGA AGAAGAGGACTT ATGTTTTT | G | gap | Ser | Tyr (9669) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |
| 7499 | cg43996402 | 1220 | TCAACTTCTGGA TCTTCTTCACCC T[gap/G]CACTTG CAACATACTCCT GTGATGG | gap | G | Glu | Ala (9670) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |
| 7500 | cg43996402 | 1249 | TGCAACATACTC CTGTGATGGATC A[gap/G]TTTGGC GTCAAGTTTCTC CCCAGTA | gap | G | Lys | Asn (9671) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |

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|------|------------|------|--|-----|-----|-----|---------------|----------------|------------------|---|----------|---|
| 7501 | cg43996402 | 1300 | ATTTCGTTTCAG TGCAAAACCCACT G[gap/G]TTTCTC ATCTCCGCTATT AGCTCCG | gap | G | Lys | Asn (9672) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |
| 7502 | cg43996402 | 1376 | TCAGTGGGAACC GAACTTGCATTG A[gap/G]TTCCAG AAAGACCAACA AAGGACA | gap | C | Ile | Ser (9673) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |
| 7503 | cg43996402 | 1427 | TTCTCGATCTGT GTTGACATGACC C[C/gap]ATTTGT GACATTTAATGC ACCTCAC | C | gap | Trp | Trp (9674) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |
| 7504 | cg43996402 | 599 | CTTCTGCTTTGC TCTTCACCAGGA T[gap/G]TTCGCT GTGCCCGTTTCC TTGTCTC | gap | G | Asn | Thr (9675) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |
| 7505 | cg43996402 | 962 | TTTTCTTTCTTT TCTTCCTTTGTA[gap/G]TTTTTTTT CTTTATTGTTACT CTC | gap | G | Ile | Thr (9676) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.6E-189 | 2 |
| 7506 | cg44002198 | 1629 | GAAGGGCCTCG GACTTCAGCGTG AG[G/gap]CCCCGA GGCGCCAGGG GCTGCTGCA | G | gap | Gly | Gly (9677) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa. | 8.8E-189 | 7 |
| 7507 | cg44002198 | 1665 | CCAGGGGCTGC TGCAGCAGGAAC AG[G/gap]CGAGG CCCGGAAACCA GCAGCGAGA | G | gap | Arg | Arg (9678) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa. | 8.8E-189 | 7 |

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| 7508 | cg44002198 | 716 | CTGGAGGACTCC TTGGAGCCTGCA G[gap/C]CCCCCTG GTGTCCCAAGGC CCCAGAA | gap | C | Leu | Ala (9679) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa. | 8.8E-189 | 7 |
| 7509 | cg43249389 | 991 | GATTGGGGCCG CCGACTACCAAGC CC[A/gap]CTGAG CAGGACATCCTC CGAACCAG | A | gap | Thr (9680) | Leu (9680) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa. | 1.4E-188 | 15 |
| 7510 | cg43947129 | 1222 | TTTTTCTAAAGC ATCATCTCCTTT G[gap]GCATTGC CAATGCGGAATG GAATAT | G | gap | Ala | Ala (9681) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa. | 3E-188 | |
| 7511 | cg43947129 | 2137 | GACCAGGCCCA AAGTTGACCACC TG[C/gap]CTGGG GGCGTCCATGGT GCGGCGGC | C | gap | Arg | Ser (9682) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa. | 3E-188 | |
| 7512 | cg43922383 | 660 | CGATGCCATTGT GGCTAAGGTACA G[C/gap]TCCCGC AGGTTCCACCAGG TTCTGCA | C | gap | Glu | Asp (9683) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |
| 7513 | cg43047610 | 604 | ACACTATCGAGG AGGCACGATG CC[C/gap]AAGGA GATGCGGACAT CATCCAGC | C | gap | Lys | Arg (9684) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB37839 TRANSDUCIN ALPHA- SUBUNIT - HOMO SAPIENS (HUMAN), 350 aa. | 7.3E-185 3 (3p21) | |

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| 7514 | cg43950796 | 1309 | GCGTGGGTCTC CCTACCCCACT TG[G/gap]CCATC GGCTCTCCTATC GCGGCGCC | G | gap | Ala (9685) | Ala | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa. | 2.5E-184 | |
| 7515 | cg43950796 | 783 | GCTCCTCAGTTT TCAGTGCTGGCT G[C/gap]CCCACT GGTCTACTGAC TCTCCAT | C | gap | Gly (9686) | Gly | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa. | 2.5E-184 | |
| 7516 | cg44007066 | 1553 | GCCTCTTGGGT TGGGCTCGGCC TG[C/gap]CTGCG GAAGTAGTCTGG CCCCTTGT | C | gap | Ser (9687) | Arg | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAB50224 HYPOTHETICAL 41.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 373 aa (fragment). | 1.7E-183 | |
| 7517 | cg44128927 | 599 | GACCCAGCCAG AGGCCCTCCCGC GGA[G/gap]CCGG GACTGCAGAGTC GACCTGGGC | G | gap | Thr (9688) | Ser | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD38070 REVERSION-INDUCED LIM PROTEIN - HOMO SAPIENS (HUMAN), 330 aa. | 2.8E-183 | 5 |
| 7518 | cg43986952 | 1388 | CAAACTGGCACT TGGCCCCGTAG CG[G/gap]CAGCG CCCACTCTCTGA GAAGGTCC | G | gap | Cys (9689) | Cys | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSPROT-ACC:P26651 TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475) - Homo sapiens (Human), 326 aa. | 2.9E-181 | 19 (19q13.1) |
| 7519 | cg43923337 | 216 | GTGGCAGGGAC GACGCCCAAGAT GG[G/gap]AGCTG ACTGATATGGTG GTGTGGGT | G | gap | Ser (9690) | Glu | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa. | 3.7E-181 | 14 |

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| 7520 | cg43299409 | 279 | TCGGCCACCAC GGCGCTGAGGA CGC[C/gap]ACGG ATGCCCTCCGTG CCTTCCATC | C | gap | Thr | Arg (9691) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD31282 DELTA-6 FATTY ACID DESATURASE - HOMO SAPIENS (HUMAN), 445 aa. | 7.9E-181 | |
| 7521 | cg43951707 | 415 | GCAGCGGCCT TGGCCGAGCGG GCG[G/gap]CCGG GGCTGCAGCC CAAGAAGCGT | G | gap | Ala | Pro (9692) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q15814 COFACTOR C - HOMO SAPIENS (HUMAN), 346 aa. | 2.7E-178 | 6 |
| 7522 | cg43961139 | 1782 | CAAAGGTGTAGA GCTGCTTCCCTT C[G/gap]TGTCGC TTCCCAATGACG GGCATGA | G | gap | His | Gln (9693) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB43360 HYPOTHETICAL 96.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 837 aa. | 2.7E-178 | 22 |
| 7523 | cg43969747 | 1720 | GCATTCACCTGG GAGTCCTGGTGC TIG[gap]CACCGT CCGGGTGCAGA TGCCGCTG | G | gap | Gln | Ser (9694) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa. | 5.1E-177 | 16 |
| 7524 | cg42733649 | 1058 | AGCCTGGAGCTC CTGTTCCCTGAA TIC[gap]CTTCGG CTTCATCACCTA TCAGGGC | C | gap | Ser | Ser (9695) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75493 CARBONIC ANHYDRASE-RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 328 aa. | 1.1E-176 | |
| 7525 | cg42733649 | 1059 | GCCTGGAGCTC CTGTTCCCTGAA TIC[gap]TTCGG CTTCATCACCTA TCAGGGCT | C | gap | Phe | Ser (9696) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75493 CARBONIC ANHYDRASE-RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 328 aa. | 1.1E-176 | |
| 7526 | cg43268525 | 820 | TGTCACCTCCAC AGCTGCCGCGG GA[G/gap]CTGCC ATCGTCACATAC AAATGCAA | G | gap | Leu | Cys (9697) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76815 KIAA0971 PROTEIN - HOMO SAPIENS (HUMAN), 648 aa. | 1.1E-176 | |

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| 7527 | cg44035397 | 1626 | TTTTGGTCTGT GGTTTCAGCCGT G[G/gap]CCTGGG CCTAAGGCTCTC CTCTGGC | G | gap | Pro | His (9698) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45826 C2H2-150 - HOMO SAPIENS (HUMAN), 326 aa. | 1.7E-176 | 7 |
| 7528 | cg44035397 | 1632 | GTCTGTGGTTTC AGCCGTGGCCT GG[G/gap]CCTAA GGCTCTCCTCTG GCTCCTCA | G | gap | Pro | Pro (9699) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45826 C2H2-150 - HOMO SAPIENS (HUMAN), 326 aa. | 1.7E-176 | 7 |
| 7529 | cg43931789 | 89 | CCGAGTCGGCC CAGGGTCCCC GGG[C/gap]CCGG CAGCGTCGCTG GAGCTGTGGC | C | gap | Pro | Arg (9700) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14564 HYPOTHETICAL 67.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 613 aa. | 2E-175 | 16 |
| 7530 | cg43941890 | 1330 | GGCATCAGGAG AAAGCTGGGTC TT[G/gap]GGACC TTGTCTCTCCCA GTTGGCCT | G | gap | Gly | Asp (9701) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD43024 MNUDC PROTEIN - HOMO SAPIENS (HUMAN), 331 aa. | 5.2E-175 | |
| 7531 | cg43941890 | 1332 | CATCAGGAGAAA GGCTGGGCTTTG G[G/gap]ACCTTG TCCTCCCCAGTT GGCCTAC | G | gap | Gly | Asp (9702) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD43024 MNUDC PROTEIN - HOMO SAPIENS (HUMAN), 331 aa. | 5.2E-175 | |
| 7532 | cg43967532 | 3773 | CACGAGTCGGC CACGGCCTCGC AGA[G/gap]CCAG CGACACGGTA GATGGGCCGG | G | gap | Leu | Ser (9703) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa. | 2.3E-174 | 8 |
| 7533 | cg43967532 | 3963 | CCATCTTCTTGT AGCCACGTTGT G[G/gap]CACAGC CGCAGGTCCGC GGGGATGT | G | gap | Cys | Cys (9704) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa. | 2.3E-174 | 8 |

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| 7534 | cg43967532 | 4074 | GGAAGCTCACGT AGTCGTACTCGC T[G/gap]GCCGAG CCCACGGCCAG AAGCGCCG | G | gap | Ala | Ala (9705) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa. | 2.3E-174 | 8 |
| 7535 | cg43967532 | 4128 | CCAGCGCCAGC AGCACGCCCGAG GGC[T/gap]GCCC CGCGCGGGCCC CCCTCGCTGC | T | gap | Ala | Ala (9706) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa. | 2.3E-174 | 8 |
| 7536 | cg43941339 | 1446 | GTTTAACTGGTA TGGCACAGGTGA T[G/gap]CCTAGG AGGCAAAAGCAA ATCACTG | G | gap | Gly | Gly (9707) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:P10451 OSTEOPONTIN PRECURSOR (BONE SIALOPROTEIN 1) (URINARY STONE PROTEIN) (SECRETED PHOSPHOPROTEIN 1) (SPP-1) (NEPHROPONTIN) (UROPONTIN) - Homo sapiens (Human), 314 aa. | 8.2E-170 | 4 (4q21) |
| 7537 | cg44032718 | 794 | GCTTCTGGAACC ACAGGTGGCCG AA[G/gap]GGTCT CAAAGGCTCTAA TGGCCTCA | G | gap | Arg | Arg (9708) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa. | 5.7E-169 | X |
| 7538 | cg44034179 | 1178 | TGGGCAGAGCC GTTTGGGGCCAC GC[C/gap]ATCGC GGACGTCATCCT GGAGGGTC | C | gap | Gly | Ala (9709) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14792 HEPARAN SULFATE 3-O- SULFOTRANSFERASE-1 PRECURSOR HOMO SAPIENS (HUMAN), 307 aa. | 1.6E-166 | 4 |
| 7539 | cg44034179 | 1272 | GGGAAGGCAC AGCTGGGGCTG GGC[C/gap]ACCA GCAGCACCCGG CCCAGGAGCA | C | gap | Val | Val (9710) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O14792 HEPARAN SULFATE 3-O- SULFOTRANSFERASE-1 PRECURSOR HOMO SAPIENS (HUMAN), 307 aa. | 1.6E-166 | 4 |

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| 7540 | cg43926509 | 1244 | CCTGCAGCAGTA ACGGGAGGATG GA[G/gap]GGGCC ACCCCCACATA CAGCGAGG | G | gap | Gly | Gly (9711) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O15165 CLONE 22 - HOMO SAPIENS (HUMAN), 306 aa. | 4.2E-166 | 18 |
| 7541 | cg44003630 | 1080 | ATGGTTGGAATT CGGACCAGATAG A[G/gap]GGCTCG CCCCAGAACATG CCCTCTTG | G | gap | Leu | Ser (9712) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa. | 5.1E-164 | |
| 7542 | cg44004690 | 826 | GCTGCTGAGGAT GCTGGAGAAGC GG[C/gap]AGATG GACCGAGCGGA GCACAAAGGG | C | gap | Gln | Arg (9713) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA74892 KIAA0869 PROTEIN - HOMO SAPIENS (HUMAN), 888 aa (fragment). | 2.5E-161 | |
| 7543 | cg43929687 | 425 | TGGTGTCTATAAT TCTCCAGCATGA G[C/gap]TCTGCT GGTCCTCTCGGT CTGACCTG | C | gap | Glu | Asp (9714) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB51351 DJ475B7.2 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 717 aa. | 8.5E-160 | |
| 7544 | cg43315424 | 341 | GCTCAGGAACAA CAGGCTGACCG GA[G/gap]GCAGT GCCAGGAGAG GCAGGCTAG | G | gap | Ala | Ala (9715) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q80525 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA 5 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 538 aa. | 8.8E-158 | |
| 7545 | cg43315424 | 342 | CTCAGGAACAC ACGCTGACCGG AG[G/gap]CAGTG GCCAGGAGAGG CAGGCTAGG | G | gap | Ala | Ala (9716) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q80525 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA 5 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 538 aa. | 8.8E-158 | |
| 7546 | cg43287561 | 468 | ACTGTGCTCTGG AAGTTGGCATCA A[T/gap]GAAGAT GGGCTCTGCCG CTGTGATT | T | gap | Ile | Leu (9717) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa. | 1.4E-156 9 (9q34) | |

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| 7547 | cg43287561 | 553 | GTTCCCTTTCTGG ATTGTTCTCAGG G[gap]/GJACAAA GGCTGCCCTGGTT TCTGTCA | gap | G | Val | Val (9718) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (human), 300 aa. | 1.4E-156 | 9 (9q34) |
| 7548 | cg43298828 | 702 | CCACTCAACTGG CTGGACACCATC A[C/gap]CTGGAT GGTGGTGACCAT GGGCAGC | C | gap | Val | End (9719) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92984 INTERFERON-INDUCED LEUCINE ZIPPER PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment). | 1.1E-155 | 17 |
| 7549 | cg43298828 | 703 | CACTCAACTGGC TGGACACCATCA C[C/gap]TGGATG GTGGTGACCATG GGCAGCT | C | gap | Gln | Gln (9720) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:Q92984 INTERFERON-INDUCED LEUCINE ZIPPER PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment). | 1.1E-155 | 17 |
| 7550 | cg41629243 | 891 | TCCTTGGCCTCC TTCTTGGCCAGC C[G/gap]CCGTGC GGCTTCTCCTC GGGCGTC | G | gap | Arg | Gly (9721) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O75229 R31449_3 - HOMO SAPIENS (HUMAN), 813 aa (fragment). | 7.8E-155 (19p13.3) | 19 |
| 7551 | cg42713596 | 380 | CTGTTGGCCGAA ATAGGGCTGAAG C[C/gap]TCTTTG GAGCGAGCTCA GAATCTCA | C | gap | Ser | Leu (9722) | FRAMES HIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD23902 ACTIVATION OF SENTRIN/SUMO PROTEIN AOS1 - HOMO SAPIENS (HUMAN), 346 aa. | 3.1E-154 | |
| 7552 | cg43981925 | 1805 | TATACTGGAAGG TCTTGCTACCAA CTT/gap]GCCCCCT GAAGTGGTGCAC CAGAAAC | T | gap | Gln | Arg (9723) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa. | 6.4E-154 | 8 |
| 7553 | cg43060941 | 1196 | TTCCCTTTTTCAT CTAGATGCAGAG T/gap]TTTTTTGA ACTTTAACCTC ATGTT | T | gap | Asn | Thr (9724) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:P70287 RETINOBLASTOMA BINDING PROTEIN 6 (PACT) - MUS MUSCULUS (MOUSE), 1587 aa (fragment). | 4.9E-153 | |

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| 7554 | cg43060941 | 960 | TCTCTGGGTGCA TAGTCAGTTTTT [T/gap]GTCTCTAT TGGGAGTGAAGT CTTTA | gap | Lys | Lys (9725) | FRAMES HIFT | UNCLAS SIFIED | Human Gene SPTREMBL-ACC:P70287 RETINOBLASTOMA BINDING PROTEIN 6 (PACT) - MUS MUSCULUS (MOUSE), 1587 aa (fragment). | 4.9E-153 | |
| 7555 | cg43990820 | 1082 | GATGTCTGTGTG ACCCAGCTTGAC C[C/gap]TGGCGG ACCCACTAGTGT TGGACAC | gap | Arg | Arg (9726) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 3.3E-150 | 3 |
| 7556 | cg43258297 | 145 | ATAGTCCATACA GTGTGGCTACTG C[C/gap]AAGGTC AGGATGGCCAG CAGACCCA | gap | Leu | Leu (9727) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB50866 DEOXYRIBONUCLEASE III (DNASE III) - HOMO SAPIENS (HUMAN), 304 aa. | 3.8E-150 | 3 |
| 7557 | cg43919239 | 576 | AAAGGTGCGGC AGAGAGCCCCA GCT[G/gap]GGCA CTTGTTAACTCC TGAGGTCCA | gap | Pro | Gln (9728) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa. | 4.2E-150 | |
| 7558 | cg43919239 | 578 | AGGTGCGGCAG AGAGCCCCAGCT GG[G/gap]CACTT GTAACTCCTGA GGTCCAGT | gap | Cys | Cys (9729) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa. | 4.2E-150 | |
| 7559 | cg43943351 | 418 | TGGGTGATATG CGGCTCCCACAA G[G/gap]TGCTGA GCACCACGTGG CTCTGTTC | gap | Pro | Leu (9730) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa. | 4.5E-150 | 17 |

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| 7560 | cg43943351 | 872 | AGGTGGTCACTG TCAATGACAAAC G[C/gap]CCCCAG GCCCTTCAGTCG CTGAGCT | C | gap | Ala | Arg (9731) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa. | 4.5E-150 | 17 |
| 7561 | cg43925047 | 754 | GTGTCCATGAAA CGGGAGCCACT GG[C/gap]CCACG GAGCCATCTTCA AAGCCAGT | C | gap | Ala | Pro (9732) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O43730 BK390B3.1 (MANIC FRINGE PRECURSOR PROTEIN) - HOMO SAPIENS (HUMAN), 321 aa. | 9.4E-150 | |
| 7562 | cg43946935 | 793 | AGCCTTATTTCA GGTTATCTACTT TTT/gap]GGAAAT GCAGGAAGTTCC CACCTTG | T | gap | Gly | Glu (9733) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60671 CELL CYCLE CHECKPOINT PROTEIN HRAD1 - HOMO SAPIENS (HUMAN), 282 aa. | 1.8E-149 | |
| 7563 | cg43930377 | 1451 | TACAAAAAGCTA GCATGGCTTCTT T[gap/A]AAAAAAA ACAATATCCCA ATAAAA | gap | A | Leu | Leu (9734) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 7.8E-149 | 4 |
| 7564 | cg43930377 | 1459 | GCTAGCATGGCT TCCTTAAAAAAA [gap/A]CAATATC CCAAATAAAATC AGAGTC | gap | A | Thr | Asn (9735) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 7.8E-149 | 4 |
| 7565 | cg43041577 | 1597 | GAAATCTCAAAG GTCGTGTAAGAA G[G/gap]CAAGCC GCAACACAAAGT CTAAGTC | G | gap | Ala | Gln (9736) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB45767 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment). | 2.7E-148 | 10 |
| 7566 | cg43943919 | 802 | TCGTAGACATGC TCCTGTTGGGAT GTT/gap]CTTCCG ACAGAGCATGAT ATAGGCC | T | gap | Thr | His (9737) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB46921 DA159A1.1 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 399 aa. | 2.7E-148 | X |

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| 7567 | cg43965796 | 1698 | GTTGACATCACT GTTGATGCTCTG G[G/gap]CCACGC CAGGGTACTGGA TCCTCAT | G | gap | Ala (9738) | Ala | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment). | 9E-148 | 1 |
| 7568 | cg43931669 | 138 | GCCGGGGGAGC CGCCATCGGAG CGC[C/gap]AGGG GACAGAGCACA GGAAAGGGAC | C | gap | Arg (9739) | Gly | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99703 ATAXIN-2 RELATED PROTEIN - HOMO SAPIENS (HUMAN), 347 aa (fragment). | 2.3E-146 | |
| 7569 | cg43937734 | 827 | CTGTGTCTTATG ATGTGGCTCTG C[C/gap]AAGACC ATCCTGAATAAT GGGAAGA | C | gap | Lys | Arg (9740) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE III) - Homo sapiens (Human), 259 aa. | 3.5E-146 | 8 |
| 7570 | cg43947808 | 846 | CCCTTTCATCCC TATGTGGAAC GT[G/gap]GGTGGC AAGTGGGAGAAA CCATCAG | T | gap | Gly | Val (9741) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34076 CGI-81 PROTEIN - HOMO SAPIENS (HUMAN), 282 aa. | 9.8E-146 | 16 |
| 7571 | cg43961927 | 442 | CCAGCTCCTCCC GGCGATGGTGG CG[C/gap]CGTTC TTGCCCTCTTC CCGGTCTG | C | gap | Arg | Arg (9742) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60928 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)) - HOMO SAPIENS (HUMAN), 265 aa. | 4E-145 | |
| 7572 | cg43946394 | 247 | AATCTGTAGCTT CCGGATACCGTA G[C/gap]CCACGG GCACCAGCTTGG AAGCCCC | C | gap | Gly | Ala (9743) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa. | 2.8E-144 | 19 |
| 7573 | cg43946394 | 586 | TACGTGCTGGGT CTGTGGGGCCG TG[G/gap]CCCCG TGGCCAGGCCA GCTCTTCTC | G | gap | Ala | Ala (9744) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa. | 2.8E-144 | 19 |

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| 7574 | cg43946394 | 840 | GGAGGATCACG CTGGCGCCGTTT TC[C/gap]TGGCG GGAGGCACCTG CCACAGGCC | C | gap | Gln (9745) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa. | 2.8E-144 | 19 |
| 7575 | cg43983449 | 1418 | TGCATGATGGAA ATGAGGCAGGAT G[G/gap]CAGAGC CAGTGCCAGCTG AGAACAC | G | gap | Ala (9746) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTRMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa. | 7.3E-144 | |
| 7576 | cg44027658 | 375 | GAAGAAAGTGCCC GTCCACGCACAG C[G/gap]AGGAGC TTCATGATTGTAT CCAAAA | G | gap | Glu (9747) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-EGS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa. | 2E-143 | 1 (1p21) |
| 7577 | cg43999829 | 1037 | AGGTGGTGAC GGCCTGGAGAA GGC[C/gap]ATCT ACAAAGGCCCA GGCAGCGAAG | C | gap | Ile (9748) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa. | 2.1E-143 | 22 (22q11.2) |
| 7578 | cg43958563 | 1417 | GAAAGCAGCTGA GATATAGTACAG G[G/gap]CACAAT GTGCTGGGCTC GGGCTCTT | G | gap | Pro (9749) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa. | 4.7E-142 | 1 (1p35) |

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| 7579 | cg43958563 | 1482 | TTGAGAAAGGTGC GGCGGATCCAAA G[C/gap]CCCCCG GGGACTGCGTG TAGCCGCC | C | gap | Gly | Ala (9750) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa. | 4.7E-142 | 1 (1p35) |
| 7580 | cg43919223 | 535 | CACITTTATCCAG GACAGCTGTCTC T[A/gap]TGAGTG CTCACCCCAACCT GGGGCCC | A | gap | Tyr | Leu (9751) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P41439 FOLATE RECEPTOR GAMMA PRECURSOR (FR- GAMMA) (FOLATE RECEPTOR 3) - Homo sapiens (Human), 243 aa. | 1.4E-140 | 11 |
| 7581 | cg42921274 | 649 | ACCAGAGTCTTT CAGGAGCCGGG GT[G/gap]CCAAG GCCAGAAATGTGG GTAATGAT | G | gap | Ala | Asp (9752) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD26417 HEMK HOMOLOG - HOMO SAPIENS (HUMAN), 338 aa. | 5E-140 | |
| 7582 | cg43260991 | 293 | CGCCCCAACCC GCCCCATGCCG CGC[gap]GJCAC AGGGAGCCAGG AGCCTGTGCG | gap | G | Pro | Arg (9753) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q60949 TBC1 - MUS MUSCULUS (MOUSE), 1141 aa. | 6.2E-140 | |
| 7583 | cg43260991 | 301 | ACCCGCCCCCATG CCGCGCCCCACA GG[G/gap]AGCCA GGAGCCTGTGC GCAGGCCCA | G | gap | Ser | Ala (9754) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q60949 TBC1 - MUS MUSCULUS (MOUSE), 1141 aa. | 6.2E-140 | |
| 7584 | cg43292703 | 992 | GCCACTCGAGC CAGATGCTTGT GT[gap]GICGGCG GAGGCCGCGCT GGTGTGACT | gap | G | Asp | Ala (9755) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99618 CHROMOSOME 12P13 SEQUENCE; HTGS PHASE 3, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 268 aa. | 1.7E-139 | |

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| 7585 | cg43305515 | 1381 | CTCAAGCATGTC GGGCCAGGGA AG[C/gap]CGAAG GCGGACATGAC CGGGGCGCA | C | gap | Gly | Ala (9756) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O35297 SECRETED APOPTOSIS RELATED PROTEIN 1 - MUS MUSCULUS (MOUSE), 295 aa. | 4.4E-139 | 4 |
| 7586 | cg43935076 | 1655 | GAACCGAGTCTC TCTTCTCTATTG [T/gap]TTCACCTC ACTGTAGAAGGT CATAA | T | gap | Lys | Asn (9757) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa. | 1.5E-136 | 1 |
| 7587 | cg43935076 | 1697 | AGGTCATAAATG CTTCCTCGGTGC T[G/gap]CCTCCG CCGCCCTGAAATC CCGCTCT | G | gap | Gly | Gly (9758) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa. | 1.5E-138 | 1 |
| 7588 | cg43952219 | 1075 | CAGTTTGCCAAA GAGCTCTACCAG A[T/gap]TTTTTTG GAGGCATAACAA TAGAAG | T | gap | Asn | Ile (9759) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa. | 2.5E-136 | X |
| 7589 | cg43952219 | 1081 | GCCAAAGAGCTC TACCAGATTTTT [T/gap]GGAGGCA TAACAATAGAAG TATTGA | T | gap | Pro | Pro (9760) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa. | 2.5E-136 | X |
| 7590 | cg43994220 | 232 | GCGGGCACCAG GTTGCTCTGGAA GA[G/gap]CTTGA GGATGTGGTTCT CGATCACC | G | gap | Leu | Ser (9761) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa. | 5.8E-135 | 19 |
| 7591 | cg43994220 | 282 | CTGTTGCACCTT CCGGTATCCCAG G[G/gap]CCACGG CAAGGTCCATCG GGGTGTA | G | gap | Ala | Ala (9762) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa. | 5.8E-135 | 19 |

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| 7592 | cg43994220 | 787 | TGGTGGAGTGCT TCAGGGAGCTG CC[gap]TCCGT GGAGAGGAAAC ACTGGCATC | gap | T | Gly | Arg (9763) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa. | 5.8E-135 | 19 |
| 7593 | cg43929878 | 1026 | CCTGACTGAGGT GGACCGGCAGG GG[gap]CCCAC ATTGTTGGCTAC TTCTCCAA | G | gap | Ala | Pro (9764) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O02193 MALES- ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-) - Drosophila melanogaster (Fruit fly), 827 aa. | 3.1E-134 | |
| 7594 | cg43942432 | 530 | AATGAGATTCTC CCAGCAACGGG AG[gap]CCAAG CCCTCCGCAGC CGAATAAT | G | gap | Ala | Ala (9765) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60573 CAP-BINDING PROTEIN 4EHP - HOMO SAPIENS (HUMAN), 245 aa. | 5.3E-134 | 2 |
| 7595 | cg43942432 | 802 | AAGTGTAGTTGT ACTGCAGGGAT G[C/gap]TCTGCC GGCCAGGGAC AACAGCCT | C | gap | Glu | Asp (9766) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60573 CAP-BINDING PROTEIN 4EHP - HOMO SAPIENS (HUMAN), 245 aa. | 5.3E-134 | 2 |
| 7596 | cg43918993 | 1557 | CAGGCTGTAAGC TCGCTGCAGATT G[gap]CGATGG CCTCATCATAGC TCTCCAT | G | gap | Ala | Ala (9767) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa. | 2.3E-133 | 16 |
| 7597 | cg43918679 | 516 | GTGAGCTGTACC TGCGGAGGAAC CG[C/gap]ATCCC CAGCCTGGCTGA GCTCTTCT | C | gap | Ile | Ser (9768) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa. | 3E-131 | 21 |
| 7598 | cg43918679 | 845 | CTGGACAGCGA GGAGGAGGCAA CCA[G/gap]CGGC GCCCAGGATGAA CGTGGCCTG | G | gap | Ser | Thr (9769) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa. | 3E-131 | 21 |

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| 7599 | cg43931621 | 2141 | TGGATTCTCCCA CAAAGCCCGCCA G[G/gap]AGGGAG CCACGCCCCAG GGTCGCAC | G | gap | Leu | Leu (9770) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment). | 4.7E-131 | 5 |
| 7600 | cg44007142 | 941 | CCAGGCTGGCG TCGCTCTCTGTG TT[C/gap]CCGCT GCCGGGACTTA GCCGCCTTC | C | gap | Glu | Asn (9771) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34089 CGI-94 PROTEIN - HOMO SAPIENS (HUMAN), 253 aa. | 3.1E-129 | |
| 7601 | cg43950545 | 766 | CTGCTACGAATT GTTTGGCGTAG G[C/gap]ACATCT CCTTGCCCCCTCT AGCTTTT | C | gap | Val | Val (9772) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa. | 3.5E-129 | 13 |
| 7602 | cg43972431 | 1944 | GGGAGGGAGAT GGCATTITTTAG CA[C/gap]CCGGG GAGGGCGTTTCT GTGAACAC | C | gap | Val | Cys (9773) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD16888 CDC42 EFFECTOR PROTEIN 3 - HOMO SAPIENS (HUMAN), 254 aa. | 7.1E-129 | 2 |
| 7603 | cg43300586 | 252 | AGTGGCTGCGG CGGGAAGATGG CGG[A/gap]GCTG CGCGTGCTCGTA GCTGTCAAG | A | gap | Glu | Gly (9774) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P38117 ELECTRON TRANSFER FLAVOPROTEIN BETA- SUBUNIT (BETA-ETF) - Homo sapiens (Human), 255 aa. | 3.6E-128 (19q13.3) | 19 |
| 7604 | cg43054809 | 335 | TTGCTCTTGGCT TTTGTGGCCTTG G[C/gap]ATCCAG CGTGCTCTGGG CATGAGTG | C | gap | Ala | Pro (9775) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15125 PHENYLALKYLAMINE BINDING PROTEIN - HOMO SAPIENS (HUMAN), 230 aa. | 2E-127 | X |
| 7605 | cg42891437 | 229 | TTGAGCACGGAG CTCAGGTCCGGA G[G/gap]AACACC ATGGTGAGGAG GCCCCAAGA | G | gap | Phe | Phe (9776) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75425 ORF3, SPLICEVARIANT_B - HOMO SAPIENS (HUMAN), 235 aa. | 2.4E-127 7 (7q21) | |

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| 7606 | cg43926784 | 933 | GATTGGACCAA TGGACCAGCCAA G[C/gap]TTCCAG CCAGTTACACTG AAAGTCT | C | gap | Lys | Asn (9777) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC: CAB44334 CYSTEINE CONJUGATE BETA-LYASE - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 419 aa. | 6.7E-127 | |
| 7607 | cg43949061 | 149 | GGAGCACCTTG GCCCTGGTCTTG GG[C/gap]CAGCA GACGCAGAAAGC AGGGAGTGTC | C | gap | Ala | Pro (9778) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC: Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa. | 2.1E-125 | 19 |
| 7608 | cg43949061 | 150 | GAGCACCTTGGC CCTGGTCTTGGG C[C/gap]AGCAGA CGCAGAAAGCAG GGAGTGCA | C | gap | Leu | Leu (9779) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC: Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa. | 2.1E-125 | 19 |
| 7609 | cg43949061 | 178 | CAGACGCAGAA GCAGGGAGTGC AGA[G/gap]CCCG GCAACACAGGTGT GTAGCCCCAG | G | gap | Ala | Val (9780) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC: Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa. | 2.1E-125 | 19 |

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| 7610 | cg43949061 | 207 | GGCAAACAGGT GTGTAGCCAG GCG[G/gap]CTCA GATGCAGGTAAT CATACATGT | G | gap | Ser (9781) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa. | 2.1E-125 | 19 |
| 7611 | cg43949061 | 390 | GATGTTGGCCTC GCGGAAGCAGG CC[C/gap]AGCAC CACAAACCCGGG CCTGGGGCT | C | gap | Leu (9782) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa. | 2.1E-125 | 19 |
| 7612 | cg43975901 | 1076 | AGCTAATGTGAA CCCTGGAGGAT GG[G/gap]CACCA GCCTCAGTGTTA AGGGCAGT | G | gap | Ala (9783) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD30288 GOODPASTURE ANTIGEN-BINDING PROTEIN (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 624 aa. | 2.6E-125 | |
| 7613 | cg43066224 | 733 | CGGGAGGCTCC CACTGCACCTGT AG[G/gap]TGGCG CTCAGCGAGGG GGCTTAGGC | G | gap | His (9784) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14213 CYTOKINE RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 229 aa. | 5.4E-125 | 19 |
| 7614 | cg44002548 | 981 | TGATGCATCAGG ACAGGGCTTTTG C[C/gap]ACTGCA CGCTTGAATTC TCCGGAC | C | gap | Thr (9785) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB45746 HYPOTHETICAL 49.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 454 aa. | 1.1E-124 | 17 |
| 7615 | cg44002548 | 1044 | GTACCCCTCTCAA CGATCCAGAAAGT TTG[gap]CCACGG CTGCTAGTTGCG TCATCCA | G | gap | Pro (9786) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB45746 HYPOTHETICAL 49.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 454 aa. | 1.1E-124 | 17 |

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| 7616 | cg43934053 | 680 | TTGGCACCTTCG GGCAAGGGGAG GG[G/gap]CTTGC AGCACCCCCAC CAGTAGGT | G | gap | Gly | Ala (9787) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD39005 RIP-LIKE KINASE - HOMO SAPIENS (HUMAN), 518 aa. | 2E-120 | |
| 7617 | cg43923128 | 2174 | GAGTGGAGATG GGCAGAGGCTC TGG[C/gap]CCCT GCTCCTCTGGCT TCTCAGCAG | C | gap | Gly | Gly (9788) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa. | 3.2E-120 | 1 |
| 7618 | cg43963595 | 156 | TCACACTCTCAC ACACACACACAC A[gap/C]TGCCAC GCACATATCCAA GCTCCAA | gap | C | Met | Ser (9789) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa. | 8.5E-120 | 17 |
| 7619 | cg43950398 | 1454 | CTGCTTGGTGGC GGCTCGTGAAG GG[G/gap]CAAGG CCGAGAACTTC TGAATGTT | G | gap | Ala | Ala (9790) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75545 HYPOTHETICAL 26.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 230 aa (fragment). | 1.4E-119 | 1 |
| 7620 | cg43994051 | 517 | AATTCTGCAAAG AACATGGCTTTG C[C/gap]GGATGG TTTGAAACCTCT GCAAAGG | C | gap | Gly | Asp (9791) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q13637 RAS- RELATED PROTEIN RAB-32 - Homo sapiens (Human), 225 aa. | 9.7E-119 | 6 |
| 7621 | cg43998873 | 188 | CTCTCAGAATTC CTGACTGTCCGC A[gap]GTTTCC AAATCCTCCAGC GCTTGAG | G | gap | Thr | Thr (9792) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB39895 GRIP1 PROTEIN - HOMO SAPIENS (HUMAN), 849 aa (fragment). | 2E-118 | |

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| 7622 | cg43917206 | 972 | GGACCAACAGG CAATATCAATCTT C[C/gap]TCCGGG CTTTAACTGATC TATTAGC | C | gap | Gly | Glu (9793) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P22061 PROTEIN-L- ISOASPARTATE(D-ASPARTATE) O- METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L- ISOASPARTYL/D- ASPARTYL METHYLTRANSFERASE) (L ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) - Homo sapiens (Human), 226 aa. | 6.9E-118 | 6 |
| 7623 | cg43258389 | 1431 | GCCACTTCTGCA GCCTGCCGTGT GG[C/gap]AAACT GGATGAAAGCAC ACTGCTGT | C | gap | Ala | Pro (9794) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q22412 T11G6.8 - CAENORHABDITIS ELEGANS, 658 aa. | 1.6E-115 | 5 |
| 7624 | cg43951899 | 460 | GCAGGCGGTGA GCTGGGGGCCG GCA[G/gap]GGGC GCGGACAGTGC GGCGTGGTCG | G | gap | Leu | Cys (9795) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa. | 3.3E-115 | 9 |
| 7625 | cg43951899 | 463 | GGCGGTGAGCT GGGGGCCGCGA GGG[G/gap]CGC GGACAGTGCGG CGTGGTCGAAC | G | gap | Pro | Pro (9796) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa. | 3.3E-115 | 9 |
| 7626 | cg43939521 | 1019 | GTGAGCATGACC CCCATGTGCTCC T[G/gap]GCCGTG GCCAAGCTGTTT TGGAGTC | G | gap | Ala | Pro (9797) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q12381 PRE-MRNA SPLICING FACTOR - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 906 aa. | 5.7E-114 | |
| 7627 | cg43939521 | 588 | AGCCCAAGATCT GTGCGAGGAGG CC[C/gap]TGCGG CACTATGAGGAC TTCCCCAA | C | gap | Leu | Cys (9798) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q12381 PRE-MRNA SPLICING FACTOR - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 906 aa. | 5.7E-114 | |

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| 7628 | cg43982971 | 501 | GCGCCATTGAGT TCGGACAGCGG ATG/gap]CTCCA GGTGGCATCTCA AGCCTCCA | gap | Leu | Ser (9799) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa. | 5.7E-114 | |
| 7629 | cg43982971 | 742 | GCCCTACCTGG GCCCATGGAACC TTC/gap]CCGGTC AGCGGCCCCGA TGTCCTCCCT | gap | Pro | Pro (9800) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa. | 5.7E-114 | |
| 7630 | cg43982971 | 744 | CTTACCCTGGGC CCATGGAACCTC C[C/gap]GGTCAG CGGCCCCGATG TCCCTCTCC | gap | Gly | Val (9801) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa. | 5.7E-114 | |
| 7631 | cg43948724 | 1060 | GGAGGAGGCCT GTCCCAATTCTG CC[C/gap]GCTCC ATGGAAGCGG GCTTGACT | gap | Pro | Arg (9802) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |
| 7632 | cg43948724 | 1165 | TTAATCCTTCTT GTAATACTTCTT A/gap]ATGTGACA TTTCTCTTCCCC TTAGA | gap | End | Tyr (9803) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |
| 7633 | cg43948724 | 1166 | TAATCCTTCTTGA TAATACTTCTA A/gap]TGTGACAT TTCTCTTCCCCT TAGAA | gap | Cys | Val (9804) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |

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| 7634 | cg43948724 | 1471 | TGGAAGCATGTA GACTGTGCCAGA G[G/gap]CCAGAC CCACGGGCTCAT GCACCCC | G | gap | Gly | Ala (9805) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |
| 7635 | cg43948724 | 1502 | CCACGGGCTC ATGCACCCCTGA GC[C/gap]AGCAG GGCATCTTGAA AAGGAACT | C | gap | Gln | Ser (9806) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |
| 7636 | cg43948724 | 800 | CTGATGAGAGAC AGCGCATGCTG GT[gap/C]GCAGC GTAAGGACGAAC TCCTCCAG | gap | C | Cys | Ser (9807) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |
| 7637 | cg43948724 | 948 | TGCGTCGAAGGA TGCTGGCTGCC GC[C/gap]GCGGA ACGGAGGCTTCA GAAGCAGC | C | gap | Pro | Arg (9808) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa. | 9.9E-114 | 16 (16q21) |
| 7638 | cg43921344 | 959 | GGGCCCTCGAAT GGTAAGAGGGG CT[G/gap]CCTGG GGGCCCATGGG TCTGGTAGA | G | gap | Gly | Gly (9809) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa. | 2.3E-112 | |
| 7639 | cg43921344 | 108 | AGGCCAAGTGG GGAAGTGCAGG TGC[A/gap]CAAG AGAGCGCTTGAG GCTCTGGTC | A | gap | Val | Gly (9810) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa. | 2.3E-112 | |

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| 7640 | cg43921344 | 228 | CAGGGCACCGT GCACCATGGGCT GG[C/gap]CCCTC TCGGTGGGAA GTAGCGTGC | C | gap | Gly | Ala (9811) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa. | 2.3E-112 | |
| 7641 | cg43921344 | 398 | CTAGCGGGGG CAGTATGGGA GAG[C/gap]CCCT CCACGCAGCTG GCATTGATGT | C | gap | Gly | Gly (9812) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa. | 2.3E-112 | |
| 7642 | cg43957889 | 325 | GGGAGATGGTT GTGGCGGCTTTG C[C/gap]TGCTCC AAGAATGCGCTT TGCCTC | C | gap | Cys | Ala (9813) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa. | 2.7E-111 | 12 |
| 7643 | cg43960984 | 777 | ATCTTTTCCCAT CGACCTGGAGTC C[C/gap]TCCTGG GAACTTAACCAT ACTTCT | C | gap | Gly | Gly (9814) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q61712 DNAJ PROTEIN HOMOLOG MTJ1 - Mus musculus (Mouse), 552 aa. | 8.6E-111 | 10 |
| 7644 | cg43986282 | 298 | AGAGCCCTGCT CCTTGGCCATAG C[C/gap]AAATCC CTTGGGCCCAA GTTCTT | C | gap | Gly | Ala (9815) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.9E-110 | 12 |
| 7645 | cg43081416 | 385 | CTGGATCCACGC CCCTGGCCCCG AG[G/gap]TCCTG CAGGTCTTCGG CCGCCCGT | G | gap | Asp | Asp (9816) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD45561 TRANSFERRIN RECEPTOR 2 ALPHA - HOMO SAPIENS (HUMAN), 801 aa. | 1E-109 | 7 |
| 7646 | cg43976845 | 137 | GGGAGCGGCTG GGATGGCGCGT CCG[C/gap]GGCC CCGCCAGTACAA AGCGGGCGA | C | gap | Arg | Gly (9817) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34137 CGI-142 PROTEIN - HOMO SAPIENS (HUMAN), 203 aa. | 3.4E-109 | 15 |

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| 7647 | cg43928772 | 1735 | ACTAAAGGCGCT TTCCGCCATCAC C[C/gap]CCACTG GCATCTTCGCGG CCGGCCT | C | gap | Gly (9818) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa. | 8.9E-109 | 2 |
| 7648 | cg44913737 | 179 | GGCAGGGGCAC TCAGTCCCTCCG CA[G/gap]GTTCT TAAGCCGTTCT CCAGGTCT | G | gap | Leu (9819) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O43633 BC-2 PROTEIN - HOMO SAPIENS (HUMAN), 222 aa. | 2.4E-108 | 19 |
| 7649 | cg44913737 | 229 | TGCATCAGCATC AGCTAGGGCTGA G[G/gap]CTGCGG CCTCTGCTTTTT CCCACC | G | gap | Ala (9820) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O43633 BC-2 PROTEIN - HOMO SAPIENS (HUMAN), 222 aa. | 2.4E-108 | 19 |
| 7650 | cg44913737 | 237 | CATCAGCTAGGG CTGAGGCTGCG GC[C/gap]TCTGC TTTTTCCACC AGCAGCCA | C | gap | Glu (9821) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O43633 BC-2 PROTEIN - HOMO SAPIENS (HUMAN), 222 aa. | 2.4E-108 | 19 |
| 7651 | cg43327495 | 1079 | CTGAAAAGGTGT GATCAATTCCAA CTT/gap]GCACGG CGGCGGTGGTG AGGACGCA | T | gap | Arg (9822) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa. | 5E-108 | 17 |
| 7652 | cg42657906 | 195 | TCATCAGGTGCT GAGGGGCCCGG GG[G/gap]CGCTG GGGGCAAAGGC AGAGTAGAG | G | gap | Pro (9823) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14919 NC2 ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 205 aa. | 6.2E-108 | 11 |

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| 7653 | cg42657906 | 431 | GCCGCCCGCTGC CTGGCTTCCGGC CC[C/gap]TCCGG GCGCCCTTGTC CCATCCAT | C | gap | Arg (9824) | Arg | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14919 NC2 ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 205 aa. | 6.2E-108 | 11 |
| 7654 | cg43296554 | 206 | TGGCCTTCTCTC TTGGGGGCTTTG C[gap/C]TCTCAT CCTCTTTGTCTG TCAAAA | gap | C | Lys (9825) | Asn | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q15527 SURFEIT LOCUS PROTEIN 2 - Homo sapiens (Human), 256 aa. | 6.4E-108 | 9 |
| 7655 | cg43942004 | 740 | ATGGAGAGAGGT GTCATGGGCTGA G[C/gap]CTCCCA GTGGAATAATCGC TTATATA | C | gap | Ser (9826) | Leu | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa. | 1E-107 | 5 (5q23) |
| 7656 | cg43942004 | 741 | TGGAGAGAGGT GTCATGGGCTGA GC[C/gap]TCCCA GTGGAATAATCGC TTATATA | C | gap | Ser (9827) | Leu | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa. | 1E-107 | 5 (5q23) |
| 7657 | cg43947512 | 344 | AAGTCAGGTTCC ATTGGCAACTG C[C/gap]GAGTGG ATCGCGGAGCC CGTGCGGC | C | gap | Ser (9828) | Glu | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q14197 DS-1 PROTEIN - Homo sapiens (Human), 206 aa. | 2.1E-107 | 17 |
| 7658 | cg42854459 | 95 | AAAAACTATATG AGAAAGCTGGCA A[G/gap]CCCAGT GAACCTCCTGGC CGGAGAG | G | gap | Gly (9829) | Gly | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD41342 HEPARANASE - HOMO SAPIENS (HUMAN), 543 aa. | 3.5E-107 | |

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| 7659 | cg42923937 | 901 | GCTGAGCATTG CCTGTGTCACG C[C/gap]TTTGAT GAGACGGACGA GGACAGGA | C | gap | Arg | Ser (9830) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O4378 R29893_1 - HOMO SAPIENS (HUMAN), 216 aa (fragment). | 4.4E-107 | |
| 7660 | cg43967668 | 248 | CGCTTGTCGAAC CACTTGCCGTTG G[C/gap]CGCGCC TGACAGGACCG CGCAGTTC | C | gap | Ala | Pro (9831) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa. | 5.6E-107 | 3 (3p22) |
| 7661 | cg43969137 | 346 | GGCTCATAGAAG ATGTGGCTGGTA G[C/gap]CTGCC TGGCCTAGGCC GCAGGAGA | C | gap | Ala | Leu (9832) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O08973 HYPOTHETICAL 33.5 KD PROTEIN - MUS MUSCULUS (MOUSE), 300 aa. | 3.6E-105 | 17 |
| 7662 | cg43981269 | 595 | ACTCTCCACG CCGAGGCGCAG GC[C/gap]GCCAT CAACGCGCTACA CGGCAGCC | C | gap | Ala | Pro (9833) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa. | 4.5E-105 | |
| 7663 | cg44912062 | 504 | AGCTGGCCGAG CTGGAGGGCCG CCA[G/gap]GAGG AGCTGCTGGG GAGAACCTAG | G | gap | Glu | Arg (9834) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15834 HEPATITIS DELTA ANTIGEN INTERACTING PROTEIN A - HOMO SAPIENS (HUMAN), 202 aa. | 1.5E-104 | 11 |
| 7664 | cg43999798 | 491 | GCGACTATCTGC TGCGCGGTACC G[C/gap]ATGCTG GGCGAGACGTG TGCGGACT | C | gap | Met | Cys (9835) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O60232 AUTOANTIGEN P27 - Homo sapiens (Human), 199 aa. | 1.4E-103 | |

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| 7665 | cg43999798 | 654 | CTCCCAAGCTCG GGAGCACCAGC TG[G/gap]CCTCA GCCTCAGAGCTC CCCCTGGG | G | gap | Ala | Pro (9836) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O60232 AUTOANTIGEN P27 - Homo sapiens (Human), 199 aa. | 1.4E-103 | |
| 7666 | cg43947566 | 547 | GCCTCGACACAA TTACCACAAAAGT G[G/gap]CTCCCC TGGTGCAGTCCT TGTGTGC | G | gap | Ala | Leu (9837) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60427 BC269730_2 - HOMO SAPIENS (HUMAN), 444 aa. | 2.9E-103 | 11 |
| 7667 | cg43250166 | 254 | AGAGACCCGGC TCGGCTTCATG GC[C/gap]GGCCT CCCGCAGGTGT CTGCCCAGC | C | gap | Gly | Ala (9838) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43382 HYPOTHETICAL 146.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 1296 aa. | 3.3E-102 | 2 |
| 7668 | cg42885795 | 440 | TAAGATGCTGTT TTCTGGGCGTCG C[C/gap]AAAATC ATAGACCACAGG GATCACC | C | gap | Gly | Ala (9839) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O88310 INTELECTIN - MUS MUSCULUS (MOUSE), 313 aa. | 4.2E-102 | |
| 7669 | cg44032186 | 1169 | TTCGGTCGTGAT GCCCTTCATGGT G[G/gap]CCTGCG TGCCCACTGGCA TGAACAC | G | gap | Ala | Ala (9840) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q23623 PUTATIVE QUEUINE TRNA- RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) - Caenorhabditis elegans, 400 aa. | 8.8E-102 | 19 |
| 7670 | cg43999564 | 760 | CCTTCTGGCTCA GTACGCGGGAC TG[G/gap]CGTAG CGCTCCTCGGCA CTCATCGC | G | gap | Arg | Arg (9841) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2) (5,10- METHENYL- TETRAHYDROFOLATE SYNTHETASE) (METHENYL-THF SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa. | 2.8E-101 | 15 |

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| 7671 | cg44911139 | 757 | AATCAGTCGTCGTTCTAAGGGGCATTG[C/gap]CTACGTGGAATTCTGTGA AATCCAG | C | gap | Ala | Ala (9842) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14499 SPLICING FACTOR - HOMO SAPIENS (HUMAN), 530 aa. | 7.9E-101 | 14 |
| 7672 | cg44911139 | 758 | ACTCACGTCGTTCTAAGGGGCATTG C[C/gap]TACGTGGAATTCTGTGA AATCCAGT | C | gap | Tyr | Thr (9843) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q14499 SPLICING FACTOR - HOMO SAPIENS (HUMAN), 530 aa. | 7.9E-101 | 14 |
| 7673 | cg43941552 | 653 | ACTTCCAGATGG AATGCTCTCTGC A[G/gap]GCCAAG CCCGCAGTGCCT ACGTCTA | G | gap | Ala | Pro (9844) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 1.6E-100 | |
| 7674 | cg43925214 | 916 | GCGTGAAGGCG TTGGAGTCGAAG GA[G/gap]CGGG ATCCGCCAGCAT CTGGAAGC | G | gap | Arg | Arg (9845) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD44480 BUP - HOMO SAPIENS (HUMAN), 195 aa. | 4.3E-100 | 10 |
| 7675 | cg43941550 | 531 | CACCTCGGCACA CAGGGTGCTCAC G[G/gap]CCATGC CCAGGAAGGCC GGGTCCCC | G | gap | Ala | Ala (9846) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |

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| 7676 | cg43941550 | 553 | ACGGCCCATGCC CAGGAAGGCCG GGT[C/gap]CCCT CCGGAGGGTGC TGAGCCTGCA | C | gap | Asp | Thr (9847) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 7677 | cg43941550 | 556 | GCCATGCCCCAG GAAGGCCGGT CCC[C/gap]TCCG GAGGGTCTGA GCCTGCATCT | C | gap | Gly | Gly (9848) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 7678 | cg43941550 | 629 | TAGACGTAGGCA CTGCGGGCTTG GC[C/gap]TGCAG AGAGCATTCCAT CTGGAAGT | C | gap | Gln | Gln (9849) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 7679 | cg43941550 | 632 | ACGTAGGCACTG CGGGCTTGGCC TG[C/gap]AGAGA GCATTCCATCTG GAAGTTGT | C | gap | Leu | Leu (9850) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |

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| 7680 | cg43941550 | 649 | TTGGCCTGCAGAG GAGCATTCATC T[G/gap]GAAGTT GTGGACTTTTCT AGTGAGA | G | gap | Gln | Arg (9851) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 7681 | cg43941550 | 729 | TATCTTCATGAT GTAGCAGCAGGT G[C/gap]CAGGGG CTGGCTTGTAGG CGATCAG | C | gap | Gly | Ala (9852) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa. | 5.5E-100 | 8 (8p21) |
| 7682 | cg43950149 | 925 | TCACTTCTACTG TGGCAAAATTTGC C[G/gap]CCTTCA CAGGCCCTTTCT TCATAGG | G | gap | Gly | Gly (9853) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa. | 7.1E-100 | 12 |
| 7683 | cg43950149 | 508 | GCCAGATCTCAT TGCGCCGTCGGT A[G/gap]GGCTTC ATGGGAGGGTC ATAACCCG | G | gap | Pro | Pro (9854) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa. | 7.1E-100 | 12 |
| 7684 | cg43950149 | 560 | GCAGAAGTAGAT GTCCCCCGGTA G[G/gap]TGGCTG TGCCCTCCAGG GCAGCACG | G | gap | Thr | Thr (9855) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa. | 7.1E-100 | 12 |
| 7685 | cg43926315 | 2128 | GAAGGTGGTGCT GGTGGTGCAACT G[C/gap]TGGTTT TGGAGACAGTAC TGGAAAT | C | gap | Ala | Gln (9856) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD2873 NY-REN-37 ANTIGEN - HOMO SAPIENS (HUMAN), 173 aa (fragment). | 1.2E-99 | 14 |

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|------|------------|-----|--|---|-----|-----|---------------|----------------|------------------|---|---------|----|
| 7686 | cg43961133 | 416 | GTGGTGGCCCT GATGCCCCGAGG TGG[G/gap]CAGC CTGCAGCACGCA CGGGTGCTG | G | gap | Gly | Ala (9857) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1 - HOMO SAPIENS (HUMAN), 358 aa. | 1.5E-99 | 20 |
| 7687 | cg44026061 | 511 | ACATGACCTGGC AGCGGGGCCGG AG[G/gap]AGCTT CATCTTCAAGGG CCAGGAGG | G | gap | Ser | Ala (9858) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60736 KE03 PROTEIN - HOMO SAPIENS (HUMAN), 367 aa (fragment). | 2.7E-97 | |
| 7688 | cg43935925 | 788 | TGACCAGGGTCC GGATTTCTGCTG C[C/gap]TTCCGG ATGTTGCTGAA GCAATGAT | C | gap | Lys | Lys (9859) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa. | 4.6E-98 | 16 |
| 7689 | cg43992729 | 691 | CTCCACACTGCT GCAAGGCTCG GC[C/gap]ATATG TTGCTGGGAATT CCCTCCAC | C | gap | His | Ile (9860) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O70303 CELL DEATH-INDUCING DNA FRAGMENTATION FACTOR, ALPHA SUBUNIT-LIKE EFFECTOR B (CELL DEATH ACTIVATOR CIDE-B) - MUS MUSCULUS (MOUSE), 219 aa. | 2.6E-95 | 14 |
| 7690 | cg43927693 | 514 | GCAGCTGGCCC TGAAGTGGGCAT GG[C/gap]CCCCC ATCTCTTTGGT GCCCCGACA | C | gap | Pro | Pro (9861) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa. | 5.3E-95 | 22 |
| 7691 | cg43927693 | 545 | ATCTCTTTGGT GCCCCGACAAATG G[G/gap]CTGGGC CTTGGTGGATCT CCTGCTG | G | gap | Gly | Ala (9862) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa. | 5.3E-95 | 22 |

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|------|------------|------|---|---|-----|-----|---------------|----------------|------------------|---|---------|----|
| 7692 | cg43927693 | 552 | TTGGTGCCCGAC AAATGGGCTGG GC[C/gap]TTGGT GGATCTCCTGCT GGTCAGTG | C | gap | Leu | Trp (9863) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa. | 5.3E-95 | 22 |
| 7693 | cg43927693 | 723 | ACAACCATGGCT GGCGTGGGGA CG[G/gap]CGGCT GCCAGAGTGAGT GCCCGGCC | G | gap | Arg | Gly (9864) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa. | 5.3E-95 | 22 |
| 7694 | cg43934685 | 664 | TGAAATATTGA TGTCAGTGAAGA G[C/gap]TTCCAG CCAGAAAGAAAT GAAATCG | C | gap | Leu | Phe (9865) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment). | 1.2E-94 | 17 |
| 7695 | cg43950632 | 723 | CTGCACAGATGG CGGCTATCAGGC C[C/gap]TTCCGG TTTTCTGCTCC TTCAGTA | C | gap | Lys | Lys (9866) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa. | 2.3E-94 | 1 |
| 7696 | cg43993152 | 1185 | GACCCAGACCA GATTTCAACACA TG[G/gap]TTCCC ATACAGGAAGGA CTGCTCTG | G | gap | Asn | Asn (9867) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD27746 CGI-37 PROTEIN - HOMO SAPIENS (HUMAN), 180 aa. | 3.7E-94 | |
| 7697 | cg42514925 | 538 | CAAGGAACCCAA CAGTCTGCATGG A[A/gap]GGAGTC AGAGGGTTTGAT AAAGTGC | A | gap | Arg | Gly (9868) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q12915 IBD1 - HOMO SAPIENS (HUMAN), 204 aa (fragment). | 2.3E-93 | |
| 7698 | cg17948203 | 321 | AGTTACAAGAGT AGTAGATGAACA A[C/gap]ACTAAA GGCGTTGCTTGA GTCCATG | C | gap | Thr | Asn (9869) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75660 DJ501N12.1 - HOMO SAPIENS (HUMAN), 247 aa (fragment). | 3.8E-93 | |

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|------|------------|------|--|---|-----|-----|---------------|----------------|------------------|--|---------|----|
| 7699 | cg42907594 | 624 | GGGAGCATCCC AAAGCATACTCG AA[G/gap]GCTCC AGCCAGGCAC ATGCCACAA | G | gap | Leu | Phe (9870) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34142 CGI-147 PROTEIN - HOMO SAPIENS (HUMAN), 179 aa. | 3.8E-92 | 17 |
| 7700 | cg43980242 | 952 | GAGAAACTGGG CCTGACCCGGAT TC[G/gap]GGACA GGAAC TGGTATG TGCAGCCC | G | gap | Arg | Arg (9871) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P26438 ADP-RIBOSYLATION FACTOR 6 - Homo sapiens (Human), Mus musculus (Mouse), and, 174 aa. | 1.7E-91 | 14 |
| 7701 | cg43930979 | 1216 | GCCACCATGGG CCTGGCTGGAA GAG[C/gap]CAGA GTGAAGGAAAAA TTTTCCCT | C | gap | Ala | Ala (9872) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q19265 SIMILAR TO M. MUSCULUS MER5 AND OTHER AHPG/TSA PROTEINS - CAENORHABDITIS ELEGANS, 576 aa. | 3.4E-90 | 9 |
| 7702 | cg43930979 | 362 | CTACGTGCTGTT CCTCGCCGACG AG[G/gap]AGTTC GACGTGGTAGTG TGCGACCA | G | gap | Glu | Ser (9873) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q19265 SIMILAR TO M. MUSCULUS MER5 AND OTHER AHPG/TSA PROTEINS - CAENORHABDITIS ELEGANS, 576 aa. | 3.4E-90 | 9 |
| 7703 | cg43963913 | 812 | GGAGTCCACAAA CTCGTCACTCAT C[C/gap]TCCGGA GCTCGCGGCCA TAGCGCTG | C | gap | Arg | Arg (9874) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment). | 5.1E-90 | 11 |
| 7704 | cg43963913 | 925 | CCATCCCTTCGT CGTCCTCCGTCC C[C/gap]GCCGGG TAGGAGCTGTGG CGACTCC | C | gap | Ala | Ala (9875) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment). | 5.1E-90 | 11 |

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|------|------------|------|---|-----|-----|-----|---------------|----------------|------------------|--|---------|----------------|
| 7705 | cg43983527 | 1032 | CGAGAGTCTGC GGCCCCGGTGC TCC[G/gap]GCTG CGATGAGATAAT ATTCGCTGA | G | gap | Gly | Ala (9876) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa. | 6.5E-90 | 3 (11q23.3) |
| 7706 | cg43983527 | 1033 | GAGAGTCTGC GCCCCGGTCT CCG[G/gap]CTGC GATGAGATAATA TTCGCTGAG | G | gap | Gly | Ala (9877) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa. | 6.5E-90 | 3 (11q23.3) |
| 7707 | cg43983527 | 837 | CAAAGAGTGGA ATACGTCTGCGA G[C/gap]TCTGCA AGGAGCGGCC CCTCCTGA | C | gap | Leu | Ser (9878) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa. | 6.5E-90 | 3 (11q23.3) |
| 7708 | cg38719198 | 543 | GCAGCAGGCGG ACGTGGTCTGT GCA[gap]A/GAAG TGACACAGCCAT CCTTGGGTG | gap | A | Glu | Arg (9879) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43598 RCL (RCL) - HOMO SAPIENS (HUMAN), 174 aa. | 1.3E-89 | 6 |
| 7709 | cg43990642 | 625 | CAGGCAGCATT AAACTTAAGCAG A[gap]A/GAGCTT AAAGCAGCGCCT GGGTAAG | gap | A | Glu | Glu (9880) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O93501 NO27 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 248 aa. | 2.4E-89 | 1 |
| 7710 | cg43950029 | 266 | TTAGTTGTGTC TGCTAGGCTCTG C[C/gap]TCAGGG ATTTTGGAGTT CTTCGG | C | gap | Arg | Ser (9881) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q17474 B0334.3A - CAENORHABDITIS ELEGANS, 623 aa. | 3.9E-89 | |
| 7711 | cg44927780 | 1406 | ATAGAGAGGAAA CAACTTGAGGGA G[C/gap]TGGGCG CCATCAATGCAG AGTGCTG | C | gap | Ser | Thr (9882) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23368 ZC518.2 - CAENORHABDITIS ELEGANS, 1030 aa. | 6.3E-89 | 4 |

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| 7712 | cg44927780 | 1544 | AACGGACCGATC CACAGCCATGTT T[G/gap]CCAGAA GGCAGATGGCA GCTTGATC | G | gap | Ala | Glu (9883) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23368 ZC518.2 - CAENORHABDITIS ELEGANS, 1030 aa. | 6.3E-89 | 4 |
| 7713 | cg43059113 | 425 | CAAGAGGGCTG GCATTCTGGCT GG[C/gap]CCTGG GCACTCAGCAGT GCGTGCTT | C | gap | Gly | Gly (9884) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa. | 7.4E-89 | 3 |
| 7714 | cg43059113 | 747 | AACAGCAGAGTT TTCACCTCCAGT G[G/gap]CTGGAG CCTGTGATTCAA AGAAAGTC | G | gap | Ala | Ala (9885) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa. | 7.4E-89 | 3 |
| 7715 | cg43941586 | 401 | TGGAAGACGGG GATAAGCGCTGT AA[G/gap]CTTCT GCTGGGGATAG GAATTCTGG | G | gap | Leu | Phe (9886) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q10589 BONE MARROW STROMAL ANTIGEN 2 (BST-2) - Homo sapiens (Human), 180 aa. | 2.5E-88 | 19 |
| 7716 | cg43960450 | 1711 | GCTTCAAGATCA GCTCAAAAGCCT G[G/gap]CCAGAG GCACGTTTGTG ATTGCT | G | gap | Gly | Gly (9887) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa. | 8.5E-88 | 8 |
| 7717 | cg43026816 | 65 | CAGTCTATGCCT GGCCCAGCGGC AG[C/gap]CCCAG GTCCAGGGGG GTCGTGTTG | C | gap | Ala | Leu (9888) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O76103 R29425.1 - HOMO SAPIENS (HUMAN), 656 aa. | 2.3E-87 | |
| 7718 | cg43931874 | 484 | CCTCTGTAATCA TCACTGGCCGCA A[G/gap]GTCCCG GATGTCCTCCTC GATGAGG | G | gap | Leu | Leu (9889) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O54745 P65 PROTEIN - RATTUS NORVEGICUS (RAT), 613 aa. | 2.4E-87 | |

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| 7719 | cg43931874 | 716 | TCAGGCGAGCT GGTCCCACCTTG GG[G/gap]CCTTC CCGGCGAATTG GTTACACAGG | G | gap | Gly (9890) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O54745 P65 PROTEIN - RATTUS NORVEGICUS (RAT), 613 aa. | 2.4E-87 | |
| 7720 | cg43296131 | 436 | GAGCTGTCCCTG GTGAGGAACGC CC[C/gap]JAGGCC CCGAGGCACCG GCCCCACGA | C | gap | Gln (9891) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB41450 CENTAURIN BETA2 - HOMO SAPIENS (HUMAN), 778 aa. | 3.7E-87 | |
| 7721 | cg43992520 | 1167 | AGCTTCGGGCCCC AGTTTGTAGTAG A[G/gap]GCCCGG CCCCACCTCACC CAGCCCGG | G | gap | Leu (9892) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa. | 6E-87 | 11 |
| 7722 | cg43946899 | 371 | TTTTGGCCGCCA TGTGCTTCCCCGA A[G/gap]GTCTCTC TCTGATGACATG AAGAAGC | G | gap | Val (9893) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P24001 NATURAL KILLER CELLS PROTEIN 4 PRECURSOR - Homo sapiens (Human), 234 aa. | 6E-87 | |
| 7723 | cg43946899 | 372 | TTTGGCCGCCAT GTGCTTCCCCGAA G[G/gap]TCCTCT CTGATGACATGA AGAAAGCT | G | gap | Ser (9894) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P24001 NATURAL KILLER CELLS PROTEIN 4 PRECURSOR - Homo sapiens (Human), 234 aa. | 6E-87 | |
| 7724 | cg42529218 | 205 | CCCCCGAGGCC AACCCCGCCGA CGG[C/gap]JAGTG ACGCTGACGAG GACGATGAGG | C | gap | Val (9895) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE), 669 aa. | 7.5E-87 | |
| 7725 | cg43970868 | 663 | ACACCGGGGAC ACTCTGGGCAGC GTC[gap]CTCCG GGGCTTCTTCAC CATCCGCA | C | gap | Ser (9896) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAA19508 Y39A1C.2 PROTEIN - CAENORHABDITIS ELEGANS, 1066 aa. | 9.8E-87 | 12 |

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| 7726 | cg43918822 | 3295 | ATTGTTCTCCAG GCGTAGCAAGG GG[G/gap]CCACC AGGCCACATT GTATGGAG | G | gap | Ala (9897) | Ala (9897) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa. | 1.1E-86 | 15 |
| 7727 | cg44018226 | 1715 | AGGCTCCCAGG CTCCAGGAGCC GGG[G/gap]CTGA CGCTTGTCACCC ACCAGGTAC | G | gap | Pro (9898) | Pro (9898) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa. | 1.6E-86 | |
| 7728 | cg44920099 | 591 | TCTCCAGTCCCC ACCACCACGATC T[C/gap]TATCCG GGGCTCCAGCA ACCAGAA | C | gap | Glu (9899) | Arg (9899) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43224 HYPOTHETICAL 22.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 207 aa (fragment). | 1.7E-86 | |
| 7729 | cg44920099 | 772 | CGATGTACATTG CCTGAGCGGCC TC[G/gap]CGTTG CAGCAGAGAGAT GCGCGTCC | G | gap | Arg (9900) | Arg (9900) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43224 HYPOTHETICAL 22.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 207 aa (fragment). | 1.7E-86 | |
| 7730 | cg43995092 | 404 | ATACTTGCTGA GGGCCCTTGAGG GC[C/gap]GATCA TCCAATCCAGTT GCAGTACT | C | gap | Arg (9901) | Asp (9901) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD18134 T41P - HOMO SAPIENS (HUMAN), 505 aa. | 1.1E-85 | 8 |
| 7731 | cg43934734 | 931 | AACCACCTTTATG TAGGGGCCGGG GA[G/gap]CCCTC CAAGGGCATTGA AGCACAGA | G | gap | Leu (9902) | Ser (9902) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment). | 7.1E-84 | 20 |
| 7732 | cg43934734 | 670 | CGATGGGAGAC AGCGTTCTTCTC CG[C/gap]CTTAG GCATCTCTGCGT ACGTCTGC | C | gap | Ala (9903) | Arg (9903) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment). | 7.1E-84 | 20 |

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| 7733 | cg44032523 | 298 | GTCCAGGTCGG GACCCTCCCGTA CG[C/gap]TGTCG TGCAGGTCTTCA GAGGAGCC | C | gap | Ser | Thr (9904) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE), 669 aa. | 9.1E-84 | |
| 7734 | cg44007579 | 255 | GCACCTCCAGGT GCACAGCGCGG GA[G/gap]CCGTC ACGGTGCTCAAG GCTCCCAA | G | gap | Ala | Pro (9905) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA83007 KIAA1055 PROTEIN - HOMO SAPIENS (HUMAN), 868 aa (fragment). | 2.2E-82 | |
| 7735 | cg43967808 | 127 | GGCGATGGGCT TGTAAGGCCCG CGG[G/gap]CAGC ACGCTTGTTTC CGAGGATGA | G | gap | Ala | Ala (9906) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q62599 METASTASIS- ASSOCIATED PROTEIN MTA1 - Rattus norvegicus (Rat), 703 aa. | 7.3E-82 | 14 |
| 7736 | cg43967808 | 73 | GTTGACGGGCG CAGGTGGCGGT GGC[gap]CJCGG CGGCAGGGCCT GGCTCTGGCG | gap | C | Arg | Arg (9907) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q62599 METASTASIS- ASSOCIATED PROTEIN MTA1 - Rattus norvegicus (Rat), 703 aa. | 7.3E-82 | 14 |
| 7737 | cg43967808 | 87 | GGTGGCGGTGG CGCGCGGCAG GGC[C/gap]TGGC TCTGGCGCAGG GCGATGGGCT | C | gap | Gln | Gln (9908) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q62599 METASTASIS- ASSOCIATED PROTEIN MTA1 - Rattus norvegicus (Rat), 703 aa. | 7.3E-82 | 14 |
| 7738 | cg43283313 | 937 | CCTGCACGTAGC AGGTGAGCAGC CG[C/gap]GTCCG CTCCCCGGTCAG GAGCGCAG | C | gap | Thr | Thr (9909) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43658 CANDIDATE TUMOR SUPPRESSOR P33ING1 - HOMO SAPIENS (HUMAN), 279 aa. | 1.9E-81 | 4 |

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|------|------------|------|--|---|-----|-----|---------------|----------------|------------------|--|---------|----------------------|
| 7739 | cg43336199 | 689 | CTCCCGGAGGA GGGCACCGTAG TTA[G/gap]CCTC CTGGCAGGCAG TGGTCATGAA | G | gap | Ala | Val (9910) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60894 MRNA ENCODING RAMP1 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.6E-79 | 2 |
| 7740 | cg44024149 | 657 | GAAGTCAACTGT GTGAGTGTGATA A[G/gap]GCTGCT GCCACCTGTTTT GCTAGAA | G | gap | Ala | Leu (9911) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa. | 5.3E-79 | 1 (1p35) |
| 7741 | cg43250517 | 354 | TCAGCATGGAAA CCTGGGAGAAA GG[C/gap]CTGTT CCTGAAGGTACA GCAGCCGG | C | gap | Ala | Pro (9912) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34037 CGI-41 PROTEIN - HOMO SAPIENS (HUMAN), 475 aa. | 1.4E-78 | |
| 7742 | cg43949675 | 367 | GTGTCCCGTGTCT TGAATGCACCGC A[G/gap]GCAGCA CAAGTTCTCATA TCCTTGC | G | gap | Leu | Cys (9913) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa. | 7.8E-78 | |
| 7743 | cg43949675 | 368 | TGTCCCGTGTCT GAATGCACCGCA G[G/gap]CAGCAC AAGTTCTCATAT CCTTGCT | G | gap | Cys | Cys (9914) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa. | 7.8E-78 | |
| 7744 | cg43304219 | 1236 | TCTATCAGCAGA GACAGCTTCTTC T[G/gap]CAGTTC CTGCAAGTCCCT TGAGATA | G | gap | Gln | Arg (9915) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00323 HYPOTHETICAL 17.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 161 aa. | 9.9E-78 | 16 (16p13.1 1) |

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|------|------------|-----|---|---|-----|-----|---------------|----------------|------------------|---|---------|----|
| 7745 | cg43936167 | 690 | TTGCAGTCTGTT CCACAGTTTTGG CT/gapTTTTTTC TTTTCTTTTTCT TTTCT | T | gap | Ser | Ala (9916) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa. | 1.2E-77 | 20 |
| 7746 | cg43936167 | 696 | TCTGTTCCACAG TTTTGGCTTTTT [T/gap]CTTTTCTT TTTTCTTTTTCTT GTCA | T | gap | Lys | Lys (9917) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa. | 1.2E-77 | 20 |
| 7747 | cg44936941 | 694 | CTCGTGCTCTCT CATCTGCATCAA A[A/gap]TACCAA ACAGTTATTGCG TACCTTG | A | gap | Tyr | Tyr (9918) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa. | 7E-77 | 1 |
| 7748 | cg43931888 | 306 | CAACGCCGAAC GCCTCCAGGA GG[C/gap]CCACC TGGGAACCCCC GACCTGAAC | C | gap | Ala | Ala (9919) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q16192 ORF3 5' OF PD-ECGF/TP - HOMO SAPIENS (HUMAN), 157 aa. | 1E-75 | 22 |
| 7749 | cg43970034 | 870 | ATTGTGCTGTTCT TTCAGGCTTCTT TTT/gapTCTGAGT CAGCATCTTTTC TCTGGC | T | gap | Lys | Lys (9920) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q64362 FUSED TOES (FT1 PROTEIN) - MUS MUSCULUS (MOUSE), 292 aa. | 1.3E-75 | 16 |
| 7750 | cg43970034 | 871 | TTGTGCTGTTCT TCAGGCTTCTT TTT/gapCTGAGT CAGCATCTTTTC TCTGGCT | T | gap | Lys | Lys (9921) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q64362 FUSED TOES (FT1 PROTEIN) - MUS MUSCULUS (MOUSE), 292 aa. | 1.3E-75 | 16 |
| 7751 | cg44924517 | 65 | CGGCTACCAGG AAGACTCTGCCG AA[G/gap]GTGAA GGCCATGGACTT CATCACCT | G | gap | Val | End (9922) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34088 CGI-93 PROTEIN - HOMO SAPIENS (HUMAN), 291 aa. | 1.6E-75 | |

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|------|------------|-----|--|-----|-----|-----|---------------|----------------|------------------|--|---------|---------------|
| 7752 | cg42897014 | 220 | ACAAGGACCTCA AAGTCACAGCG A[G/gap]CTTCTC CTGCTGGCCCC CTGCTGCC | G | gap | Leu | Cys (9923) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa. | 1.7E-75 | 11 (11q13) |
| 7753 | cg42897014 | 234 | GTACACAGGCA GCTTCTCCTGCT GC[G/gap]CCCCCT GCTGCCAGGGG GCAAGTGGT | G | gap | Ala | Gly (9924) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa. | 1.7E-75 | 11 (11q13) |
| 7754 | cg42897014 | 449 | CGGCCGCTGC GCCGCCCTTCTGC AC[C/gap]TGCGG GTCGTCGGGG ACAGGTCCC | C | gap | Gln | Gln (9925) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa. | 1.7E-75 | 11 (11q13) |
| 7755 | cg42897014 | 523 | TGCGGCCGGC CCGGCGTCTGC GTG[G/gap]CAGC GCCAGGAGCA GAATGCGACC | G | gap | Pro | His (9926) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa. | 1.7E-75 | 11 (11q13) |
| 7756 | cg44909359 | 206 | CATAGACGAG GCAAAGCGGCG TCAIgap/GICCA GTTAATCAGATC AACACTGAG | gap | G | Thr | Ser (9927) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03700 INTEGRASE - Bacteriophage lambda, 356 aa. | 4.1E-75 | |
| 7757 | cg44909359 | 248 | AACACTGAGCGA TGCATTCCGAGA G[G/gap]CAATAG CTGAAGGCCATA TAACAAC | G | gap | Ala | Gln (9928) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03700 INTEGRASE - Bacteriophage lambda, 356 aa. | 4.1E-75 | |
| 7758 | cg43971400 | 386 | GGAAACATCTCT TGTAATGCGACT A[G/gap]CAACCA AGGAACAAGAGA TGCAAGA | G | gap | Ala | Gln (9929) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15007 HYPOTHETICAL PROTEIN KIAA0105 - Homo sapiens (Human), 151 aa. | 4.4E-75 | 6 |

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| 7759 | cg44012742 | 1302 | GGAGCGCAACTA CTGCCGCTGC GG[G/gap]AGGCT CTGCAGCCCCCTG CTTACCCA | G | gap | Glu | Arg (9930) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa. | 1.8E-74 | |
| 7760 | cg43272466 | 1780 | CAGTTCTTGGTG GATGCAGTGAAA C[C/gap]TTCGGC CTTTGCTGTGAC CACATAC | C | gap | Gly | Val (9931) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa. | 1.9E-74 | 10 |
| 7761 | cg43969639 | 775 | TCATCCCCGGGCA GGAGAGGCTGT GG[C/gap]CACAT ACACCTGATTAT CAACAGCC | C | gap | Ala | Pro (9932) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa. | 2.3E-74 | 3 |
| 7762 | cg43969639 | 776 | CATCCCCGGGCA GGAGAGGCTGT GG[C/gap]ACAT ACACCTGATTAT CAACAGCCC | C | gap | Val | Val (9933) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa. | 2.3E-74 | 3 |
| 7763 | cg43962490 | 395 | GTCAGCTTCACC ATCATGGGCGAG A[G/gap]CTCATA GAGGACGAAGA CTCCGGGA | G | gap | Leu | Ser (9934) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD34049 CGI-54 PROTEIN - HOMO SAPIENS (HUMAN), 383 aa. | 1.4E-73 | 2 (10q21) |
| 7764 | cg43981873 | 641 | CCGAGGTGTGTT TGGTGGCCGGG GC[C/gap]GAGGT GGGATCCCCGGG CACAGGCAG | C | gap | Arg | Glu (9935) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa. | 1.7E-73 | |
| 7765 | cg43981873 | 670 | GTGGGATCCCG GGCACAGGCAG AGG[C/gap]CAGC CAGAGAAAGAGC CTGGCAGAC | C | gap | Gln | Ser (9936) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa. | 1.7E-73 | |

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| 7766 | cg43981873 | 671 | TGGGATCCCG GCACAGGCAGA GGC[<i>gap</i>]AGCC AGAGAAGAAGCC TGGCAGACA | C | <i>gap</i> | Gln | Ser (9937) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa. | 1.7E-73 | |
| 7767 | cg43933021 | 645 | CTCTGCTGGTCG ACGTCGGCGTCT G[G <i>gap</i>]CCGTTT GGCCGAGGGCT GCAAGTAC | G | <i>gap</i> | Pro | Gln (9938) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD38506 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa. | 2.8E-73 | 13 |
| 7768 | cg43933021 | 653 | GTCGACGTCGG CGTCTGGCCGTT TG[G <i>gap</i>]CCGAG GGCTGCAAGTAC TCAGCGTA | G | <i>gap</i> | Ala | Ala (9939) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD38506 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa. | 2.8E-73 | 13 |
| 7769 | cg43271682 | 164 | AGTTCACTGCCC CGCACCTGCGC CC[T <i>gap</i>]CAGCC CCGCCAGCGC TTCTGCCCGT | T | <i>gap</i> | End | Trp (9940) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa. | 1.3E-70 | 1 |
| 7770 | cg43923124 | 261 | TATAGAGGGCTG CTGTATTGTCAG A[G <i>gap</i>]CTAAGT CCTCCAGTTCTC GATTAC | G | <i>gap</i> | Ala | Leu (9941) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa. | 2.9E-70 | |
| 7771 | cg42696021 | 457 | CACAATGAAGTG AACCGGAAGCTG G[G <i>gap</i>]CAAGCC TGATTTGACTG CTCAAGA | G | <i>gap</i> | Gly | Ala (9942) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa. | 1.4E-69 | |
| 7772 | cg3003900 | 333 | CGTGCGGGAGC GGGGGCCGCTG CGC[G <i>gap</i>]GTCT TGGGCCTCTGCT GCAGCCCCGG | G | <i>gap</i> | Val | Ser (9943) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01178 OXYTOCIN- NEUROPHYSIN 1 PRECURSOR (OCYTOCIN-NEUROPHYSIN 1) - Homo sapiens (Human), 125 aa. | 1.8E-69 | 20 (20p13) |

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| 7773 | cg3003900 | 334 | GTGCGGGAGCG GGGGCCGCTGC GCG[G/gap]TCTT GGCCTCTGCT GCAGCCCGGA | G | gap | Val | Ser (9944) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01178 OXYTOCIN- NEUROPHYSIN 1 PRECURSOR (OCYTOCIN-NEUROPHYSIN 1) - Homo sapiens (Human), 125 aa. | 1.8E-69 | 20 (20p13) |
| 7774 | cg42921698 | 337 | CCCCGCCACCT CCACCAGGCGC AC[G/gap]CGCGC CAGCGGCAGGC GGTGGCGGA | G | gap | Arg | Arg (9945) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa. | 2.3E-69 | 19 |
| 7775 | cg42921698 | 472 | GGAAAGGAACG CCCGGCCCGCG CTC[G/gap]TCGC GGCCCCAGGAG CCTTGCTCCT | C | gap | Glu | Glu (9946) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa. | 2.3E-69 | 19 |
| 7776 | cg42921698 | 478 | GAACGCCCGGC CCGCGCTCCTC GCG[G/gap]CCCC AGGAGCCTTGCT CCTTGCTGT | G | gap | Gly | Gly (9947) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa. | 2.3E-69 | 19 |
| 7777 | cg42921698 | 644 | GCCGCGAATTCT CAGCACCGTGC CA[G/gap]GGCGG ATGCCCTCGGG CAGCGAGGA | G | gap | Pro | Leu (9948) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa. | 2.3E-69 | 19 |
| 7778 | cg42921698 | 646 | CGCGAATTCTCA GCACCGTGCCA GG[G/gap]CGGAT GCCCTCGGGCA GCGAGGACT | G | gap | Arg | Arg (9949) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa. | 2.3E-69 | 19 |

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| 7779 | cg42921698 | 652 | TTCTCAGCACCG TGCCAGGGCGG AT[G/gap]CCCTC GGCAGCGAGG ACTTGTGGG | G | gap | Gly (9950) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa. | 2.3E-69 | 19 |
| 7780 | cg43266481 | 341 | CTGAAAGAATAA TTCAATATTATG G[G/gap]CCCAGC CACCTGGGGCA GAAGATGG | G | gap | Pro (9951) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14264 ENVELOPE PROTEIN - HOMO SAPIENS (HUMAN), 564 aa. | 5.3E-69 | |
| 7781 | cg43930848 | 596 | CAACGCGTTCAG GACCCCGGCGC GG[G/gap]CAGGG CGCCACGAGC TGGCTGGCT | G | gap | Ala (9952) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75817 RIBONUCLEASE P PROTEIN SUBUNIT P20 - HOMO SAPIENS (HUMAN), 140 aa. | 7.9E-69 | 7 (7q21) |
| 7782 | cg42925004 | 580 | AGCCACCCTATC TCCATGGCTGTG G[C/gap]CCTTCA GGACTACATGGC CCCCGAC | C | gap | Ala (9953) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16674 MELANOMA DERIVED GROWTH REGULATORY PROTEIN PRECURSOR (MELANOMA INHIBITORY ACTIVITY) - Homo sapiens (Human), 131 aa. | 1.6E-68 | |
| 7783 | cg42925004 | 671 | TCCTTCTCCAAGC TGAAGGGCCGT GG[G/gap]CGGCT CTTCTGGGGAG GCAGCGTTC | G | gap | Gly (9954) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16674 MELANOMA DERIVED GROWTH REGULATORY PROTEIN PRECURSOR (MELANOMA INHIBITORY ACTIVITY) - Homo sapiens (Human), 131 aa. | 1.6E-68 | |
| 7784 | cg44004331 | 524 | GGCAAAAGCAAA CTTGAGGCGGTA G[G/gap]CCTCGG CCAGCAACAGG CTGATGTC | G | gap | Ala (9955) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB48628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa. | 7.1E-68 | |

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| 7785 | cg43958562 | 301 | GCATGTTGTCCTT CAGTCTGCTTTG C[A/gap]GCATCT AAAAATTTTCGT GCAGAAA | A | gap | Ala (9956) | Ala | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD33909 COLON CANCER- ASSOCIATED PROTEIN MIC1 - HOMO SAPIENS (HUMAN), 609 aa. | 9.1E-68 | 18 (18q11) |
| 7786 | cg42831353 | 481 | GCGGCTCCACA CGTACACCAGCA TG[G/gap]CCATG AGGCCTGGCCC AGGAAGAAC | G | gap | Ala (9957) | Ala | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa. | 1.3E-67 | 22 |
| 7787 | cg43980385 | 446 | GGCAGGAACCC TCCTTATCATTG GG[gap]G[CAGAG AGCAGAAAGGTG GCACAGCCC | gap | G | Pro (9958) | Pro | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa. | 1.5E-67 | 20 |
| 7788 | cg43980385 | 452 | AACCTCCTTAT CATTGGGCAGAG A[gap/A]GCAGAA GGTGGCACAGC CCGCGCTG | gap | A | Phe (9959) | Ser | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa. | 1.5E-67 | 20 |
| 7789 | cg43980385 | 463 | ATCATTGGGCAG AGAGCAGAAAGGT GG[gap]CACAGC CCGCGCTGCAG CACTTGAG | G | gap | Ala (9960) | Ala | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa. | 1.5E-67 | 20 |

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| 7790 | cg43980385 | 469 | GGGCAGAGAGC AGAAAGGTGGCA CAGC/gap]CCGC GCTGCAGCACTT GAGGTTGTC | C | gap | Gly | Ala (9961) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa. | 1.5E-67 | 20 |
| 7791 | cg43980385 | 555 | AGTTCTGGTCAG CCTGGAGCTCG GG[G/gap]CACAC GCCAGTCTTCTC TGCTCCTG | G | gap | Cys | Cys (9962) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa. | 1.5E-67 | 20 |
| 7792 | cg43080742 | 289 | AAC TGGGCCCGGT GTGGGAACCTG GC[C/gap]TGCCG GTCAGACCTCCA GGTGGCGG | C | gap | Cys | Ala (9963) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P53603 FORMINOTRANSFERASE- CYCLODEAMINASE (FTCD) [INCLUDES: GLUTAMATE FORMINOTRANSFERASE (EC 2.1.2.5) (GLUTAMATE FORMYLTRANSFERASE) FORMINOTETRAHYDROFOLATE CYCLODEAMINASE (EC 4.3.1.4)] - Sus scrofa (Fig. 541 aa. | 2.2E-66 | 21 |

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| 7793 | cg43080742 | 324 | CTGCCGGTCAGAG CCTCCAGGTGG CG[G/gap]CCAAA GCCCTGGAGAT GGGCGTGTT | gap | Ala | Pro (9964) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P53803 FORMINOTRANSFERASE- CYCLODEAMINASE (FTCD) [INCLUDES: GLUTAMATE FORMINOTRANSFERASE (EC 2.1.2.5) (GLUTAMATE FORMYLTRANSFERASE) FORMINOTETRAHYDROFOLATE CYCLODEAMINASE (EC 4.3.1.4)] - Sus scrofa (Pig), 541 aa. | 2.2E-66 | 21 |
| 7794 | cg44911411 | 438 | GAATCTCGTGAC ATTGGCCACAG C[C/gap]TGAGCA AGACCTGTTCCC CGGCCCTG | gap | Leu | End (9965) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa. | 4.5E-66 | |
| 7795 | cg44911411 | 454 | GGCCACAGCCT GAGCAAGACCTG TT[C/gap]CCCCG CCTGCCCATCC CAGAAAGGC | gap | Ser | Ser (9966) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa. | 4.5E-66 | |
| 7796 | cg44911411 | 553 | CTGTGCAATTC AGTGGGCCCA TG[G/gap]CGGC TGCGGGCAAGC GTCACCCCTG | gap | Gly | Ala (9967) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa. | 4.5E-66 | |
| 7797 | cg43294227 | 351 | CAGGCGCGGG CCTGCGGGCCA AGG[G/gap]CCCC GGGGGCACGAG CGACGCGTAC | gap | Gly | Ala (9968) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment). | 6.1E-66 | 8 |
| 7798 | cg43294227 | 571 | GCCTCGACAAGT TCCTGGGCCGC GC[C/gap]GAGGT GGACCTGCGGG ATCTGCACC | gap | Glu | Arg (9969) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment). | 6.1E-66 | 8 |

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|------|------------|-----|---|---|-----|---------------|---------------|----------------|------------------|--|---------|---|
| 7799 | cg43294227 | 612 | GATCTGCACCGC GACCAGGGCCG CA[G/gap]GAAGA CGCAGTGGTATA AGTTGAAA | G | gap | Arg (9970) | Arg (9970) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment). | 6.1E-66 | 8 |
| 7800 | cg43294227 | 613 | ATCTGCACCGC ACCAGGGCCG AG[G/gap]AAGAC GCAGTGGTATA GTTGAAAT | G | gap | Lys (9971) | Arg (9971) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment). | 6.1E-66 | 8 |
| 7801 | cg43294227 | 622 | GCGACCAGGC CGCAGGAAGAC GCA[G/gap]TGGT ATAAGTTGAAAT CCAAACCAG | G | gap | Trp (9972) | Gly (9972) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment). | 6.1E-66 | 8 |
| 7802 | cg44010741 | 114 | GAGGCGCGCG GAGCCTGCCCT GG[G/gap]CGCCA GGTGTTCGGG GTGCGGGTC | G | gap | Gly (9973) | Ala (9973) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O75380 NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A) - Homo sapiens (Human), 124 aa. | 6.6E-65 | 5 |
| 7803 | cg44010741 | 143 | CAGGTGTTTCGG GGTGCGGGTCT CG[C/gap]CGACC GGGGAGAAGGT CACGCACAC | C | gap | Pro (9974) | Arg (9974) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O75380 NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A) - Homo sapiens (Human), 124 aa. | 6.6E-65 | 5 |
| 7804 | cg42722355 | 80 | TCGCCTCTTTCA TCCTGGCCTTTG G[C/gap]ACCGGA GTGGAGTTCGTG CGCTTTA | C | gap | Thr (9975) | Pro (9975) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD45885 MULTISPANNING NUCLEAR ENVELOPE MEMBRANE PROTEIN NURIM - HOMO SAPIENS (HUMAN), 261 aa (fragment). | 1.8E-64 | |

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| 7805 | cg44001502 | 188 | AACGCTCTCACC GGGAGCCAGAG CT[C/gap]CCATG CTTCTCTGCGCA ATATCCAT | C | gap | Ser (9976) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14849 MLN64 MRNA - HOMO SAPIENS (HUMAN), 445 aa. | 7.6E-64 | |
| 7806 | cg43969715 | 585 | GAGCTCGTCATG ATTGGCCAGGTG T[G/gap]CTCTGC AGTGGATACAGC TGTACGT | G | gap | Ala (9977) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60688 HYPOTHETICAL 13.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 119 aa. | 3.3E-63 | 22 |
| 7807 | cg40360053 | 217 | TCGCTCACTGGC TCCTCCGGCGG CA[G/gap]CTCGT GCTGAGGGAGC TCCTGGGCTG | G | gap | Leu (9978) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O14598 TESTIS-SPECIFIC BASIC PROTEIN Y 1 - Homo sapiens (Human), 125 aa. | 8.7E-63 | |
| 7808 | cg43969918 | 999 | ACGGATGTATAC CTGCTCCAGCTG T[G/gap]CCACTC GGCCATCTCTGT ATGTGAC | G | gap | Ala (9979) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P43331 SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) - Homo sapiens (Human), 126 aa. | 2.9E-62 | 22 |
| 7809 | cg44017203 | 137 | GTAGATGCTAGT GGAGGGCGCCC GC[C/gap]TGGCG ACGAGGCAGAG GCAGGCAGC | C | gap | Ser (9980) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa. | 6E-62 | 11 |
| 7810 | cg44017203 | 141 | ATGCTAGTGGAG GGCGCCCGCCT GG[C/gap]GACGA GGCAGAGGCAG GCAGCAAGA | C | gap | Pro (9981) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa. | 6E-62 | 11 |
| 7811 | cg43950850 | 465 | CAAGATAATATC CAGCAAAAAA A[gap]A[GGCCGT AATATATAGAAG CTGGCGA | gap | A | Phe (9982) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I- B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa. | 7.8E-62 | 11 |

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| 7812 | cg43329229 | 183 | GCCCGTGCAG ATCGGCTGCTGA AA[G/gap]CCCCGT GCCCTGAAGATC CGGGAGGA | G | gap | Ala | Pro (9983) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA83047 KIAA1095 PROTEIN - HOMO SAPIENS (HUMAN), 1098 aa (fragment). | 5.4E-61 | |
| 7813 | cg43329229 | 207 | AGCCCGTGCCT GAAGATCCGGG AG[G/gap]AGCGC AGCGTTATGACG ACCGACGA | G | gap | Glu | Ser (9984) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA83047 KIAA1095 PROTEIN - HOMO SAPIENS (HUMAN), 1098 aa (fragment). | 5.4E-61 | |
| 7814 | cg40157055 | 196 | GGACTGCTCGTG GCCGCGGCGGT GG[C/gap]CGGCG CTGCGCTCTTGC TGGTCCAC | C | gap | Ala | Ala (9985) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35675 M-DELTA-LIKE 3 GENE PRECURSOR - MUS MUSCULUS (MOUSE), 585 aa. | 5.5E-61 | |
| 7815 | cg43298020 | 237 | TGGTGGATCACC TCAATGTGGGTG T[G/gap]GCCCCAG GCCTACATGAAC CAGAGAA | G | gap | Ala | Pro (9986) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa. | 7E-61 | |
| 7816 | cg43298020 | 238 | GGTGGATCACCT CAATGTGGGTGT G[G/gap]CCCCAGG CCTACATGAACC AGAGAAA | G | gap | Ala | Pro (9987) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa. | 7E-61 | |
| 7817 | cg43298020 | 245 | CACCTCAATGTG GGTGTGGCCCA GG[C/gap]CTACA TGAACCAAGAGAA AGCTGGAC | C | gap | Ala | Ala (9988) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa. | 7E-61 | |
| 7818 | cg43285334 | 613 | GATTGCTTCAT TAAACGCTTGGT T[C/gap]CCGTTT CGGTCGTAGGC GGCCACAGA | C | gap | Gly | Gly (9989) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa. | 1.9E-60 | 1 |

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|------|------------|-----|--|---|-----|---------------|----------------|------------------|---|---------|----|
| 7818 | cg43285334 | 615 | TTGTCCTTCATTAA ACGCTTGTTCC [C/gap]GTTCCGG TCGTAGGCGGC CCAGATG | C | gap | Gly (9990) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa. | 1.9E-60 | 1 |
| 7820 | cg43985327 | 248 | GGGACCTCAGT GGACACTTCGGT GG[G/gap]CACTG CCAGCCGCCCTG GGGGGCACA | G | gap | Pro (9991) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa. | 2.1E-59 | 1 |
| 7821 | cg43985327 | 255 | CAGTGGACACTT CCGTGGGCACT GC[C/gap]AGCCG CCTGGGGGCA CATAGGATC | C | gap | Leu (9992) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa. | 2.1E-59 | 1 |
| 7822 | cg43985327 | 499 | CTGGGGTCTGTG CGGATCCCTGAG GC[C/gap]GCAGC TCGCGGTGAATC TCATCCAA | C | gap | Arg (9993) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa. | 2.1E-59 | 1 |
| 7823 | cg43278994 | 422 | GGCCCATACCCT GCCAGCCGCCA CA[G/gap]CTCCT CTGTCTCCCCCG ACAGCGTG | G | gap | Cys (9994) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA83030 KIAA1078 PROTEIN - HOMO SAPIENS (HUMAN), 856 aa (fragment). | 3E-59 | 19 |
| 7824 | cg43278994 | 572 | GCGGTTCTGTTCA CCTTGCCCGCCA G[G/gap]CAGCAG TGTGATAGGGCA TTGTGGA | G | gap | Cys (9995) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:BAA83030 KIAA1078 PROTEIN - HOMO SAPIENS (HUMAN), 856 aa (fragment). | 3E-59 | 19 |
| 7825 | cg43976473 | 761 | TGGGATGCGATG GAGCTGCCATAG G[C/gap]CATAGC CACATTGGCCAT TGGGTCC | C | gap | Pro (9996) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa. | 3.5E-59 | 11 |

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| 7826 | cg43939569 | 807 | AGCCTTTTCTAC TATCACCGGCAC C[C/gap]GGTCCG GGTATTTCTTTC GGATCTT | C | gap | Arg (9997) | Arg | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa. | 3.5E-59 | 17 |
| 7827 | cg44011422 | 729 | GAGAAAGATGCAC GAGGGTGACGA GG[G/gap]CCCTG GCCACCACCCATA AGCCAGGC | G | gap | Gly | Ala (9998) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa. | 4.4E-59 | 1 (1q12) |
| 7828 | cg44011422 | 737 | GCACGAGGGTG ACGAGGGCCCT GGC[C/gap]ACCA CCATAAGCCAGG CCTCGGGGA | C | gap | His | Thr (9999) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa. | 4.4E-59 | 1 (1q12) |
| 7829 | cg44011422 | 765 | CACCATAAGCCA GGCCTCGGGGA GG[G/gap]CACCC CCTAAGACCACA GTGGCCAA | G | gap | Gly | Ala (10000) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa. | 4.4E-59 | 1 (1q12) |
| 7830 | cg44937260 | 130 | TCCGAGCACGTC GCCGAGATCGTC G[G/gap]CCGCCA GGGTTGTAAAT TAAAGCA | G | gap | Gly | Ala (10001) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q94140 MEX-3 - CAENORHABDITIS ELEGANS, 415 aa. | 4.4E-59 | |

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| 7831 | cg44914411 | 669 | AGGCCCGCTCC GGAGAGCCCG GAC[C/gap]TGAC GGGTGCCAATAC TAGCCAGCG | C | gap | Arg | Ser (10002) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment). | 7.2E-59 | 22 |
| 7832 | cg44915744 | 243 | AAGATTCGAGCG AAATATCCCGAC A[G/gap]GGTTCC GGTGATTGTGGA AAAGGTC | G | gap | Arg | Arg (10003) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:O08765 GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2) - Homo sapiens (Human), and Rattus norvegicus (Rat), 117 aa. | 1.9E-58 | 16 |
| 7833 | cg42717343 | 380 | TCCTACTGATG TTGAGACAGTCT C[C/gap]TCCGGC TTTCTGGAAGAA TTCACTG | C | gap | Ser | Pro (10004) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P15267 KIDNEY ANDROGEN- REGULATED PROTEIN PRECURSOR (KAP) - Homo sapiens (Human), and Mus musculus (Mouse), 121 aa. | 1.9E-58 | |
| 7834 | cg43253299 | 428 | GGAAGCTCCTT CTGGACGAATGT C[C/gap]ATCGTT AAGAACCTGCAG AACCTGG | C | gap | Ile | Ser (10005) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P06307 PROCHOLECYSTOKININ PRECURSOR (CCK) - Homo sapiens (Human), 115 aa. | 4.6E-57 | 3 |
| 7835 | cg43962116 | 616 | CTGCAGGTCAAA TAGACAGTCCGA A[G/gap]GCACTG ACGATGCAGTAC ATGGTCT | G | gap | Ala | Ala (10006) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15763 CYTOPLASMIC DYNEIN LIGHT CHAIN (T-COMPLEX TESTIS- SPECIFIC PROTEIN 1 HOMOLOG) (PROTEIN CW-1) - Homo sapiens (Human), and Bos taurus (Bovine), 113 aa. | 5.9E-57 | 6 |
| 7836 | cg43962116 | 617 | TGCAGGTCAAAT AGACAGTCCGAA G[G/gap]CACTGA CGATGCAGTACA TGGTCTT | G | gap | Ala | Ala (10007) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q15763 CYTOPLASMIC DYNEIN LIGHT CHAIN (T-COMPLEX TESTIS- SPECIFIC PROTEIN 1 HOMOLOG) (PROTEIN CW-1) - Homo sapiens (Human), and Bos taurus (Bovine), 113 aa. | 5.9E-57 | 6 |

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| 7837 | cg43934461 | 580 | GAGGTGGATGC CGGCCCTAGCA CTG[G/gap]CCCT GGCCCTCATACT GGCTTCAGC | G | gap | Ala (10008) | Ala (10008) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD33392 BREAST CANCER ASSOCIATED GENE 1 PROTEIN - HOMO SAPIENS (HUMAN), 606 aa. | 8.8E-57 | 3 |
| 7838 | cg43919432 | 1237 | CTTGGATTCTG CAGTTCAGTAA C[C/gap]TCGGC GGCGCTCACTCT GCTCCAA | C | gap | Arg | Ser (10009) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa. | 1.2E-56 | 15 |
| 7839 | cg43919432 | 459 | TCTTGTGCTCCA TAATCTGCTGGA G[C/gap]TGGTGC CCAGCATAGTCT GGCTTGG | C | gap | Gln | His (10010) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa. | 1.2E-56 | 15 |
| 7840 | cg43919432 | 537 | CACCAAGGACAT CTGACACCATGT A[G/gap]GGCGC AGCCAGCCAC CAAGGGAG | G | gap | Pro | Pro (10011) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa. | 1.2E-56 | 15 |
| 7841 | cg43919432 | 540 | CAAGGACATCTG ACACCATGTAGG G[G/gap]CGCAGC CAGCCCAACAAG GGAGTGC | G | gap | Arg | Arg (10012) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa. | 1.2E-56 | 15 |
| 7842 | cg43991184 | 51 | CGGACCTCACCA AGCACCGGCGC AC[G/gap]CACAC GGCGGAGAAGC CCTACCGCT | G | gap | His | Thr (10013) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment). | 2E-56 | 1 |

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| 7843 | cg43991184 | 67 | CCGGCGCAGCG ACACGGCGGAG AAG[C/gap]CCTA CCGCTGCGAACT GTGCGGCAA | C | gap | Pro | Pro (10014) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment). | 2E-56 | 1 |
| 7844 | cg43991184 | 69 | GGCGCACGCAC ACGGCGGAGAA GCC[C/gap]TACC GCTGCGAACTGT GCGGCAAGC | C | gap | Tyr | Thr (10015) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment). | 2E-56 | 1 |
| 7845 | cg43991184 | 93 | CCTACCGCTGCG AACTGTGCGGCA A[G/gap]CGGTTC ACGTGCGGTGTC AATCTCA | G | gap | Arg | Gly (10016) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment). | 2E-56 | 1 |
| 7846 | cg44011808 | 666 | CACCATCTCCAG CAGTCCGTGCG CA[G/gap]CCGCT TCTGAAAAGCG GCCTCCAA | G | gap | Gly | Gly (10017) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O95178 NADH-UBIQUINONE OXIDOREDUCTASE AGGG SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-AGGG) (CI-AGGG) - Homo sapiens (Human), 105 aa. | 2.5E-56 | |
| 7847 | cg43999272 | 171 | ATCGCGGACGG AAGATGGCGTCC GC[C/gap]ACCCG TCTCATCCAGCG GCTGCGGA | C | gap | Thr | Pro (10018) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD05427 NADH-UBIQUINONE OXIDOREDUCTASE B14.5A SUBUNIT - HOMO SAPIENS (HUMAN), 113 aa. | 3.2E-56 | 19 |
| 7848 | cg43999272 | 290 | CAGCCTCCTCCC AAGCTCCCTGTG G[G/gap]TCCTAG CCACAAGCTCTC CAACAAT | G | gap | Gly | Val (10019) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD05427 NADH-UBIQUINONE OXIDOREDUCTASE B14.5A SUBUNIT - HOMO SAPIENS (HUMAN), 113 aa. | 3.2E-56 | 19 |

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| 7849 | cg42697199 | 304 | ATGTTGATGTAG ACTTTGCCATCT T[C/gap]TTGGGC GGGGCTGCGGC GTGGGCGT | C | gap | Glu | Lys (10020) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB43303 HYPOTHETICAL 13.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 131 aa (fragment). | 1.1E-55 | 19 |
| 7850 | cg43935092 | 198 | GC GTTCAGACCA ACTCCTGGATAT G[gap/G]AGCTCA ACCTTCAACAAG ACTACAC | gap | G | Ser | Glu (10021) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD28992 VAMP5-LIKE PROTEIN HOMO SAPIENS (HUMAN), 116 aa. | 1.8E-55 | 2 |
| 7851 | cg44019498 | 1102 | TAGCCTGTCTAC CATGAAATCAAT G[G/gap]CATCAG CCATCATAGGGT CCACCGG | G | gap | Ala | Ala (10022) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45970 HYPOTHETICAL 43.5 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 392 aa. | 1.8E-55 | 15 |
| 7852 | cg43269198 | 618 | AGCATTGCCATT CCAGACACAGG TG[G/gap]CTGTG CCCATGTACAGG CGGGACAG | G | gap | Ala | Ala (10023) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB41301 DJ596C15.1.1 (NOVEL PROTEIN) (ISOFORM 1) - HOMO SAPIENS (HUMAN), 162 aa (fragment). | 1.8E-55 | 20 |
| 7853 | cg43917989 | 763 | CCCCTCTGGCCA TGGGCATGCTTG CTT/gap]GGGGCC GCCACGGGTGC TGCTCTTG | T | gap | Gly | Gly (10024) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa. | 2.3E-55 | 11 |
| 7854 | cg43916991 | 719 | CCCTTCTTGTC CTGCAGCGTGTG G[G/gap]TCATTTT GACCCCGTGAC CCGGAGC | G | gap | Gly | Val (10025) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD33400 CARBOXY TERMINUS OF HSP70-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa. | 3E-55 | 16 |
| 7855 | cg43129880 | 187 | CTGGACACTGTG GAAGTGTGAAA G[C/gap]AATTCA GAAAGCCCAAGGA GGTCAAG | C | gap | Ala | Glu (10026) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa. | 1.1E-54 | 3 |

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| 7856 | cg43957773 | 453 | CGTAGAGCAACT GCAATCGCTCTG G[G/gap]CCTGGG CCTGGACAGGA CGGAGACC | G | gap | Ala | Ala (10027) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43914 DNAX ACTIVATION PROTEIN 12 - HOMO SAPIENS (HUMAN), 113 aa. | 3.3E-54 | 19 |
| 7857 | cg43123055 | 468 | AGCTGCAGTCGC TGGTCCCTCAGG G[gap]GJAGGTGT GGGAGAGCTGTC CCCAATGG | gap | G | Ser | Ser (10028) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P08949 NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN B] - Homo sapiens (Human), 121 aa. | 8.8E-54 | 2 |
| 7858 | cg43123055 | 495 | GGTGTGGGAG CTGTCCCAATG GG[G/gap]ATGGG CTGGAAGGCTCC AGACTCTT | G | gap | Ser | Ser (10029) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P08949 NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN B] - Homo sapiens (Human), 121 aa. | 8.8E-54 | 2 |
| 7859 | cg43969772 | 707 | CAGATTCTGTAGT CAGCATAAGTTC T[G/gap]CCTTCT GGCCTCTTGGTA GGCTGTA | G | gap | Gly | Gly (10030) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa. | 4.9E-53 | 14 |
| 7860 | cg43969772 | 728 | TTCTGCCCTTCTG GCCTCTTGGTAG G[C/gap]TGTAAC AGCAAAATGGTG TGAGACA | C | gap | Gln | His (10031) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa. | 4.9E-53 | 14 |
| 7861 | cg43047973 | 270 | CTTGGCGAGCG CTCTGGGCTGGT GC[C/gap]ACCGG GTGATCTCTTAC CGGGGCCA | C | gap | Gly | Ala (10032) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q02080 MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2) - Homo sapiens (Human), 365 aa. | 1.9E-51 | 19 |

| | | | | | | | | | | | | |
|------|------------|-----|---|---|-----|-----|----------------|----------------|-------------------|--|---------|----|
| 7862 | cg42903443 | 120 | CGCGGCAGCCA GAGCGCTGGTC CGC[G/gap]CAGG TTGGCCAGCAGC GGCGGCACC | G | gap | Arg | Ala (10033) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:CAB45012 573K1.15 (MM17M1-6 (NOVEL 7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY) (OLFACTORY RECEPTOR LIKE) PROTEIN)) - MUS MUSCULUS (MOUSE), 309 aa (fragment). | 1.9E-51 | |
| 7863 | cg43511776 | 96 | TTTTCTAGTTAAG TCCCAAGGTGTC [A/gap]ACGACAA TGAGGAGGGTTT CTTCAG | A | gap | Asn | Thr (10034) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa. | 3.1E-51 | 4 |
| 7864 | cg44341684 | 96 | TTTTCTAGTTAAG TCCCAAGGTGTC [A/gap]ACGACAA TGAGGAGGGTTT CTTCAG | A | gap | Asn | Thr (10035) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa. | 3.1E-51 | 4 |
| 7865 | cg43924435 | 847 | GTAGGACCTTCT GCCACTGGCA AG[C/gap]TCCGC CTGCCGCATGGA ATGCAGTT | C | gap | Glu | Asp (10036) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD20971 HSPC009 - HOMO SAPIENS (HUMAN), 106 aa. | 2.8E-50 | 17 |
| 7866 | cg44010855 | 596 | CACTGCCTGCAC CCCAAGCTGCAG A[G/gap]CACCAA GCGCTTCATCAA GTGGTAC | G | gap | Ser | Thr (10037) | FRAMES HIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa. | 5.8E-50 | 5 |
| 7867 | cg43298240 | 375 | CAACCAGCAATG AAGGTGAAGATG C[G/gap]GGGGG GGCAGGTCCCG GGACGGGTT | G | gap | Arg | Ala (10038) | FRAMES HIFT | water_ch annel | Human Gene Similar to SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa. | 4.9E-65 | |

WHAT IS CLAIMED IS:

1. An isolated polynucleotide selected from the group consisting of:
 - a) a nucleotide sequence comprising one or more polymorphic sequences
5 selected from the group consisting of SEQ ID NOS:1 - 7867;
 - b) a fragment of said nucleotide sequence, provided that the fragment
includes a polymorphic site in said polymorphic sequence;
 - c) a complementary nucleotide sequence comprising a sequence
10 complementary to one or more of said polymorphic sequences selected
from the group consisting of SEQ ID NOS:1-7867; and
 - d) a fragment of said complementary nucleotide sequence, provided that the
fragment includes a polymorphic site in said polymorphic sequence.
2. The polynucleotide of claim 1, wherein said polynucleotide sequence is DNA.
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3. The polynucleotide of claim 1, wherein said polynucleotide sequence is RNA.
4. The polynucleotide of claim 1, wherein said polynucleotide sequence is between
about 10 and about 100 nucleotides in length.
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5. The polynucleotide of claim 1, wherein said polynucleotide sequence is between
about 10 and about 90 nucleotides in length.
6. The polynucleotide of claim 1, wherein said polynucleotide sequence is between
25 about 10 and about 75 nucleotides in length.
7. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and
about 50 bases in length.
- 30 8. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and
about 40 bases in length.

9. The polynucleotide of claim 1, wherein said polynucleotide is between about 15 and about 30 bases in length.
10. The polynucleotide of claim 1, wherein said polymorphic site includes a nucleotide other than the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
11. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of said polymorphic sequence.
12. The polynucleotide of claim 1, wherein said polymorphic site includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
13. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes the complement of the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
14. An isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is selected from the group consisting of:
- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867 provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence;
 - b) a nucleotide sequence that is a fragment of said polymorphic sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
 - c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867, provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and

d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

5 15. The oligonucleotide of claim 14, wherein the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide selected from the group consisting of:

a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867, wherein said
10 polymorphic sequence includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence;

b) a nucleotide sequence that is a fragment of any of said nucleotide sequences;

c) a complementary nucleotide sequence comprising a sequence
15 complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867, wherein said polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and

d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic
20 sequence.

16. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 51 bases in length.

25 17. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 40 bases in length.

18. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 15 and about 30 bases in length.

30 19. A method of detecting a polymorphic site in a nucleic acid, the method comprising:

a) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS:

1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;
and

b) determining whether said nucleic acid and said oligonucleotide hybridize; whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphic site in said nucleic acid.

20. The method of claim 19, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

21. The method of claim 19, wherein said oligonucleotide is between about 10 and about 51 bases in length.

22. The method of claim 19, wherein said oligonucleotide is between about 10 and about 40 bases in length.

23. A method of detecting the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a nucleic acid from said subject;

b) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;
and

c) determining whether said nucleic acid and said oligonucleotide hybridize; whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphism in said subject.

24. A method of determining the relatedness of a first and second nucleic acid, the method comprising:

a) providing a first nucleic acid and a second nucleic acid;

b) contacting said first nucleic acid and said second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;

c) determining whether said first nucleic acid and said second nucleic acid hybridize to said oligonucleotide; and

d) comparing hybridization of said first and second nucleic acids to said oligonucleotide, wherein hybridization of first and second nucleic acids to said nucleic acid indicates the first and second subjects are related.

25. The method of claim 24, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

26. The method of claim 24, wherein the oligonucleotide is between about 10 and about 51 bases in length.

27. The method of claim 24, wherein the oligonucleotide is between about 10 and about 40 bases in length.

28. The method of claim 24, wherein the oligonucleotide is between about 15 and about 30 bases in length.

29. An isolated polypeptide comprising a polymorphic site at one or more amino acid residues, wherein the protein is encoded by a polynucleotide selected from the group

consisting of polymorphic sequences SEQ ID NOS:1-7867, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

30. The polypeptide of claim 29, wherein said polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

31. The polypeptide of claim 29, wherein the polypeptide encoded by said polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

32. An antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

33. The antibody of claim 32, wherein said antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

34. The antibody of claim 32, wherein said antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

35. A method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject, the method comprising
a) providing a protein sample from said subject;

b) contacting said sample with the antibody of claim 34 under conditions that allow for the formation of antibody-antigen complexes; and
c) detecting said antibody-antigen complexes,
whereby the presence of said complexes indicates the presence of said polypeptide.

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36. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

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a) providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement; and

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b) administering to the subject an effective therapeutic dose of a second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele, thereby treating said subject.

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37. The method of claim 36, wherein the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

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38. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a subject suffering from a pathology associated with aberrant expression of a polymorphic sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1 - 7867, or its complement; and

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b) administering to the subject an effective therapeutic dose of a polypeptide,

wherein said polypeptide is encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7867, provided that said polymorphic

sequence includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

39. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement; and

b) administering to the subject an effective dose of the antibody of claim 34, thereby treating said subject.

40. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement; and

b) administering to the subject an effective dose of an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7867, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for said polymorphic sequence,

thereby treating said subject.

41. An oligonucleotide array, comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is chosen from the group consisting of:

a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867;

- b) a nucleotide sequence that is a fragment of any of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
- c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867; and
- d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

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42. The array of claim 41, wherein said array comprises about 10 oligonucleotides.

43. The array of claim 41, wherein said array comprises about 100 oligonucleotides.

15 44. The array of claim 41, wherein said array comprises about 1000 oligonucleotides.